

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Harold Kleanthous et al.
- (ii) TITLE OF THE INVENTION: Identification of Polynucleotides
Encoding Novel Helicobacter Polypeptides in the Helicobacter
Genome
- (iii) NUMBER OF SEQUENCES: 370
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Clark & Elbing LLP
(B) STREET: 176 Federal Street
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02110
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/833,457
(B) FILING DATE: 01-APR-97
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Clark, Paul T.
(B) REGISTRATION NUMBER: 30,162
(C) REFERENCE/DOCKET NUMBER: 06132/041001
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 617-428-0200
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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 265 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:
(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...212
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTAGTT TGTTTTGTAG TATAATCCTA CGAAAATTTT AAGGAACGGC ATG GAG 56
Met Glu
1

TTT TTG GGA CTG ATT TTA AGT CTG GCC GCT ATT TTG ATA GCG TTT AAA 104
Phe Leu Gly Leu Ile Leu Ser Leu Ala Ala Ile Leu Ile Ala Phe Lys
5 10 15

AAG CCT GAA AAA GAA AAT TGG GCG TTT GGG ATT TTG ATG GTG GTG TGG 152
Lys Pro Glu Lys Glu Asn Trp Ala Phe Gly Ile Leu Met Val Val Trp
20 25 30

TTA GTG GAG CTT ATT ATT TTT ATA GCC CAC AGC TCT AGC GTT TTG CCT 200
Leu Val Glu Leu Ile Ile Phe Ile Ala His Ser Ser Ser Val Leu Pro
35 40 45 50

AAC ATG AAT CTA TAAGGGGGAT GCATGGATAA AGAAACCCGA TTTTACAACC TTTT 257
Asn Met Asn Leu

TCTTTGGC 265

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Phe Leu Gly Leu Ile Leu Ser Leu Ala Ala Ile Leu Ile Ala
1 5 10 15
Phe Lys Lys Pro Glu Lys Glu Asn Trp Ala Phe Gly Ile Leu Met Val
20 25 30
Val Trp Leu Val Glu Leu Ile Ile Phe Ile Ala His Ser Ser Val
35 40 45
Leu Pro Asn Met Asn Leu
50

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...617
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCATAGACG ACAAATCAA GCGGTTTTAT CAAAACCAAA AAACCTTTAGA ATG AAA	56
Met Lys	
1	
AAA ATT GCT TTC ATT TTG GCT TTA TGG GTG GGC TTG TTA GGG GCG TTT	104
Lys Ile Ala Phe Ile Leu Ala Leu Trp Val Gly Leu Leu Gly Ala Phe	
5 10 15	
GAG CCT AAA AAA AGT CAT ATT TAT TTT GGG GCT ATG GTG GGT TTA GCT	152
Glu Pro Lys Lys Ser His Ile Tyr Phe Gly Ala Met Val Gly Leu Ala	
20 25 30	
CCT ATT AAA ATA ACC CCA AAA CCG GCT AGT GAT TCT TCT TAT ACG GCT	200
Pro Ile Lys Ile Thr Pro Lys Pro Ala Ser Asp Ser Ser Tyr Thr Ala	
35 40 45 50	
TTT TTA TGG GGG GCT AAA GGA GGG TAT CAA TTC GCT TTT TTT AAA GCT	248
Phe Leu Trp Gly Ala Lys Gly Gly Tyr Gln Phe Ala Phe Phe Lys Ala	
55 60 65	
CTA GCG TTA AGG GGT GAA TTT TCC TAC CTT ATG GCA ATC AAA CCC ACC	296
Leu Ala Leu Arg Gly Glu Phe Ser Tyr Leu Met Ala Ile Lys Pro Thr	
70 75 80	
GCA CTG CAC ACG ATT AAC ACT TCT TTA TTG AGC TTA AAT ATT GAT GTG	344
Ala Leu His Thr Ile Asn Thr Ser Leu Leu Ser Leu Asn Ile Asp Val	
85 90 95	
TTA AGC GAT TTT TAC ACT TAC AAA AAA TAC AGC TTT GGG GTG TAT GGG	392
Leu Ser Asp Phe Tyr Thr Tyr Lys Lys Tyr Ser Phe Gly Val Tyr Gly	
100 105 110	
GGG CTT GGG ATA GGG TAT TTT TAT CAA AGC AAC CAT TTA GGC ATG AAA	440
Gly Leu Gly Ile Gly Tyr Phe Tyr Gln Ser Asn His Leu Gly Met Lys	
115 120 125 130	
AAT AGT TCG TTT ATG GGT TAT AAC GGC TTG TTT AAT GTG GGG CTT GGC	488
Asn Ser Ser Phe Met Gly Tyr Asn Gly Leu Phe Asn Val Gly Leu Gly	
135 140 145	
AGC ACG ATC GAT CGC CAC CAC CGC ATA GAG CTT GGG GCT AAA ATC CCT	536
Ser Thr Ile Asp Arg His His Arg Ile Glu Leu Gly Ala Lys Ile Pro	
150 155 160	
TTT TCA AAG ACT AGA AAT TCT TTT AAA AAT CCT TAT TTT TTA GAG AGC	584
Phe Ser Lys Thr Arg Asn Ser Phe Lys Asn Pro Tyr Phe Leu Glu Ser	
165 170 175	
GTT TTT ATC CAT GCG ACT TAT AGC TAT ATG TTT TAAGAGAGAA TAGCCTATTA	637
Val Phe Ile His Ala Thr Tyr Ser Tyr Met Phe	
180 185	

670

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met 1	Lys	Lys	Ile	Ala 5	Phe	Ile	Leu	Ala	Leu 10	Trp	Val	Gly	Leu	Leu 15	Gly
Ala	Phe	Glu	Pro	Lys 20	Lys	Ser	His	Ile 25	Tyr	Phe	Gly	Ala	Met 30	Val	Gly
Leu	Ala	Pro	Ile	Lys 35	Ile	Thr	Pro 40	Lys	Pro	Ala	Ser	Asp 45	Ser	Ser	Tyr
Thr	Ala 50	Phe	Leu	Trp	Gly	Ala 55	Lys	Gly	Gly	Tyr	Gln 60	Phe	Ala	Phe	Phe
Lys 65	Ala	Leu	Ala	Leu	Arg 70	Gly	Glu	Phe	Ser	Tyr 75	Leu	Met	Ala	Ile	Lys 80
Pro	Thr	Ala	Leu	His 85	Thr	Ile	Asn	Thr	Ser 90	Leu	Leu	Ser	Leu	Asn 95	Ile
Asp	Val	Leu	Ser 100	Asp	Phe	Tyr	Thr	Tyr 105	Lys	Lys	Tyr	Ser	Phe 110	Gly	Val
Tyr	Gly	Gly 115	Leu	Gly	Ile	Gly	Tyr 120	Phe	Tyr	Gln	Ser	Asn 125	His	Leu	Gly
Met	Lys 130	Asn	Ser	Ser	Phe	Met 135	Gly	Tyr	Asn	Gly	Leu 140	Phe	Asn	Val	Gly
Leu 145	Gly	Ser	Thr	Ile	Asp 150	Arg	His	His	Arg	Ile 155	Glu	Leu	Gly	Ala	Lys 160
Ile	Pro	Phe	Ser	Lys 165	Thr	Arg	Asn	Ser	Phe 170	Lys	Asn	Pro	Tyr	Phe 175	Leu
Glu	Ser	Val	Phe 180	Ile	His	Ala	Thr	Tyr 185	Ser	Tyr	Met	Phe			

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...380
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGCGTGAAAA AAATTGAGTT GAATCAAAAC CTGCATTAAG GATTAAAAGA ATG CTC 56
Met Leu
1

AAA AAA AGT TTG TTA TTG CTT GTT TTT TTA GTC TTA CAG CTT AGC GGC 104
Lys Lys Ser Leu Leu Leu Leu Val Phe Leu Val Leu Gln Leu Ser Gly
5 10 15

GCT GAA GAA AAC AAT CAA GCC CCA AAA AAC ACG CCC CCT GAA TTA AAC 152
Ala Glu Glu Asn Asn Gln Ala Pro Lys Asn Thr Pro Pro Glu Leu Asn
20 25 30

CCC GCT AAC GCT AAG GGC GCG CCA AAC TCT AAC ACC CAG ATC ACC CCT 200
Pro Ala Asn Ala Lys Gly Ala Pro Asn Ser Asn Thr Gln Ile Thr Pro
35 40 45 50

AAA AAC GAT AAC TCT AAC CTG TTA GAC AAA TTA GGT TCG CCT GAA AAC 248
Lys Asn Asp Asn Ser Asn Leu Leu Asp Lys Leu Gly Ser Pro Glu Asn
55 60 65

GCT CAA ACC GAG CTT TCT GCC GGT ATT GAT TTG GCT AAA AAG GGC GAT 296
Ala Gln Thr Glu Leu Ser Ala Gly Ile Asp Leu Ala Lys Lys Gly Asp
70 75 80

TAT CAA GGG GCT TTC AAG CTT TTT TCC CAA TCG TGC GAT AAT GGT AAT 344
Tyr Gln Gly Ala Phe Lys Leu Phe Ser Gln Ser Cys Asp Asn Gly Asn
85 90 95

GCG GCC GGG TGT TTT GCA AGT GGG GGC GAT GTA TGC TAATGGGGTA GGGATC 396
Ala Ala Gly Cys Phe Ala Ser Gly Gly Asp Val Cys
100 105 110

CAAACCAACA GATTAAAAGC CGCTCGCTAT TATGAATG 434

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Leu Lys Lys Ser Leu Leu Leu Leu Val Phe Leu Val Leu Gln Leu
1 5 10 15
Ser Gly Ala Glu Glu Asn Asn Gln Ala Pro Lys Asn Thr Pro Pro Glu
20 25 30
Leu Asn Pro Ala Asn Ala Lys Gly Ala Pro Asn Ser Asn Thr Gln Ile
35 40 45
Thr Pro Lys Asn Asp Asn Ser Asn Leu Leu Asp Lys Leu Gly Ser Pro
50 55 60
Glu Asn Ala Gln Thr Glu Leu Ser Ala Gly Ile Asp Leu Ala Lys Lys
65 70 75 80
Gly Asp Tyr Gln Gly Ala Phe Lys Leu Phe Ser Gln Ser Cys Asp Asn

85 90 95
 Gly Asn Ala Ala Gly Cys Phe Ala Ser Gly Gly Asp Val Cys
 100 105 110

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 575 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 73...522
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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CCACAAAAGC TTAATGAATA TTAAATTAAA AACATGTTAA TCTTTAGTTA TTTTTAAAAT      60
TTAGGAAATC CC ATG CAT CAA AAC AAT AAA ACT TTT TTA CCC AGC CAA TCC      111
      Met His Gln Asn Asn Lys Thr Phe Leu Pro Ser Gln Ser
        1              5              10

GCT CAC CTC TCT AAA ATC ATT CTT TTT TTA AAC ACC GGC TTT TTA GCC      159
Ala His Leu Ser Lys Ile Ile Leu Phe Leu Asn Thr Gly Phe Leu Ala
      15              20              25

TAT CTG TTA AGC GCT TGT GGG GCG AAT GTG CCT ATA GAA GAA GTG TTG      207
Tyr Leu Leu Ser Ala Cys Gly Ala Asn Val Pro Ile Glu Glu Val Leu
      30              35              40              45

GTT AAA GAT CCT AAA GAG ACC AAA GCC CAA GAA GTC GCC AGA GAA GAA      255
Val Lys Asp Pro Lys Glu Thr Lys Ala Gln Glu Val Ala Arg Glu Glu
              50              55              60

AAG GCT ATC CAG CAA GAA AAC GCC ACT ATT GAT GCG CGC ACC ACG CCT      303
Lys Ala Ile Gln Gln Glu Asn Ala Thr Ile Asp Ala Arg Thr Thr Pro
              65              70              75

TTA ATC AAT CGT TTC ACT AAT TAT AGC GCT TAT GGC TCT TTA AAC GGC      351
Leu Ile Asn Arg Phe Thr Asn Tyr Ser Ala Tyr Gly Ser Leu Asn Gly
      80              85              90

TTT TAC AAT TCA GTG GAT AAT CTC AAT TCG CCC ATG CAA AAC GGG ATG      399
Phe Tyr Asn Ser Val Asp Asn Leu Asn Ser Pro Met Gln Asn Gly Met
      95              100              105

TAT GGA GGC TAT TAC ATG CCT TAT TAT TAC ATG CCC TAT GGT TTC ATG      447
Tyr Gly Gly Tyr Tyr Met Pro Tyr Tyr Tyr Met Pro Tyr Gly Phe Met
      110              115              120              125

CCT TAT GGG TCA GGT CTT ATG CCT TAT GGG CCT TAT GGG TAT GGA GCG      495
Pro Tyr Gly Ser Gly Leu Met Pro Tyr Gly Pro Tyr Gly Tyr Gly Ala

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130

135

140

CCT GGA TAC TTC CCT TAC GCT TTT TAT TGATTGAGTG GCTTTAGAAA GCGTGGT 549
 Pro Gly Tyr Phe Pro Tyr Ala Phe Tyr
 145 150

GGTGTGGTG TTTTACTCA AACACG 575

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	His	Gln	Asn	Asn	Lys	Thr	Phe	Leu	Pro	Ser	Gln	Ser	Ala	His	Leu
1				5					10					15	
Ser	Lys	Ile	Ile	Leu	Phe	Leu	Asn	Thr	Gly	Phe	Leu	Ala	Tyr	Leu	Leu
		20						25					30		
Ser	Ala	Cys	Gly	Ala	Asn	Val	Pro	Ile	Glu	Glu	Val	Leu	Val	Lys	Asp
		35					40					45			
Pro	Lys	Glu	Thr	Lys	Ala	Gln	Glu	Val	Ala	Arg	Glu	Glu	Lys	Ala	Ile
		50				55					60				
Gln	Gln	Glu	Asn	Ala	Thr	Ile	Asp	Ala	Arg	Thr	Thr	Pro	Leu	Ile	Asn
					70					75				80	
Arg	Phe	Thr	Asn	Tyr	Ser	Ala	Tyr	Gly	Ser	Leu	Asn	Gly	Phe	Tyr	Asn
				85					90					95	
Ser	Val	Asp	Asn	Leu	Asn	Ser	Pro	Met	Gln	Asn	Gly	Met	Tyr	Gly	Gly
			100					105					110		
Tyr	Tyr	Met	Pro	Tyr	Tyr	Tyr	Met	Pro	Tyr	Gly	Phe	Met	Pro	Tyr	Gly
		115					120					125			
Ser	Gly	Leu	Met	Pro	Tyr	Gly	Pro	Tyr	Gly	Tyr	Gly	Ala	Pro	Gly	Tyr
		130				135					140				
Phe	Pro	Tyr	Ala	Phe	Tyr										
145					150										

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 910 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...860
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATTATGTTAT TATTATACGA AATGTAGACT TTTAGAAGGA AAAATGTTGT ATG AAA	56
Met Lys	
1	
AAG TTT GTA GTG TTT AAA ACG CTC TGT TTA TCG GTA GTG TTA GGT AAT	104
Lys Phe Val Val Phe Lys Thr Leu Cys Leu Ser Val Val Leu Gly Asn	
5 10 15	
AGT CTT GTG GCA GCA GAA GGC AGC ACA GAA GTG CAA AAG CAA TTG GAA	152
Ser Leu Val Ala Ala Glu Gly Ser Thr Glu Val Gln Lys Gln Leu Glu	
20 25 30	
AAG CCA AAA GAG TAT AAA GCA GTG AAA GGC GAG AAA AAC GCT TGG TAT	200
Lys Pro Lys Glu Tyr Lys Ala Val Lys Gly Glu Lys Asn Ala Trp Tyr	
35 40 45 50	
TTG GGG ATT AGC TAT CAA GTC GGT CAG GCT TCG CAA AGC GTT AAA AAC	248
Leu Gly Ile Ser Tyr Gln Val Gly Gln Ala Ser Gln Ser Val Lys Asn	
55 60 65	
CCC CCC AAA AGC AGT GAA TTT AAC TAC CCT AAG TTC CCT GTG GGT AAA	296
Pro Pro Lys Ser Ser Glu Phe Asn Tyr Pro Lys Phe Pro Val Gly Lys	
70 75 80	
ACC GAC TAT CTG GCC GTT ATG CAA GGC TTA GGG CTT ACT GTG GGT TAT	344
Thr Asp Tyr Leu Ala Val Met Gln Gly Leu Gly Leu Thr Val Gly Tyr	
85 90 95	
AAG CAG TTT TTC GGG GAA AAG AGA TGG TTT GGT GCA CGC TAT TAC GGC	392
Lys Gln Phe Phe Gly Glu Lys Arg Trp Phe Gly Ala Arg Tyr Tyr Gly	
100 105 110	
TTC ATG GAT TAT GGG CAT GCC GTA TTT GGA GCG AAC GCT TTA ACA TCG	440
Phe Met Asp Tyr Gly His Ala Val Phe Gly Ala Asn Ala Leu Thr Ser	
115 120 125 130	
GAT AAT GGT GGG GTG TGT GAG CTT CAC CAA CCA TGT GCG ACC AAA GTA	488
Asp Asn Gly Gly Val Cys Glu Leu His Gln Pro Cys Ala Thr Lys Val	
135 140 145	
GGG ACA ATG GGC AAT CTG TCT GAC ATG TTC ACT TAT GGT GTG GGT ATT	536
Gly Thr Met Gly Asn Leu Ser Asp Met Phe Thr Tyr Gly Val Gly Ile	
150 155 160	
GAC ACT TTA TAC AAT GTC ATC AAT AAA GAA GAT GCG AGT TTT GGT TTC	584
Asp Thr Leu Tyr Asn Val Ile Asn Lys Glu Asp Ala Ser Phe Gly Phe	
165 170 175	
TTT TTT GGG GCT CAA ATC GCG GGT AAC TCT TGG GGT AAT ACG ACA GGG	632
Phe Phe Gly Ala Gln Ile Ala Gly Asn Ser Trp Gly Asn Thr Thr Gly	
180 185 190	
GCC TTT TTG GAA ACT AAA AGC CCT TAT AAG CAC ACT TCC TAT AGC CTT	680
Ala Phe Leu Glu Thr Lys Ser Pro Tyr Lys His Thr Ser Tyr Ser Leu	
195 200 205 210	

GAT CCG GCG ATT TTC CAG TTC CTT TTT AAT TTA GGG ATC CGC ACC CAT	728
Asp Pro Ala Ile Phe Gln Phe Leu Phe Asn Leu Gly Ile Arg Thr His	
215 220 225	
ATT GGC CGG CAT CAA GAA TTT GAC TTT GGC GTG AAG ATT CCC ACT ATC	776
Ile Gly Arg His Gln Glu Phe Asp Phe Gly Val Lys Ile Pro Thr Ile	
230 235 240	
AAT GTT TAT TAT TTT AAC CAT GGG AAT TTG AGC TTC ACT TAC CGC CGT	824
Asn Val Tyr Tyr Phe Asn His Gly Asn Leu Ser Phe Thr Tyr Arg Arg	
245 250 255	
CAA TAC AGC CTT TAT GTG GGG TAT CGT TAC AAT TTC TGATTAAAA CGCTTG	876
Gln Tyr Ser Leu Tyr Val Gly Tyr Arg Tyr Asn Phe	
260 265 270	
TTTTTCTCTA ATTGAATTTT CAATTAGAGT TTTT	910

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Lys	Lys	Phe	Val	Val	Phe	Lys	Thr	Leu	Cys	Leu	Ser	Val	Val	Leu
1				5					10					15	
Gly	Asn	Ser	Leu	Val	Ala	Ala	Glu	Gly	Ser	Thr	Glu	Val	Gln	Lys	Gln
			20					25					30		
Leu	Glu	Lys	Pro	Lys	Glu	Tyr	Lys	Ala	Val	Lys	Gly	Glu	Lys	Asn	Ala
		35					40					45			
Trp	Tyr	Leu	Gly	Ile	Ser	Tyr	Gln	Val	Gly	Gln	Ala	Ser	Gln	Ser	Val
	50					55				60					
Lys	Asn	Pro	Pro	Lys	Ser	Ser	Glu	Phe	Asn	Tyr	Pro	Lys	Phe	Pro	Val
65				70					75					80	
Gly	Lys	Thr	Asp	Tyr	Leu	Ala	Val	Met	Gln	Gly	Leu	Gly	Leu	Thr	Val
			85					90					95		
Gly	Tyr	Lys	Gln	Phe	Phe	Gly	Glu	Lys	Arg	Trp	Phe	Gly	Ala	Arg	Tyr
		100					105						110		
Tyr	Gly	Phe	Met	Asp	Tyr	Gly	His	Ala	Val	Phe	Gly	Ala	Asn	Ala	Leu
		115				120					125				
Thr	Ser	Asp	Asn	Gly	Gly	Val	Cys	Glu	Leu	His	Gln	Pro	Cys	Ala	Thr
	130					135					140				
Lys	Val	Gly	Thr	Met	Gly	Asn	Leu	Ser	Asp	Met	Phe	Thr	Tyr	Gly	Val
145				150					155					160	
Gly	Ile	Asp	Thr	Leu	Tyr	Asn	Val	Ile	Asn	Lys	Glu	Asp	Ala	Ser	Phe
			165					170					175		
Gly	Phe	Phe	Phe	Gly	Ala	Gln	Ile	Ala	Gly	Asn	Ser	Trp	Gly	Asn	Thr
		180				185						190			
Thr	Gly	Ala	Phe	Leu	Glu	Thr	Lys	Ser	Pro	Tyr	Lys	His	Thr	Ser	Tyr
	195					200					205				
Ser	Leu	Asp	Pro	Ala	Ile	Phe	Gln	Phe	Leu	Phe	Asn	Leu	Gly	Ile	Arg

210	215	220
Thr His Ile Gly Arg His Gln Glu Phe Asp Phe Gly Val Lys Ile Pro		
225	230	235
Thr Ile Asn Val Tyr Tyr Phe Asn His Gly Asn Leu Ser Phe Thr Tyr		240
	245	250
Arg Arg Gln Tyr Ser Leu Tyr Val Gly Tyr Arg Tyr Asn Phe		255
	260	265
		270

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic RNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 58...1305
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGCAATTAAA AGGAATTTTA ACTAAAATAT TGAGTTTAAA TCCACGATGA GTTTTTA ATG	60
Met	
1	
CAA TAT AAG AAA AAT AAG AAA AGA TAT TAT TAT TTA GCG TTA GGG ATC	108
Gln Tyr Lys Lys Asn Lys Lys Arg Tyr Tyr Tyr Leu Ala Leu Gly Ile	
5 10 15	
TTT TTT TTA AAT GGT CTG TCT TTG AAA GCT TTA GAA ATC GCC GTC AAA	156
Phe Phe Leu Asn Gly Leu Ser Leu Lys Ala Leu Glu Ile Ala Val Lys	
20 25 30	
CCT TTT GGC TAT CTG GGG CTA TTA TAT AAT CAA GGG GCG CAA AAA AAC	204
Pro Phe Gly Tyr Leu Gly Leu Leu Tyr Asn Gln Gly Ala Gln Lys Asn	
35 40 45	
CCT CAC AGC TAT GTG GGG GCT TTA GCG CGT CTT GGG GTG GAT TTT TCT	252
Pro His Ser Tyr Val Gly Ala Leu Ala Arg Leu Gly Val Asp Phe Ser	
50 55 60 65	
TAT AGC AAC GGG TGG TCC TTT GGT ATT GGA GCG ATT GGG GCT TGG AAT	300
Tyr Ser Asn Gly Trp Ser Phe Gly Ile Gly Ala Ile Gly Ala Trp Asn	
70 75 80	
ATT TAT AAC AAA CAG CGT TTG GCT AAC CTT TAT ATC AGT CTA GGG AAT	348
Ile Tyr Asn Lys Gln Arg Leu Ala Asn Leu Tyr Ile Ser Leu Gly Asn	
85 90 95	
TTT TTT GGT AGT TCT AAA AAT GTT AAA CCT TAT TTG AGC GCT GGC GAT	396
Phe Phe Gly Ser Ser Lys Asn Val Lys Pro Tyr Leu Ser Ala Gly Asp	
100 105 110	

GTT TCT GAT GCG TAT GTT CAA TAC ACT AAC CAG CGT TTT AAA ATC GCT Val Ser Asp Ala Tyr Val Gln Tyr Thr Asn Gln Arg Phe Lys Ile Ala 115 120 125	444
TTA GGG CGT TTC AAT ACC GAT TTT GTG GAT TTT GAT TGG ATA GGG GGC Leu Gly Arg Phe Asn Thr Asp Phe Val Asp Phe Asp Trp Ile Gly Gly 130 135 140 145	492
AAT ATT CAA GGG GTT TCT GTA GCT TTT AAG CAA AAT TCC ATG CGT TAT Asn Ile Gln Gly Val Ser Val Ala Phe Lys Gln Asn Ser Met Arg Tyr 150 155 160	540
TTT GGG ATT TTT ATG GAT AGC ATG CTT TAT AAT GGG CAT CAA ATC AAC Phe Gly Ile Phe Met Asp Ser Met Leu Tyr Asn Gly His Gln Ile Asn 165 170 175	588
AAA GAG CAA GGG AAT CGG ATC GCT ACT TCC CTA AAC GCT CTA GCG TCT Lys Glu Gln Gly Asn Arg Ile Ala Thr Ser Leu Asn Ala Leu Ala Ser 180 185 190	636
TAT GAC CCT GTG TCT AAA CGC TTG TAT GTG GGG GGG GAA GTG TTT GTT Tyr Asp Pro Val Ser Lys Arg Leu Tyr Val Gly Gly Glu Val Phe Val 195 200 205	684
TTA GGT GCA GAA TAC AGG CAT GAA AAT CTT AAA GTG GTG CCT TTT ATT Leu Gly Ala Glu Tyr Arg His Glu Asn Leu Lys Val Val Pro Phe Ile 210 215 220 225	732
TTA ACG GAC ACC CGC TTG CCT TTA TCC ACC CAA AAT GTT TTA GTG CAA Leu Thr Asp Thr Arg Leu Pro Leu Ser Thr Gln Asn Val Leu Val Gln 230 235 240	780
GTG GGG GGT AAG TTG GAG TAT GAC GCT TCT TTA GCT AAG GGT TTC ACT Val Gly Gly Lys Leu Glu Tyr Asp Ala Ser Leu Ala Lys Gly Phe Thr 245 250 255	828
TCG CAC ACT CTA GTG CAT GGC ATG TAT CAA TAC GGC AAC ACT GAT GCG Ser His Thr Leu Val His Gly Met Tyr Gln Tyr Gly Asn Thr Asp Ala 260 265 270	876
GCT ACA AGC GTT AAA AAT GCC GGC TTG TTT TTG ATC GAT CAA ACT TTT Ala Thr Ser Val Lys Asn Ala Gly Leu Phe Leu Ile Asp Gln Thr Phe 275 280 285	924
AAA TAC AAA ATT TTT AAT TTT GGA ACG GGT TTT TAT ATC GTT CCG GCA Lys Tyr Lys Ile Phe Asn Phe Gly Thr Gly Phe Tyr Ile Val Pro Ala 290 295 300 305	972
AGA AAC AAT AAG GGC TAT CTA TGG ACT TTT AAT GAC AGG ACT AAA TTC Arg Asn Asn Lys Gly Tyr Leu Trp Thr Phe Asn Asp Arg Thr Lys Phe 310 315 320	1020
TAT GGC CGT GGG ATC AAT GCG CCC GGC GTG CCA GCG ATT TAT TTT GCA Tyr Gly Arg Gly Ile Asn Ala Pro Gly Val Pro Ala Ile Tyr Phe Ala 325 330 335	1068
AAC TCT AGC ATT TCA GGC TAT GTT TTT TTA GGG CTT AAG ACT AAA AGG Asn Ser Ser Ile Ser Gly Tyr Val Phe Leu Gly Leu Lys Thr Lys Arg	1116

340	345	350	
GTG CGT TTA GAC GCG ATG	GTG GCT TTT GGG GAT	TAC CAA GAA TAT TCT	1164
Val Arg Leu Asp Ala Met	Val Ala Phe Gly Asp Tyr	Gln Glu Tyr Ser	
355	360	365	
TTA ATG AGC AGT TTT AGG	GTT TGG ACT TAT AGG	AGT TTG TCT TTT GAT	1212
Leu Met Ser Ser Phe Arg	Val Trp Thr Tyr Arg Ser	Leu Ser Phe Asp	
370	375	380	385
ATG GGT GGG GGG TAT GTG	TAT GCT TAC AAT TCT	AAA GCC ACG AGA AAA	1260
Met Gly Gly Gly Tyr Val	Tyr Ala Tyr Asn Ser	Lys Ala Thr Arg Lys	
390	395	400	
AGT CTT GGA AAT AGT TCT	TTT GTC TTT TTT GGG	AAG TTT TTG TTT TAAAA	1310
Ser Leu Gly Asn Ser Ser	Phe Val Phe Gly Lys	Phe Leu Phe	
405	410	415	
AATACCATTT CTACAATCAA TAGTGAAGAG TTTGCAATAA AGTAAGC			1357

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Gln	Tyr	Lys	Lys	Asn	Lys	Lys	Arg	Tyr	Tyr	Tyr	Leu	Ala	Leu	Gly
1				5					10					15	
Ile	Phe	Phe	Leu	Asn	Gly	Leu	Ser	Leu	Lys	Ala	Leu	Glu	Ile	Ala	Val
			20					25					30		
Lys	Pro	Phe	Gly	Tyr	Leu	Gly	Leu	Leu	Tyr	Asn	Gln	Gly	Ala	Gln	Lys
			35				40					45			
Asn	Pro	His	Ser	Tyr	Val	Gly	Ala	Leu	Ala	Arg	Leu	Gly	Val	Asp	Phe
			50			55				60					
Ser	Tyr	Ser	Asn	Gly	Trp	Ser	Phe	Gly	Ile	Gly	Ala	Ile	Gly	Ala	Trp
65				70				75					80		
Asn	Ile	Tyr	Asn	Lys	Gln	Arg	Leu	Ala	Asn	Leu	Tyr	Ile	Ser	Leu	Gly
			85					90					95		
Asn	Phe	Phe	Gly	Ser	Ser	Lys	Asn	Val	Lys	Pro	Tyr	Leu	Ser	Ala	Gly
			100				105						110		
Asp	Val	Ser	Asp	Ala	Tyr	Val	Gln	Tyr	Thr	Asn	Gln	Arg	Phe	Lys	Ile
			115				120				125				
Ala	Leu	Gly	Arg	Phe	Asn	Thr	Asp	Phe	Val	Asp	Phe	Asp	Trp	Ile	Gly
			130			135				140					
Gly	Asn	Ile	Gln	Gly	Val	Ser	Val	Ala	Phe	Lys	Gln	Asn	Ser	Met	Arg
145				150					155					160	
Tyr	Phe	Gly	Ile	Phe	Met	Asp	Ser	Met	Leu	Tyr	Asn	Gly	His	Gln	Ile
			165					170					175		
Asn	Lys	Glu	Gln	Gly	Asn	Arg	Ile	Ala	Thr	Ser	Leu	Asn	Ala	Leu	Ala
			180				185					190			
Ser	Tyr	Asp	Pro	Val	Ser	Lys	Arg	Leu	Tyr	Val	Gly	Gly	Glu	Val	Phe

195	200	205
Val Leu Gly Ala Glu Tyr Arg His Glu Asn Leu Lys Val Val Pro Phe		
210	215	220
Ile Leu Thr Asp Thr Arg Leu Pro Leu Ser Thr Gln Asn Val Leu Val		
225	230	235
Gln Val Gly Gly Lys Leu Glu Tyr Asp Ala Ser Leu Ala Lys Gly Phe		
245	250	255
Thr Ser His Thr Leu Val His Gly Met Tyr Gln Tyr Gly Asn Thr Asp		
260	265	270
Ala Ala Thr Ser Val Lys Asn Ala Gly Leu Phe Leu Ile Asp Gln Thr		
275	280	285
Phe Lys Tyr Lys Ile Phe Asn Phe Gly Thr Gly Phe Tyr Ile Val Pro		
290	295	300
Ala Arg Asn Asn Lys Gly Tyr Leu Trp Thr Phe Asn Asp Arg Thr Lys		
305	310	315
Phe Tyr Gly Arg Gly Ile Asn Ala Pro Gly Val Pro Ala Ile Tyr Phe		
325	330	335
Ala Asn Ser Ser Ile Ser Gly Tyr Val Phe Leu Gly Leu Lys Thr Lys		
340	345	350
Arg Val Arg Leu Asp Ala Met Val Ala Phe Gly Asp Tyr Gln Glu Tyr		
355	360	365
Ser Leu Met Ser Ser Phe Arg Val Trp Thr Tyr Arg Ser Leu Ser Phe		
370	375	380
Asp Met Gly Gly Gly Tyr Val Tyr Ala Tyr Asn Ser Lys Ala Thr Arg		
385	390	395
Lys Ser Leu Gly Asn Ser Ser Phe Val Phe Phe Gly Lys Phe Leu Phe		
405	410	415

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1562 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 73...1509
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTATGCTTCT TTGTTTTAG ATCAGTTAAG AATTGTAGTC TTTAAGATGT ATTGGCTATT	60
AAAAGGAAAA AA ATG AAA AAT AGC ACG CCT TTA AAG AAT CAA GTT TTT TGT	111
Met Lys Asn Ser Thr Pro Leu Lys Asn Gln Val Phe Cys	
1 5 10	
GGG TTA TAT GTT TTA AGT TTG AGC GCT TCT TTG CAA GCG TTT GAT TAT	159
Gly Leu Tyr Val Leu Ser Leu Ser Ala Ser Leu Gln Ala Phe Asp Tyr	
15 20 25	
AAA ATT GAA GTT TCA GCG GAG TCC TTT TCT AAA GTT GGC TTT AAT AAA	207
Lys Ile Glu Val Ser Ala Glu Ser Phe Ser Lys Val Gly Phe Asn Lys	

30	35	40	45	
AAA AAG ATT GAT ATA GCT AGG GGG ATT TAT CCT ACA GAG ACT TTT GTA Lys Lys Ile Asp Ile Ala Arg Gly Ile Tyr Pro Thr Glu Thr Phe Val 50 55 60	255			
ACC GCT GTA GGG CAG GGC AAT ATC TAT GCG GAT TTT TTA CCC AAA GGC Thr Ala Val Gly Gln Gly Asn Ile Tyr Ala Asp Phe Leu Pro Lys Gly 65 70 75	303			
CTT AAA GAT CAA GGG CAT GTT TTA GAG GGA AAA ATC GGT GGC ACG CTA Leu Lys Asp Gln Gly His Val Leu Glu Gly Lys Ile Gly Gly Thr Leu 80 85 90	351			
GGA GGG GTC GCT TAT GAT AGC ACG AAA TTC AAT CAA GGC GGA TCG GTT Gly Gly Val Ala Tyr Asp Ser Thr Lys Phe Asn Gln Gly Gly Ser Val 95 100 105	399			
ATT TAT AAC TAC ATC GGT TAT TGG GAT GGC TAT TTA GGG GGT AAA AGA Ile Tyr Asn Tyr Ile Gly Tyr Trp Asp Gly Tyr Leu Gly Gly Lys Arg 110 115 120 125	447			
GCC TTG CTT GAT GGC ACG AGT ATC CAT GAG TGC GCG CTT GGA TCT GAT Ala Leu Leu Asp Gly Thr Ser Ile His Glu Cys Ala Leu Gly Ser Asp 130 135 140	495			
GGC AAG GTG ATT GAT TCT ATA GCG TGC GGG AAC GCT AGG GCC AAT AAA Gly Lys Val Ile Asp Ser Ile Ala Cys Gly Asn Ala Arg Ala Asn Lys 145 150 155	543			
ATC CGC CGT AAT TAC TTG ATG AAT AAC GCT TTT TTA GAA TAC CGC TAT Ile Arg Arg Asn Tyr Leu Met Asn Asn Ala Phe Leu Glu Tyr Arg Tyr 160 165 170	591			
AAA GAT ATT TTT TTA GCT AAG GGA GGG CGT TAT CAA TCC AAT GCT CCT Lys Asp Ile Phe Leu Ala Lys Gly Gly Arg Tyr Gln Ser Asn Ala Pro 175 180 185	639			
TAT ATG AGC GGT TAC ACG CAA GGC TTT GAA ATC AGC GCT AAA GTC AAG Tyr Met Ser Gly Tyr Thr Gln Gly Phe Glu Ile Ser Ala Lys Val Lys 190 195 200 205	687			
GAT AAA AAT GAA GGA ATC CAC AAA TTA TGG TGG TTT AGC TCA TGG GGT Asp Lys Asn Glu Gly Ile His Lys Leu Trp Trp Phe Ser Ser Trp Gly 210 215 220	735			
AGG GCG TTC GCT TAT GGG GAG TGG ATT TAT GAT TTT TAT TCT CCA AGA Arg Ala Phe Ala Tyr Gly Glu Trp Ile Tyr Asp Phe Tyr Ser Pro Arg 225 230 235	783			
ACC GTG GTT AAA AAC GGG CGC ACT TTG AAT TAT GGT ATC CAT TTA GTG Thr Val Val Lys Asn Gly Arg Thr Leu Asn Tyr Gly Ile His Leu Val 240 245 250	831			
AAT TAT ACT TAT GAA AGA AAA GGG GTT AGC GTT AGC CCT TTT TTC CAA Asn Tyr Thr Tyr Glu Arg Lys Gly Val Ser Val Ser Pro Phe Phe Gln 255 260 265	879			

TTT TCG CCT GGG ACT TAT TAT AGC CCT GGG GTG GTT GTA GGC TAT GAT	927
Phe Ser Pro Gly Thr Tyr Tyr Ser Pro Gly Val Val Val Gly Tyr Asp	
270 275 280 285	
AGT AAC CCT AAT TTT AAC GGC GTT GGC TTT AGA TCC GAA ACA AAA GCT	975
Ser Asn Pro Asn Phe Asn Gly Val Gly Phe Arg Ser Glu Thr Lys Ala	
290 295 300	
TAT ATT TTG CTC CCT GTC CAT GAC CCC TTA AGA AGG GAT ACT TAT CGT	1023
Tyr Ile Leu Leu Pro Val His Asp Pro Leu Arg Arg Asp Thr Tyr Arg	
305 310 315	
TAC GCT ATA AAG GCT GGC ACT GCC GGG CAA AGC TTG CTC ATT AGG CAA	1071
Tyr Ala Ile Lys Ala Gly Thr Ala Gly Gln Ser Leu Leu Ile Arg Gln	
320 325 330	
CGA TTT GAT TAC AAT GAA TTT AAT TTT GGG GGA GCG TTT TAT AAA GTA	1119
Arg Phe Asp Tyr Asn Glu Phe Asn Phe Gly Gly Ala Phe Tyr Lys Val	
335 340 345	
TGG AAA AAC GCA AAC GCT TAC ATC GGC ACG ACA GGA AAC CCT TTA GGC	1167
Trp Lys Asn Ala Asn Ala Tyr Ile Gly Thr Thr Gly Asn Pro Leu Gly	
350 355 360 365	
ATT GAT TTT TGG ACC AAT AGC GTT TAT GAT ATA GGG CAA GCT TTA AGC	1215
Ile Asp Phe Trp Thr Asn Ser Val Tyr Asp Ile Gly Gln Ala Leu Ser	
370 375 380	
CAT GTG GTA ACC GCT GAT GCC GTC TCT GGT TGG GTT TTT GGT GGG GGC	1263
His Val Val Thr Ala Asp Ala Val Ser Gly Trp Val Phe Gly Gly Gly	
385 390 395	
GTG CAT AAA AAG TGG CTG TGG GGG ACT TTA TGG CGT TGG ACT AGC GGC	1311
Val His Lys Lys Trp Leu Trp Gly Thr Leu Trp Arg Trp Thr Ser Gly	
400 405 410	
ACT TTA GCC AAT GAA GCG AGT GCG GCT GTT AAT GTG GGC TAT AAG ATC	1359
Thr Leu Ala Asn Glu Ala Ser Ala Ala Val Asn Val Gly Tyr Lys Ile	
415 420 425	
AGT AAG AGT TTG ACA GCG AGC GTG AAA TTA GAA TAT TTG GGC GTG ATG	1407
Ser Lys Ser Leu Thr Ala Ser Val Lys Leu Glu Tyr Leu Gly Val Met	
430 435 440 445	
ACG CAT GCA GGC TTT ACG GTA GGG AGT TAC AGG CCC ACG CCC GGC TCT	1455
Thr His Ala Gly Phe Thr Val Gly Ser Tyr Arg Pro Thr Pro Gly Ser	
450 455 460	
AAA GCG CTT TAT TCA GAC AGG AGT CAT TTG ATG ACA ACT CTT AGC GCT	1503
Lys Ala Leu Tyr Ser Asp Arg Ser His Leu Met Thr Thr Leu Ser Ala	
465 470 475	
AAA TTC TAACCAATCG CTTTAAGCTG TTTATTAAAG CGTTAAAAAT CCCTTAATAA AA	1561
Lys Phe	

A

1562

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Lys	Asn	Ser	Thr	Pro	Leu	Lys	Asn	Gln	Val	Phe	Cys	Gly	Leu	Tyr
1				5					10					15	
Val	Leu	Ser	Leu	Ser	Ala	Ser	Leu	Gln	Ala	Phe	Asp	Tyr	Lys	Ile	Glu
			20					25					30		
Val	Ser	Ala	Glu	Ser	Phe	Ser	Lys	Val	Gly	Phe	Asn	Lys	Lys	Lys	Ile
		35					40					45			
Asp	Ile	Ala	Arg	Gly	Ile	Tyr	Pro	Thr	Glu	Thr	Phe	Val	Thr	Ala	Val
		50				55					60				
Gly	Gln	Gly	Asn	Ile	Tyr	Ala	Asp	Phe	Leu	Pro	Lys	Gly	Leu	Lys	Asp
65					70				75					80	
Gln	Gly	His	Val	Leu	Glu	Gly	Lys	Ile	Gly	Gly	Thr	Leu	Gly	Gly	Val
			85						90					95	
Ala	Tyr	Asp	Ser	Thr	Lys	Phe	Asn	Gln	Gly	Gly	Ser	Val	Ile	Tyr	Asn
			100					105					110		
Tyr	Ile	Gly	Tyr	Trp	Asp	Gly	Tyr	Leu	Gly	Gly	Lys	Arg	Ala	Leu	Leu
		115					120					125			
Asp	Gly	Thr	Ser	Ile	His	Glu	Cys	Ala	Leu	Gly	Ser	Asp	Gly	Lys	Val
		130				135					140				
Ile	Asp	Ser	Ile	Ala	Cys	Gly	Asn	Ala	Arg	Ala	Asn	Lys	Ile	Arg	Arg
145					150				155					160	
Asn	Tyr	Leu	Met	Asn	Asn	Ala	Phe	Leu	Glu	Tyr	Arg	Tyr	Lys	Asp	Ile
			165						170					175	
Phe	Leu	Ala	Lys	Gly	Gly	Arg	Tyr	Gln	Ser	Asn	Ala	Pro	Tyr	Met	Ser
			180					185					190		
Gly	Tyr	Thr	Gln	Gly	Phe	Glu	Ile	Ser	Ala	Lys	Val	Lys	Asp	Lys	Asn
		195					200					205			
Glu	Gly	Ile	His	Lys	Leu	Trp	Trp	Phe	Ser	Ser	Trp	Gly	Arg	Ala	Phe
		210				215					220				
Ala	Tyr	Gly	Glu	Trp	Ile	Tyr	Asp	Phe	Tyr	Ser	Pro	Arg	Thr	Val	Val
225					230				235					240	
Lys	Asn	Gly	Arg	Thr	Leu	Asn	Tyr	Gly	Ile	His	Leu	Val	Asn	Tyr	Thr
			245						250					255	
Tyr	Glu	Arg	Lys	Gly	Val	Ser	Val	Ser	Pro	Phe	Phe	Gln	Phe	Ser	Pro
			260					265					270		
Gly	Thr	Tyr	Tyr	Ser	Pro	Gly	Val	Val	Val	Gly	Tyr	Asp	Ser	Asn	Pro
		275					280					285			
Asn	Phe	Asn	Gly	Val	Gly	Phe	Arg	Ser	Glu	Thr	Lys	Ala	Tyr	Ile	Leu
		290				295					300				
Leu	Pro	Val	His	Asp	Pro	Leu	Arg	Arg	Asp	Thr	Tyr	Arg	Tyr	Ala	Ile
305					310				315					320	
Lys	Ala	Gly	Thr	Ala	Gly	Gln	Ser	Leu	Leu	Ile	Arg	Gln	Arg	Phe	Asp
			325						330					335	
Tyr	Asn	Glu	Phe	Asn	Phe	Gly	Gly	Ala	Phe	Tyr	Lys	Val	Trp	Lys	Asn
			340					345					350		
Ala	Asn	Ala	Tyr	Ile	Gly	Thr	Thr	Gly	Asn	Pro	Leu	Gly	Ile	Asp	Phe

355	360	365
Trp Thr Asn Ser Val Tyr	Asp Ile Gly Gln Ala Leu	Ser His Val Val
370	375	380
Thr Ala Asp Ala Val Ser	Gly Trp Val Phe Gly	Gly Gly Val His Lys
385	390	395
Lys Trp Leu Trp Gly Thr	Leu Trp Arg Trp Thr	Ser Gly Thr Leu Ala
405	410	415
Asn Glu Ala Ser Ala Ala	Val Asn Val Gly Tyr Lys	Ile Ser Lys Ser
420	425	430
Leu Thr Ala Ser Val Lys	Leu Glu Tyr Leu Gly Val	Met Thr His Ala
435	440	445
Gly Phe Thr Val Gly Ser	Tyr Arg Pro Thr Pro Gly	Ser Lys Ala Leu
450	455	460
Tyr Ser Asp Arg Ser His	Leu Met Thr Thr Leu Ser	Ala Lys Phe
465	470	475

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 98...757
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTAATATTTA TTTTAACTT TGTTATTATT TAAGGTGTGA TTTGATTTTA GTCTGTATGG	60
GGCAAGTGTG GGGCAGGATA ACATAAGGAA TTGGGTT ATG AAT AAA ACA ACG GTT	115
Met Asn Lys Thr Thr Val	
1 5	
AAA ATA TTA ATG GGC ATG GCG TTA TTA TCA TCG CTT CAA GCC GCA GAG	163
Lys Ile Leu Met Gly Met Ala Leu Leu Ser Ser Leu Gln Ala Ala Glu	
10 15 20	
GCA GAG CTT GAT GAA AAA TCA AAA AAA CCT AAA TTT GCG GAC AGG AAT	211
Ala Glu Leu Asp Glu Lys Ser Lys Lys Pro Lys Phe Ala Asp Arg Asn	
25 30 35	
ACA TTT TAT TTA GGG GTT GGG TAT CAA CTT AGT GCG ATC AAC ACA TCT	259
Thr Phe Tyr Leu Gly Val Gly Tyr Gln Leu Ser Ala Ile Asn Thr Ser	
40 45 50	
TTT AGC ACC GAG TCT GTA GAT AAA TCG TAT TTT ATG ACC GGC AAT GGC	307
Phe Ser Thr Glu Ser Val Asp Lys Ser Tyr Phe Met Thr Gly Asn Gly	
55 60 65 70	
TTT GGT GTG GTG TTA GGG GGG AAA TTT GTG GCT AAA ACG CAA GCT GTA	355
Phe Gly Val Val Leu Gly Gly Lys Phe Val Ala Lys Thr Gln Ala Val	

75										80					85					
GAG	CAT	GTG	GGT	TTC	CGT	TAC	GGG	TTG	TTT	TAT	GAT	CAG	ACC	TTT	TCT	403				
Glu	His	Val	Gly	Phe	Arg	Tyr	Gly	Leu	Phe	Tyr	Asp	Gln	Thr	Phe	Ser					
		90						95					100							
TCT	CAC	AAA	TCC	TAT	ATT	TCT	ACC	TAT	GGT	TTA	GAA	TTT	AGC	GGT	TTG	451				
Ser	His	Lys	Ser	Tyr	Ile	Ser	Thr	Tyr	Gly	Leu	Glu	Phe	Ser	Gly	Leu					
		105					110					115								
TGG	GAC	GCT	TTC	AAT	TCG	CCA	AAG	ATG	TTT	TTA	GGG	TTA	GAG	TTT	GGC	499				
Trp	Asp	Ala	Phe	Asn	Ser	Pro	Lys	Met	Phe	Leu	Gly	Leu	Glu	Phe	Gly					
	120					125					130									
TTA	GGC	ATC	GCT	GGG	GCG	ACT	TAT	ATG	CCA	GGA	GGG	GCT	ATG	CAT	GGG	547				
Leu	Gly	Ile	Ala	Gly	Ala	Thr	Tyr	Met	Pro	Gly	Gly	Ala	Met	His	Gly					
135					140					145					150					
ATT	ATC	GCT	CAA	AAT	TTA	GGC	AAA	GAA	AAT	TCG	CTT	TTC	CAA	TTG	CTT	595				
Ile	Ile	Ala	Gln	Asn	Leu	Gly	Lys	Glu	Asn	Ser	Leu	Phe	Gln	Leu	Leu					
			155					160						165						
GTG	AAA	GTG	GGT	TTT	CGT	TTT	GGC	TTT	TTG	CAC	AAT	GAA	ATC	ACT	TTC	643				
Val	Lys	Val	Gly	Phe	Arg	Phe	Gly	Phe	Leu	His	Asn	Glu	Ile	Thr	Phe					
		170					175					180								
GGG	TTG	AAA	TTC	CCT	GTC	ATT	CCT	AAC	AAA	AGA	ACG	GAA	ATC	ATT	GAT	691				
Gly	Leu	Lys	Phe	Pro	Val	Ile	Pro	Asn	Lys	Arg	Thr	Glu	Ile	Ile	Asp					
		185					190					195								
GGC	TTG	AGC	ACG	ACT	ACT	TTA	TGG	CAC	CGC	TTA	CCG	GTA	GCT	TAT	TTC	739				
Gly	Leu	Ser	Thr	Thr	Thr	Leu	Trp	His	Arg	Leu	Pro	Val	Ala	Tyr	Phe					
	200					205					210									
AAT	TAT	ATC	TAT	AAT	TTT	TAGATATGGT	TATTTAGAGG	TTTTAGATTT	GACAAAAT							795				
Asn	Tyr	Ile	Tyr	Asn	Phe															
215					220															
CAATCAACTC	TCGTG															810				

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met	Asn	Lys	Thr	Thr	Val	Lys	Ile	Leu	Met	Gly	Met	Ala	Leu	Leu	Ser
1				5					10					15	
Ser	Leu	Gln	Ala	Ala	Glu	Ala	Glu	Leu	Asp	Glu	Lys	Ser	Lys	Lys	Pro
		20					25					30			
Lys	Phe	Ala	Asp	Arg	Asn	Thr	Phe	Tyr	Leu	Gly	Val	Gly	Tyr	Gln	Leu

		35					40					45			
Ser	Ala	Ile	Asn	Thr	Ser	Phe	Ser	Thr	Glu	Ser	Val	Asp	Lys	Ser	Tyr
	50					55					60				
Phe	Met	Thr	Gly	Asn	Gly	Phe	Gly	Val	Val	Leu	Gly	Gly	Lys	Phe	Val
65					70					75					80
Ala	Lys	Thr	Gln	Ala	Val	Glu	His	Val	Gly	Phe	Arg	Tyr	Gly	Leu	Phe
				85					90					95	
Tyr	Asp	Gln	Thr	Phe	Ser	Ser	His	Lys	Ser	Tyr	Ile	Ser	Thr	Tyr	Gly
			100					105					110		
Leu	Glu	Phe	Ser	Gly	Leu	Trp	Asp	Ala	Phe	Asn	Ser	Pro	Lys	Met	Phe
		115					120					125			
Leu	Gly	Leu	Glu	Phe	Gly	Leu	Gly	Ile	Ala	Gly	Ala	Thr	Tyr	Met	Pro
	130					135					140				
Gly	Gly	Ala	Met	His	Gly	Ile	Ile	Ala	Gln	Asn	Leu	Gly	Lys	Glu	Asn
145					150					155					160
Ser	Leu	Phe	Gln	Leu	Leu	Val	Lys	Val	Gly	Phe	Arg	Phe	Gly	Phe	Leu
				165					170					175	
His	Asn	Glu	Ile	Thr	Phe	Gly	Leu	Lys	Phe	Pro	Val	Ile	Pro	Asn	Lys
			180					185					190		
Arg	Thr	Glu	Ile	Ile	Asp	Gly	Leu	Ser	Thr	Thr	Thr	Leu	Trp	His	Arg
		195					200					205			
Leu	Pro	Val	Ala	Tyr	Phe	Asn	Tyr	Ile	Tyr	Asn	Phe				
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1516 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1463
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTTATCTTTA	AAAGTATTTG	CATTTATCAA	TCTCATTTTA	GGAGGCATGC	ATG	AAA	56
					Met	Lys	
					1		
AAG GCA AGT CAG GTT TTA TTC TTT GGG GCA TTT TTA AGC TCT TCT TTG							104
Lys Ala Ser Gln Val Leu Phe Phe Gly Ala Phe Leu Ser Ser Leu							
	5				10	15	
CAA GGT TTT GAA GCT AAG CTC AAC GGC TTT GTG GAT CAA TCC AGC ACT							152
Gln Gly Phe Glu Ala Lys Leu Asn Gly Phe Val Asp Gln Ser Ser Thr							
	20			25		30	
ATC GGT TTT AAC CAG CAT AAA ATC AAT AAA GAA AGA GGT ATC TAC CCT							200
Ile Gly Phe Asn Gln His Lys Ile Asn Lys Glu Arg Gly Ile Tyr Pro							
35			40		45	50	

ATG CAG CAA TTC GCA ACG ATT GCG GGC TAT TTA GGG CTT GGT TTT AGC	248
Met Gln Gln Phe Ala Thr Ile Ala Gly Tyr Leu Gly Leu Gly Phe Ser	
55 60 65	
CTG TTA CCC AAA AAG GTT TCA GAC CAT GTT CTA AAA GGC AAA ATA GGA	296
Leu Leu Pro Lys Lys Val Ser Asp His Val Leu Lys Gly Lys Ile Gly	
70 75 80	
GGC ATG GTG GGA TCT ATT TTC TAT GAT GGC ACG AAG AAG TTT GAA GAC	344
Gly Met Val Gly Ser Ile Phe Tyr Asp Gly Thr Lys Lys Phe Glu Asp	
85 90 95	
AGC TCT GTA GCT TAC AAC CTC TTT GGT TAT TAT GAT GGG TTC ATG GGG	392
Ser Ser Val Ala Tyr Asn Leu Phe Gly Tyr Tyr Asp Gly Phe Met Gly	
100 105 110	
GGT TAT ACA AAC ATC TTA CAA AGC GAT GAT TTA GCG ACA CAA AAC ATG	440
Gly Tyr Thr Asn Ile Leu Gln Ser Asp Asp Leu Ala Thr Gln Asn Met	
115 120 125 130	
AAA TAC AAT AAA AAT GTC CGC AAC TAT GTC TTT AGC GAC GCG TAT TTA	488
Lys Tyr Asn Lys Asn Val Arg Asn Tyr Val Phe Ser Asp Ala Tyr Leu	
135 140 145	
GAA TAC GCT TAT AAG AAT TAT TTT GAA ATA AAA GCC GGG CGC TAT TTA	536
Glu Tyr Ala Tyr Lys Asn Tyr Phe Glu Ile Lys Ala Gly Arg Tyr Leu	
150 155 160	
TCC ACT ATG CCT TAT AAA AGC GGT CAA ACG CAA GGC TTT CAA ATT TCT	584
Ser Thr Met Pro Tyr Lys Ser Gly Gln Thr Gln Gly Phe Gln Ile Ser	
165 170 175	
GGG CAA TAC AAG AAA GCG CGC TTG ACT TGG TTT AGC TCT TTT GGG AGG	632
Gly Gln Tyr Lys Lys Ala Arg Leu Thr Trp Phe Ser Ser Phe Gly Arg	
180 185 190	
GCG TTC GCT TAC GGC TCG TTT TTG ATG GAT TGG TTT GCC GCT AGG ACC	680
Ala Phe Ala Tyr Gly Ser Phe Leu Met Asp Trp Phe Ala Ala Arg Thr	
195 200 205 210	
ACT TAT AGC GGA GGT TTT ACC AAA AAC GAT AAG GGA GGT TAT GAT AGC	728
Thr Tyr Ser Gly Gly Phe Thr Lys Asn Asp Lys Gly Gly Tyr Asp Ser	
215 220 225	
CAT GGG CGA AAG GTG CTT TAT GGC ACG CAT GCG GTG CAA CTC ACC TAT	776
His Gly Arg Lys Val Leu Tyr Gly Thr His Ala Val Gln Leu Thr Tyr	
230 235 240	
AAA CCT CAT CGT TTC CTC ATA GAA GGC TTT TAT TAC CTT TCG CCT CAA	824
Lys Pro His Arg Phe Leu Ile Glu Gly Phe Tyr Tyr Leu Ser Pro Gln	
245 250 255	
ATC TTT AAC GCT CCG GGC GTT AAG ATT GGT TGG GAT TCT AAC CCT AAT	872
Ile Phe Asn Ala Pro Gly Val Lys Ile Gly Trp Asp Ser Asn Pro Asn	
260 265 270	
TTT AGC GGC ACA GGC TTT CGC TCT GAT ACA GCT ATC ATA GGG TTT TTC	920
Phe Ser Gly Thr Gly Phe Arg Ser Asp Thr Ala Ile Ile Gly Phe Phe	

275	280	285	290	
CCC ATT TAC TAC CCT TGG ATG ATC GTT AAA TCC AAT GGA AGC CCG GTC	Pro Ile Tyr Tyr Pro Trp Met Ile Val Lys Ser Asn Gly Ser Pro Val			968
	295	300	305	
TAT AAA TAC GAC ACG CCT GCC ACT CAA AAT GGG CAA AAC CTC ATT ATC	Tyr Lys Tyr Asp Thr Pro Ala Thr Gln Asn Gly Gln Asn Leu Ile Ile			1016
	310	315	320	
CTC CAA CGC TTT GAC ATC AAC AAT TAC AAT GTT TCC ATC GCT TTT TAT	Leu Gln Arg Phe Asp Ile Asn Asn Tyr Asn Val Ser Ile Ala Phe Tyr			1064
	325	330	335	
AAA GTC TTT CAA AAC GCT AAT GGT TGG ATA GGC AAC ATG GGG AAT CCA	Lys Val Phe Gln Asn Ala Asn Gly Trp Ile Gly Asn Met Gly Asn Pro			1112
	340	345	350	
AGC GGT GTG ATC ATG GGG AGT AAC AGC GTC TAT GCG GGT TTT ACA GGC	Ser Gly Val Ile Met Gly Ser Asn Ser Val Tyr Ala Gly Phe Thr Gly			1160
	355	360	365	
ACA GCC CTT AAA AGA GAT GCC GCT ACC ATT TTC CTT TCT TGT GGC GGC	Thr Ala Leu Lys Arg Asp Ala Ala Thr Ile Phe Leu Ser Cys Gly Gly			1208
	375	380	385	
ACT CAT TTT GCC AAA AAA TTC ACA TGG AAA TTC GCC ACG CAA TAC TCC	Thr His Phe Ala Lys Lys Phe Thr Trp Lys Phe Ala Thr Gln Tyr Ser			1256
	390	395	400	
AAT TCA GTG GTT TCT TGG GAA GCG AGA GCG ATG ATC TCT TTA GGT TAT	Asn Ser Val Val Ser Trp Glu Ala Arg Ala Met Ile Ser Leu Gly Tyr			1304
	405	410	415	
AAA TTC ACT GAA TAC TTG AGC GGT AGC GTG GAT CTT GCA TAT TAT GGC	Lys Phe Thr Glu Tyr Leu Ser Gly Ser Val Asp Leu Ala Tyr Tyr Gly			1352
	420	425	430	
GTG TAT ACT AAC AAA GGA TTT AAA CCG GGT GAA AAC GGG CCT GTG CCT	Val Tyr Thr Asn Lys Gly Phe Lys Pro Gly Glu Asn Gly Pro Val Pro			1400
	435	440	445	
AAA GAC TTC CCC GCC CTT TAT TCT GAC AGG AGC GCG TTA TAC ACG GCT	Lys Asp Phe Pro Ala Leu Tyr Ser Asp Arg Ser Ala Leu Tyr Thr Ala			1448
	455	460	465	
CTA GTA GCA TCT TTT TGATGCTACC CTATGATTAT GGTGGGCGTC TTTTGATGCT G	Leu Val Ala Ser Phe			1504
	470			
TTTCTCTAGT CT				1516

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met	Lys	Lys	Ala	Ser	Gln	Val	Leu	Phe	Phe	Gly	Ala	Phe	Leu	Ser	Ser	1	5	10	15
Ser	Leu	Gln	Gly	Phe	Glu	Ala	Lys	Leu	Asn	Gly	Phe	Val	Asp	Gln	Ser	20	25	30	
Ser	Thr	Ile	Gly	Phe	Asn	Gln	His	Lys	Ile	Asn	Lys	Glu	Arg	Gly	Ile	35	40	45	
Tyr	Pro	Met	Gln	Gln	Phe	Ala	Thr	Ile	Ala	Gly	Tyr	Leu	Gly	Leu	Gly	50	55	60	
Phe	Ser	Leu	Leu	Pro	Lys	Lys	Val	Ser	Asp	His	Val	Leu	Lys	Gly	Lys	65	70	75	80
Ile	Gly	Gly	Met	Val	Gly	Ser	Ile	Phe	Tyr	Asp	Gly	Thr	Lys	Lys	Phe	85	90	95	
Glu	Asp	Ser	Ser	Val	Ala	Tyr	Asn	Leu	Phe	Gly	Tyr	Tyr	Asp	Gly	Phe	100	105	110	
Met	Gly	Gly	Tyr	Thr	Asn	Ile	Leu	Gln	Ser	Asp	Asp	Leu	Ala	Thr	Gln	115	120	125	
Asn	Met	Lys	Tyr	Asn	Lys	Asn	Val	Arg	Asn	Tyr	Val	Phe	Ser	Asp	Ala	130	135	140	
Tyr	Leu	Glu	Tyr	Ala	Tyr	Lys	Asn	Tyr	Phe	Glu	Ile	Lys	Ala	Gly	Arg	145	150	155	160
Tyr	Leu	Ser	Thr	Met	Pro	Tyr	Lys	Ser	Gly	Gln	Thr	Gln	Gly	Phe	Gln	165	170	175	
Ile	Ser	Gly	Gln	Tyr	Lys	Lys	Ala	Arg	Leu	Thr	Trp	Phe	Ser	Ser	Phe	180	185	190	
Gly	Arg	Ala	Phe	Ala	Tyr	Gly	Ser	Phe	Leu	Met	Asp	Trp	Phe	Ala	Ala	195	200	205	
Arg	Thr	Thr	Tyr	Ser	Gly	Gly	Phe	Thr	Lys	Asn	Asp	Lys	Gly	Gly	Tyr	210	215	220	
Asp	Ser	His	Gly	Arg	Lys	Val	Leu	Tyr	Gly	Thr	His	Ala	Val	Gln	Leu	225	230	235	240
Thr	Tyr	Lys	Pro	His	Arg	Phe	Leu	Ile	Glu	Gly	Phe	Tyr	Tyr	Leu	Ser	245	250	255	
Pro	Gln	Ile	Phe	Asn	Ala	Pro	Gly	Val	Lys	Ile	Gly	Trp	Asp	Ser	Asn	260	265	270	
Pro	Asn	Phe	Ser	Gly	Thr	Gly	Phe	Arg	Ser	Asp	Thr	Ala	Ile	Ile	Gly	275	280	285	
Phe	Phe	Pro	Ile	Tyr	Tyr	Pro	Trp	Met	Ile	Val	Lys	Ser	Asn	Gly	Ser	290	295	300	
Pro	Val	Tyr	Lys	Tyr	Asp	Thr	Pro	Ala	Thr	Gln	Asn	Gly	Gln	Asn	Leu	305	310	315	320
Ile	Ile	Leu	Gln	Arg	Phe	Asp	Ile	Asn	Asn	Tyr	Asn	Val	Ser	Ile	Ala	325	330	335	
Phe	Tyr	Lys	Val	Phe	Gln	Asn	Ala	Asn	Gly	Trp	Ile	Gly	Asn	Met	Gly	340	345	350	
Asn	Pro	Ser	Gly	Val	Ile	Met	Gly	Ser	Asn	Ser	Val	Tyr	Ala	Gly	Phe	355	360	365	
Thr	Gly	Thr	Ala	Leu	Lys	Arg	Asp	Ala	Ala	Thr	Ile	Phe	Leu	Ser	Cys	370	375	380	
Gly	Gly	Thr	His	Phe	Ala	Lys	Lys	Phe	Thr	Trp	Lys	Phe	Ala	Thr	Gln	385	390	395	400
Tyr	Ser	Asn	Ser	Val	Val	Ser	Trp	Glu	Ala	Arg	Ala	Met	Ile	Ser	Leu				

				405						410					415				
Gly	Tyr	Lys	Phe	Thr	Glu	Tyr	Leu	Ser	Gly	Ser	Val	Asp	Leu	Ala	Tyr				
			420					425					430						
Tyr	Gly	Val	Tyr	Thr	Asn	Lys	Gly	Phe	Lys	Pro	Gly	Glu	Asn	Gly	Pro				
		435					440					445							
Val	Pro	Lys	Asp	Phe	Pro	Ala	Leu	Tyr	Ser	Asp	Arg	Ser	Ala	Leu	Tyr				
	450					455					460								
Thr	Ala	Leu	Val	Ala	Ser	Phe													
465					470														

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 87...323
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AAATTTATGT TATAATTAAA CGCATTGTAA ATAAATTCTC ATTTTGATAC ATTTTACAA	60
TAAAACATTA CTTTAAGGAA CATCTT ATG AAA AAA ACG AAA AAA ACG ATT CTG	113
Met Lys Lys Thr Lys Lys Thr Ile Leu	
1 5	
CTT TCT CTA ACT CTC GCG GCG TCA TTG CTC CAT GCT GAA GAC AAC GGC	161
Leu Ser Leu Thr Leu Ala Ala Ser Leu Leu His Ala Glu Asp Asn Gly	
10 15 20 25	
GTT TTT TTA AGC GTG GGT TAT CAA ATC GGT GAA GCG GTT CAA AAA GTG	209
Val Phe Leu Ser Val Gly Tyr Gln Ile Gly Glu Ala Val Gln Lys Val	
30 35 40	
AAA AAC GCC GAC AAG GTG CAA AAA CTT TCA GAC ACT TAT GAA CAA TTA	257
Lys Asn Ala Asp Lys Val Gln Lys Leu Ser Asp Thr Tyr Glu Gln Leu	
45 50 55	
AGC CGG CTT TTA ACC AAC GAT AAT GGC ACA AAC TCA AAG ACA AGC GCG	305
Ser Arg Leu Leu Thr Asn Asp Asn Gly Thr Asn Ser Lys Thr Ser Ala	
60 65 70	
CAA NAT CAA CCA AGC GGT TAATAATTTG AACGAACGCG CAAAACTTT AGCCGGTG	361
Gln Xaa Gln Pro Ser Gly	
75	
GGACAACCAA TTCCCC	377

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

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Met Lys Lys Thr Lys Lys Thr Ile Leu Leu Ser Leu Thr Leu Ala Ala
 1             5             10             15
Ser Leu Leu His Ala Glu Asp Asn Gly Val Phe Leu Ser Val Gly Tyr
          20             25             30
Gln Ile Gly Glu Ala Val Gln Lys Val Lys Asn Ala Asp Lys Val Gln
          35             40             45
Lys Leu Ser Asp Thr Tyr Glu Gln Leu Ser Arg Leu Leu Thr Asn Asp
          50             55             60
Asn Gly Thr Asn Ser Lys Thr Ser Ala Gln Xaa Gln Pro Ser Gly
65             70             75

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(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 60...2039
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

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CCCTATCATA GGGCGTGGCA TGAAGAAAAA AGCAAAAGTC TTTTGGTATT GTTTTAATC      59

ATG ATT TAT TGG TTG TAT TTG GCG GTC TTT TTT TTG TTG AGC GCA TTA      107
Met Ile Tyr Trp Leu Tyr Leu Ala Val Phe Phe Leu Leu Ser Ala Leu
 1             5             10             15

GAC GCT AAA GAA ATC GCT ATG CAA CGA TTT GAC AAA CAA AAC CAT AAG      155
Asp Ala Lys Glu Ile Ala Met Gln Arg Phe Asp Lys Gln Asn His Lys
          20             25             30

ATT TTT GAA ATC CTT GCG GAT AAA GTG AGC GCT AAA GAC AAT GTG ATA      203
Ile Phe Glu Ile Leu Ala Asp Lys Val Ser Ala Lys Asp Asn Val Ile
          35             40             45

ACC GCA TCA GGG AAT GCG ATC TTA TTG AAT TAT GAT GTG TAT ATT CTA      251
Thr Ala Ser Gly Asn Ala Ile Leu Leu Asn Tyr Asp Val Tyr Ile Leu
          50             55             60

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GCG	GAC	AAG	GTG	CGT	TAT	GAC	ACT	AAA	ACC	AAA	GAA	GCG	TTA	TTA	GAG	299
Ala	Asp	Lys	Val	Arg	Tyr	Asp	Thr	Lys	Thr	Lys	Glu	Ala	Leu	Leu	Glu	
65					70					75					80	
GGG	AAT	ATC	AAG	GTT	TAT	AGG	GGC	GAG	GGT	TTG	CTC	GTT	AAA	ACC	GAT	347
Gly	Asn	Ile	Lys	Val	Tyr	Arg	Gly	Glu	Gly	Leu	Leu	Val	Lys	Thr	Asp	
				85					90					95		
TAC	GTG	AAA	TTG	AGT	TTG	AAT	GAA	AAA	TAT	GAA	ATC	ATT	TTC	CCC	TTT	395
Tyr	Val	Lys	Leu	Ser	Leu	Asn	Glu	Lys	Tyr	Glu	Ile	Ile	Phe	Pro	Phe	
			100					105					110			
TAT	GTC	CAA	GAC	AGC	GTG	AGC	GGG	ATT	TGG	GTG	AGC	GCG	GAT	ATT	GCC	443
Tyr	Val	Gln	Asp	Ser	Val	Ser	Gly	Ile	Trp	Val	Ser	Ala	Asp	Ile	Ala	
		115					120					125				
AGC	GGA	AAG	GAT	CAA	AAA	TAT	AAG	GTT	AAA	AAC	ATG	AGC	ACT	TCA	GGG	491
Ser	Gly	Lys	Asp	Gln	Lys	Tyr	Lys	Val	Lys	Asn	Met	Ser	Thr	Ser	Gly	
	130					135					140					
TGC	AGC	ATT	GAT	AAC	CCC	ATT	TGG	CAT	GTC	AAT	GCG	ACT	TCA	GGC	TCA	539
Cys	Ser	Ile	Asp	Asn	Pro	Ile	Trp	His	Val	Asn	Ala	Thr	Ser	Gly	Ser	
145					150					155					160	
TTC	AAC	ATG	CAA	AAA	TCG	CAT	TTG	TCT	ATG	TGG	AAT	CCT	AAG	ATC	TAT	587
Phe	Asn	Met	Gln	Lys	Ser	His	Leu	Ser	Met	Trp	Asn	Pro	Lys	Ile	Tyr	
				165					170					175		
GTC	GGT	GAT	ATT	CCT	GTA	TTG	TAT	TTG	CCC	TAT	ATT	TTC	ATG	TCC	ACG	635
Val	Gly	Asp	Ile	Pro	Val	Leu	Tyr	Leu	Pro	Tyr	Ile	Phe	Met	Ser	Thr	
			180					185					190			
AGC	AAT	AAA	AGA	ACT	ACT	GGG	TTT	TTA	TAC	CCT	GAG	TTT	GGC	ACT	TCC	683
Ser	Asn	Lys	Arg	Thr	Thr	Gly	Phe	Leu	Tyr	Pro	Glu	Phe	Gly	Thr	Ser	
		195					200					205				
AAC	TTA	GAC	GGC	TTT	ATT	TAT	TTG	CAA	CCC	TTT	TAT	TTA	GCC	CCC	AAA	731
Asn	Leu	Asp	Gly	Phe	Ile	Tyr	Leu	Gln	Pro	Phe	Tyr	Leu	Ala	Pro	Lys	
	210					215					220					
AAC	TCA	TGG	GAT	ATG	ACC	TTT	ACC	CCA	CAA	ATC	CGC	TAT	AAA	AGG	GGT	779
Asn	Ser	Trp	Asp	Met	Thr	Phe	Thr	Pro	Gln	Ile	Arg	Tyr	Lys	Arg	Gly	
225					230					235					240	
TTT	GGC	TTG	AAT	TTT	GAA	GCG	CGC	TAC	ATT	AAC	TCT	AAA	AAC	GAC	AGG	827
Phe	Gly	Leu	Asn	Phe	Glu	Ala	Arg	Tyr	Ile	Asn	Ser	Lys	Asn	Asp	Arg	
				245					250					255		
TTT	TTA	TTC	AAC	GCG	CGC	TAT	TTT	AGG	AAT	TAC	ACC	CAA	TAT	GTC	AAA	875
Phe	Leu	Phe	Asn	Ala	Arg	Tyr	Phe	Arg	Asn	Tyr	Thr	Gln	Tyr	Val	Lys	
			260				265						270			
CGC	TAC	GAT	TTG	AGG	AAT	CAA	AAT	ATC	TAC	GGG	TTT	GAA	TTT	TTA	AGC	923
Arg	Tyr	Asp	Leu	Arg	Asn	Gln	Asn	Ile	Tyr	Gly	Phe	Glu	Phe	Leu	Ser	
		275					280					285				
TCT	AGC	AGG	GAC	ACT	TTA	CAA	AAA	TAC	TTC	CAC	CTT	AAG	TCT	AAT	ATT	971
Ser	Ser	Arg	Asp	Thr	Leu	Gln	Lys	Tyr	Phe	His	Leu	Lys	Ser	Asn	Ile	

290	295	300	
GAC AAC GGG CAT TAC ATT GAC TTT TTA TAC ATG AAC GAT TTG GAC TAT	1019		
Asp Asn Gly His Tyr Ile Asp Phe Leu Tyr Met Asn Asp Leu Asp Tyr			
305 310 315 320			
GTG CGT TTT GAA AAG GTT AAT AAG CGT ATC ACA GAC GCC ACG CAC ATG	1067		
Val Arg Phe Glu Lys Val Asn Lys Arg Ile Thr Asp Ala Thr His Met			
325 330 335			
TCT AGG GCG AAT TAC TAT TTG CAA ACA GAA AAC AAT TAT TAC GGC TTG	1115		
Ser Arg Ala Asn Tyr Tyr Leu Gln Thr Glu Asn Asn Tyr Tyr Gly Leu			
340 345 350			
AAT ATC AAG TAT TTT TTA AAC CTG AAT AAA ATC AAC AAT AAC CGC ACT	1163		
Asn Ile Lys Tyr Phe Leu Asn Leu Asn Lys Ile Asn Asn Asn Arg Thr			
355 360 365			
TTC CAA TCT GTC CCT AAT TTG CAA TAC CAT AAA TAT TTA AAT TCT TTG	1211		
Phe Gln Ser Val Pro Asn Leu Gln Tyr His Lys Tyr Leu Asn Ser Leu			
370 375 380			
TAT TTT AGA AAT TTG TTG TAT TCG GTG GAT TAT CAG TTT AGA AAC ACC	1259		
Tyr Phe Arg Asn Leu Leu Tyr Ser Val Asp Tyr Gln Phe Arg Asn Thr			
385 390 395 400			
GCA AGA GAG ATT GGT TAT GGC TAT GTG CAA AAC GCT TTG AAT GTG CCG	1307		
Ala Arg Glu Ile Gly Tyr Gly Tyr Val Gln Asn Ala Leu Asn Val Pro			
405 410 415			
GTG GGC TTG CAA TTT TCT TTG TTT AAA AAG TAT TTG TCT TTA GGG CTT	1355		
Val Gly Leu Gln Phe Ser Leu Phe Lys Lys Tyr Leu Ser Leu Gly Leu			
420 425 430			
TGG AAT GAT CTC CAA CTA TCT AAT GTG GCT TTA ATG CAA TCT AAA AAT	1403		
Trp Asn Asp Leu Gln Leu Ser Asn Val Ala Leu Met Gln Ser Lys Asn			
435 440 445			
TCC TTC GTG CCT ACG ATC CCT AAT GAA TCA AGG GAA TTT GGG AAT TTT	1451		
Ser Phe Val Pro Thr Ile Pro Asn Glu Ser Arg Glu Phe Gly Asn Phe			
450 455 460			
GTG TCT TCA AAT TTT TCC ATG TAT GTC AAT ACG GAT TTG GCT AGA GAA	1499		
Val Ser Ser Asn Phe Ser Met Tyr Val Asn Thr Asp Leu Ala Arg Glu			
465 470 475 480			
TAC AAC AAG CTT TTC CAC ACG ATC CAA CTA GAA GCG ATT TTC AAC ATC	1547		
Tyr Asn Lys Leu Phe His Thr Ile Gln Leu Glu Ala Ile Phe Asn Ile			
485 490 495			
CCT TAT TAC ACC TTT AAA AAC GGC TTA TTT TCT CAA AAC ATG TAT GCT	1595		
Pro Tyr Tyr Thr Phe Lys Asn Gly Leu Phe Ser Gln Asn Met Tyr Ala			
500 505 510			
TTA AGC GCG CAA GCC TTA AAC AGC TAC ACT TCG CCT TTA TTG AGA GAT	1643		
Leu Ser Ala Gln Ala Leu Asn Ser Tyr Thr Ser Pro Leu Leu Arg Asp			
515 520 525			

TAT GAT TAT CAA GGG CGT TTG TAT GAC TCG GTG TGG AAT CCT AGC AGT	1691
Tyr Asp Tyr Gln Gly Arg Leu Tyr Asp Ser Val Trp Asn Pro Ser Ser	
530 535 540	
ATT TTA CCT AGC AAT GCG AGC AAC AAG ACG GTG GAT TTA ACC CTA ACG	1739
Ile Leu Pro Ser Asn Ala Ser Asn Lys Thr Val Asp Leu Thr Leu Thr	
545 550 555 560	
CAA TAC CTT TAT GGC TTA GGG GGG CAA GAG TTA TTG TAT TTT AAA ATA	1787
Gln Tyr Leu Tyr Gly Leu Gly Gly Gln Glu Leu Leu Tyr Phe Lys Ile	
565 570	575
TCG CAA CTC ATC AAT CTT GAC GAT AAA GTT TCG CCC TTT AGA ATG CCA	1835
Ser Gln Leu Ile Asn Leu Asp Asp Lys Val Ser Pro Phe Arg Met Pro	
580 585 590	
CTA GAG AGC AAG ATC GGG TTT TCG CCC TTA ACG GGA TTG AAC ATC TTT	1883
Leu Glu Ser Lys Ile Gly Phe Ser Pro Leu Thr Gly Leu Asn Ile Phe	
595 600 605	
GGG AAT GTC TTT TAT TCG TTT TAT CAA AAC CGC TTA GAA GAA ATC TCT	1931
Gly Asn Val Phe Tyr Ser Phe Tyr Gln Asn Arg Leu Glu Glu Ile Ser	
610 615 620	
GTG AAC GCC AAT TAC CAA CGC AAG TTT TTA AGC TTT AAC CTC TCT TAT	1979
Val Asn Ala Asn Tyr Gln Arg Lys Phe Leu Ser Phe Asn Leu Ser Tyr	
625 630 635 640	
TTT TTA AAA AAC AAT TTT AGC AGT GGG ATT AAT AGC ATT GTA GAA AAT	2027
Phe Leu Lys Asn Asn Phe Ser Ser Gly Ile Asn Ser Ile Val Glu Asn	
645 650 655	
CTG CGG ATT ATT TAAAGGCGGG TTTTAGCAAC GACTTTGGCT ATTTTTCAT GAGCGC	2085
Leu Arg Ile Ile	
660	
GGATGTGGGT TATGATATTA GAAACAATGT GGTTTTAAAT TGGAATGTGG GGATTTATAA	2145
AAAAATCCGT TGTTTTGGGA TTGG	2169

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met	Ile	Tyr	Trp	Leu	Tyr	Leu	Ala	Val	Phe	Phe	Leu	Leu	Ser	Ala	Leu
1				5					10					15	
Asp	Ala	Lys	Glu	Ile	Ala	Met	Gln	Arg	Phe	Asp	Lys	Gln	Asn	His	Lys
			20					25					30		
Ile	Phe	Glu	Ile	Leu	Ala	Asp	Lys	Val	Ser	Ala	Lys	Asp	Asn	Val	Ile
		35					40					45			

Thr	Ala	Ser	Gly	Asn	Ala	Ile	Leu	Leu	Asn	Tyr	Asp	Val	Tyr	Ile	Leu
50						55					60				
Ala	Asp	Lys	Val	Arg	Tyr	Asp	Thr	Lys	Thr	Lys	Glu	Ala	Leu	Leu	Glu
65					70					75					80
Gly	Asn	Ile	Lys	Val	Tyr	Arg	Gly	Glu	Gly	Leu	Leu	Val	Lys	Thr	Asp
				85					90					95	
Tyr	Val	Lys	Leu	Ser	Leu	Asn	Glu	Lys	Tyr	Glu	Ile	Ile	Phe	Pro	Phe
			100					105					110		
Tyr	Val	Gln	Asp	Ser	Val	Ser	Gly	Ile	Trp	Val	Ser	Ala	Asp	Ile	Ala
		115					120					125			
Ser	Gly	Lys	Asp	Gln	Lys	Tyr	Lys	Val	Lys	Asn	Met	Ser	Thr	Ser	Gly
						135					140				
Cys	Ser	Ile	Asp	Asn	Pro	Ile	Trp	His	Val	Asn	Ala	Thr	Ser	Gly	Ser
145					150					155					160
Phe	Asn	Met	Gln	Lys	Ser	His	Leu	Ser	Met	Trp	Asn	Pro	Lys	Ile	Tyr
				165					170					175	
Val	Gly	Asp	Ile	Pro	Val	Leu	Tyr	Leu	Pro	Tyr	Ile	Phe	Met	Ser	Thr
			180					185					190		
Ser	Asn	Lys	Arg	Thr	Thr	Gly	Phe	Leu	Tyr	Pro	Glu	Phe	Gly	Thr	Ser
			195				200					205			
Asn	Leu	Asp	Gly	Phe	Ile	Tyr	Leu	Gln	Pro	Phe	Tyr	Leu	Ala	Pro	Lys
						215					220				
Asn	Ser	Trp	Asp	Met	Thr	Phe	Thr	Pro	Gln	Ile	Arg	Tyr	Lys	Arg	Gly
225					230					235					240
Phe	Gly	Leu	Asn	Phe	Glu	Ala	Arg	Tyr	Ile	Asn	Ser	Lys	Asn	Asp	Arg
				245					250					255	
Phe	Leu	Phe	Asn	Ala	Arg	Tyr	Phe	Arg	Asn	Tyr	Thr	Gln	Tyr	Val	Lys
			260					265					270		
Arg	Tyr	Asp	Leu	Arg	Asn	Gln	Asn	Ile	Tyr	Gly	Phe	Glu	Phe	Leu	Ser
			275				280					285			
Ser	Ser	Arg	Asp	Thr	Leu	Gln	Lys	Tyr	Phe	His	Leu	Lys	Ser	Asn	Ile
					295						300				
Asp	Asn	Gly	His	Tyr	Ile	Asp	Phe	Leu	Tyr	Met	Asn	Asp	Leu	Asp	Tyr
305					310					315					320
Val	Arg	Phe	Glu	Lys	Val	Asn	Lys	Arg	Ile	Thr	Asp	Ala	Thr	His	Met
				325					330					335	
Ser	Arg	Ala	Asn	Tyr	Tyr	Leu	Gln	Thr	Glu	Asn	Asn	Tyr	Tyr	Gly	Leu
			340					345					350		
Asn	Ile	Lys	Tyr	Phe	Leu	Asn	Leu	Asn	Lys	Ile	Asn	Asn	Asn	Arg	Thr
			355				360					365			
Phe	Gln	Ser	Val	Pro	Asn	Leu	Gln	Tyr	His	Lys	Tyr	Leu	Asn	Ser	Leu
						375					380				
Tyr	Phe	Arg	Asn	Leu	Leu	Tyr	Ser	Val	Asp	Tyr	Gln	Phe	Arg	Asn	Thr
385					390					395					400
Ala	Arg	Glu	Ile	Gly	Tyr	Gly	Tyr	Val	Gln	Asn	Ala	Leu	Asn	Val	Pro
				405					410					415	
Val	Gly	Leu	Gln	Phe	Ser	Leu	Phe	Lys	Lys	Tyr	Leu	Ser	Leu	Gly	Leu
			420					425					430		
Trp	Asn	Asp	Leu	Gln	Leu	Ser	Asn	Val	Ala	Leu	Met	Gln	Ser	Lys	Asn
							440					445			
Ser	Phe	Val	Pro	Thr	Ile	Pro	Asn	Glu	Ser	Arg	Glu	Phe	Gly	Asn	Phe
						455					460				
Val	Ser	Ser	Asn	Phe	Ser	Met	Tyr	Val	Asn	Thr	Asp	Leu	Ala	Arg	Glu
465					470					475					480
Tyr	Asn	Lys	Leu	Phe	His	Thr	Ile	Gln	Leu	Glu	Ala	Ile	Phe	Asn	Ile
				485					490					495	
Pro	Tyr	Tyr	Thr	Phe	Lys	Asn	Gly	Leu	Phe	Ser	Gln	Asn	Met	Tyr	Ala
			500					505					510		

Leu Ser Ala Gln Ala Leu Asn Ser Tyr Thr Ser Pro Leu Leu Arg Asp
 515 520 525
 Tyr Asp Tyr Gln Gly Arg Leu Tyr Asp Ser Val Trp Asn Pro Ser Ser
 530 535 540
 Ile Leu Pro Ser Asn Ala Ser Asn Lys Thr Val Asp Leu Thr Leu Thr
 545 550 555 560
 Gln Tyr Leu Tyr Gly Leu Gly Gly Gln Glu Leu Leu Tyr Phe Lys Ile
 565 570 575
 Ser Gln Leu Ile Asn Leu Asp Asp Lys Val Ser Pro Phe Arg Met Pro
 580 585 590
 Leu Glu Ser Lys Ile Gly Phe Ser Pro Leu Thr Gly Leu Asn Ile Phe
 595 600 605
 Gly Asn Val Phe Tyr Ser Phe Tyr Gln Asn Arg Leu Glu Glu Ile Ser
 610 615 620
 Val Asn Ala Asn Tyr Gln Arg Lys Phe Leu Ser Phe Asn Leu Ser Tyr
 625 630 635 640
 Phe Leu Lys Asn Asn Phe Ser Ser Gly Ile Asn Ser Ile Val Glu Asn
 645 650 655
 Leu Arg Ile Ile
 660

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...401
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TCAAGGTGTG CCAAACATGC CTTGAAACTC AATTTTGTAA TCTCAATTTT ATG AAA	56
Met Lys	
1	
GGA TTT GTT ATG AGT GGA TTA AAA GCA TTT AGT TGT GTA GTG GTT TTA	104
Gly Phe Val Met Ser Gly Leu Lys Ala Phe Ser Cys Val Val Val Leu	
5 10 15	
TGC GGT GCA ATG GCT AAT ACG GCT ATA GCT GGT CCT AAA ATA GAA GCA	152
Cys Gly Ala Met Ala Asn Thr Ala Ile Ala Gly Pro Lys Ile Glu Ala	
20 25 30	
AGG GGT GAG TTT GGC AGA TTT TGG GGG GGA GCT GTT GGT GGT GCA ATT	200
Arg Gly Glu Phe Gly Arg Phe Trp Gly Gly Ala Val Gly Gly Ala Ile	
35 40 45 50	
GGG GGT GGT GTT GGT GGT GCA GTG GGG GGA GCT GTT GGT GGT CCT GCG	248
Gly Gly Gly Val Gly Gly Ala Val Gly Gly Ala Val Gly Gly Pro Ala	

55	60	65	
GGT GGT TGG GCT GGC AGA TTA GTT GGT GGT TCT GTG GGG AGA GAG TTT			296
Gly Gly Trp Ala Gly Arg Leu Val Gly Gly Ser Val Gly Arg Glu Phe			
70	75	80	
GGT CGG GAA ATA GGC GAT AGG GTA GAA GAT TAC ATC CGT GGC GTT GAT			344
Gly Arg Glu Ile Gly Asp Arg Val Glu Asp Tyr Ile Arg Gly Val Asp			
85	90	95	
AGA GAG CCA CAA GCC CCA AGA GAA CCC ACC TAT GAT CGT CAT TTC GTG			392
Arg Glu Pro Gln Ala Pro Arg Glu Pro Thr Tyr Asp Arg His Phe Val			
100	105	110	
TAT GAC AGG TAGCTTTGGG CGAGAAAGGA GAGAGCATGA ATGTCAAAAA TCGTTTGAG			450
Tyr Asp Arg			
115			
CGAT			454

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Lys	Gly	Phe	Val	Met	Ser	Gly	Leu	Lys	Ala	Phe	Ser	Cys	Val	Val
1				5					10					15	
Val	Leu	Cys	Gly	Ala	Met	Ala	Asn	Thr	Ala	Ile	Ala	Gly	Pro	Lys	Ile
			20					25					30		
Glu	Ala	Arg	Gly	Glu	Phe	Gly	Arg	Phe	Trp	Gly	Gly	Ala	Val	Gly	Gly
		35					40					45			
Ala	Ile	Gly	Gly	Gly	Val	Gly	Gly	Ala	Val	Gly	Gly	Ala	Val	Gly	Gly
	50					55				60					
Pro	Ala	Gly	Gly	Trp	Ala	Gly	Arg	Leu	Val	Gly	Gly	Ser	Val	Gly	Arg
65					70				75					80	
Glu	Phe	Gly	Arg	Glu	Ile	Gly	Asp	Arg	Val	Glu	Asp	Tyr	Ile	Arg	Gly
			85						90					95	
Val	Asp	Arg	Glu	Pro	Gln	Ala	Pro	Arg	Glu	Pro	Thr	Tyr	Asp	Arg	His
			100					105					110		
Phe	Val	Tyr	Asp	Arg											
115															

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 856 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 59...802

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCCATTTTAA GCTAATATAA TATAGAGCGA TTATCAAAAA ATAAAGGGAA AAGACTGA	58
ATG TTG AAA AGA ATG ATA TTA TTA GGG GCT TTG GGT GTT TTA GCG AGC	106
Met Leu Lys Arg Met Ile Leu Leu Gly Ala Leu Gly Val Leu Ala Ser	
1 5 10 15	
GCT GAA GAG AGT GCG GCT TTT GTG GGA GTC AAT TAC CAG GTG AGC ATG	154
Ala Glu Glu Ser Ala Ala Phe Val Gly Val Asn Tyr Gln Val Ser Met	
20 25 30	
ATA CAA AAT CAG ACT AAA ATG GTG AAT GAC AAC GGC TTG CAA AAG CCT	202
Ile Gln Asn Gln Thr Lys Met Val Asn Asp Asn Gly Leu Gln Lys Pro	
35 40 45	
TTG ATA AAG TTT CCG CCT TAC GCA GGA GCG GGT TTT GAA GTG GGC TAT	250
Leu Ile Lys Phe Pro Pro Tyr Ala Gly Ala Gly Phe Glu Val Gly Tyr	
50 55 60	
AAG CAA TTT TTT GGT AAG AAA AAA TGG TTT GGC ATG CGT TAT TAT GGG	298
Lys Gln Phe Phe Gly Lys Lys Lys Trp Phe Gly Met Arg Tyr Tyr Gly	
65 70 75 80	
TTT TTT GAC TAC GCG CAC AAC CGC TTT GGC GTG ATG AAA AAG GGC ATT	346
Phe Phe Asp Tyr Ala His Asn Arg Phe Gly Val Met Lys Lys Gly Ile	
85 90 95	
CCG GTG GGC GAT AGT GGG TTT ATT TAC AAT AGT TTT AGT TTT GGA GGG	394
Pro Val Gly Asp Ser Gly Phe Ile Tyr Asn Ser Phe Ser Phe Gly Gly	
100 105 110	
AAC ACT TTA ACG GAA AGG GAT TCC TAT CAG GGC CAA TAC TAT GTC AAT	442
Asn Thr Leu Thr Glu Arg Asp Ser Tyr Gln Gly Gln Tyr Tyr Val Asn	
115 120 125	
TTA TTC ACT TAT GGC GTG GGG TTA GAT ACG CTG TGG AAT TTT GTG AAT	490
Leu Phe Thr Tyr Gly Val Gly Leu Asp Thr Leu Trp Asn Phe Val Asn	
130 135 140	
AAA GAA AAC ATG GTT TTT GGT TTT GTG GTG GGG ATC CAA TTA GCG GGG	538
Lys Glu Asn Met Val Phe Gly Phe Val Val Gly Ile Gln Leu Ala Gly	
145 150 155 160	
GAT AGT TGG GCA ACG AGC ATC AGT AAA GAA ATC GCT CAT TAT GCA AAA	586
Asp Ser Trp Ala Thr Ser Ile Ser Lys Glu Ile Ala His Tyr Ala Lys	
165 170 175	
CAC CAC AGC AAT TCC AGT TAT AGC CCG GCC AAT TTC CAG TTT TTA TGG	634

His His Ser Asn Ser Ser Tyr Ser Pro Ala Asn Phe Gln Phe Leu Trp
180 185 190

AAG TTT GGG GTC CGC ACC CAT ATC GCT AAA CAC AAT AGC CTA GAA TTA 682
Lys Phe Gly Val Arg Thr His Ile Ala Lys His Asn Ser Leu Glu Leu
195 200 205

GGG ATT AAA GTG CCT ACG ATC ACA CAC CAG CTT TTC TCT CTT ACC AAC 730
Gly Ile Lys Val Pro Thr Ile Thr His Gln Leu Phe Ser Leu Thr Asn
210 215 220

GAA AAG GGA TAC ACC TTA CAG GCT GAT GTG CGT AGA GTT TAT GCG TTT 778
Glu Lys Gly Tyr Thr Leu Gln Ala Asp Val Arg Arg Val Tyr Ala Phe
225 230 235 240

CAA ATC AGT TAC TTG AGG GAT TTT TAACCCCTTT TTAGATACAA TCACGCCTGA AA 834
Gln Ile Ser Tyr Leu Arg Asp Phe
245

CTATCCATTT AAAGGTGTGA AA 856

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Leu Lys Arg Met Ile Leu Leu Gly Ala Leu Gly Val Leu Ala Ser
1 5 10 15
Ala Glu Glu Ser Ala Ala Phe Val Gly Val Asn Tyr Gln Val Ser Met
20 25 30
Ile Gln Asn Gln Thr Lys Met Val Asn Asp Asn Gly Leu Gln Lys Pro
35 40 45
Leu Ile Lys Phe Pro Pro Tyr Ala Gly Ala Gly Phe Glu Val Gly Tyr
50 55 60
Lys Gln Phe Phe Gly Lys Lys Lys Trp Phe Gly Met Arg Tyr Tyr Gly
65 70 75 80
Phe Phe Asp Tyr Ala His Asn Arg Phe Gly Val Met Lys Lys Gly Ile
85 90 95
Pro Val Gly Asp Ser Gly Phe Ile Tyr Asn Ser Phe Ser Phe Gly Gly
100 105 110
Asn Thr Leu Thr Glu Arg Asp Ser Tyr Gln Gly Gln Tyr Tyr Val Asn
115 120 125
Leu Phe Thr Tyr Gly Val Gly Leu Asp Thr Leu Trp Asn Phe Val Asn
130 135 140
Lys Glu Asn Met Val Phe Gly Phe Val Val Gly Ile Gln Leu Ala Gly
145 150 155 160
Asp Ser Trp Ala Thr Ser Ile Ser Lys Glu Ile Ala His Tyr Ala Lys
165 170 175
His His Ser Asn Ser Ser Tyr Ser Pro Ala Asn Phe Gln Phe Leu Trp

AAC ACC GTG ATC GAT CCT AAC ATG ATT AAA GAA GTG GAA GTG ATC AAG Asn Thr Val Ile Asp Pro Asn Met Ile Lys Glu Val Glu Val Ile Lys 115 120 125	446
GGG GCG GCG AAC GCT TCA GCA GGC CCA GGT GCG GTG GCG GGT AAA TTG Gly Ala Ala Asn Ala Ser Ala Gly Pro Gly Ala Val Ala Gly Lys Leu 130 135 140	494
TCT TTC ACC ACG ATT GAC GCT AAC GAC TTC TTA AGA AAG AAT CAA ACT Ser Phe Thr Thr Ile Asp Ala Asn Asp Phe Leu Arg Lys Asn Gln Thr 145 150 155	542
TAT GGC GCT AAA GCG GAA GCG GCC TTT TAT ACC AAC TTC GGG TAT CGC Tyr Gly Ala Lys Ala Glu Ala Ala Phe Tyr Thr Asn Phe Gly Tyr Arg 160 165 170	590
ATG AAC GCC ACT GCG GCT TAC CGG GGG AAA AAC TGG GAC ATC CTA GCC Met Asn Ala Thr Ala Ala Tyr Arg Gly Lys Asn Trp Asp Ile Leu Ala 175 180 185 190	638
TAT TAC AAC CAT CAA AAT ATT TTT TAC TAC AGA GAC GGG AAC AAC GCT Tyr Tyr Asn His Gln Asn Ile Phe Tyr Tyr Arg Asp Gly Asn Asn Ala 195 200 205	686
TTT AGG AAT GTC TTC CAC CCT AAC TAC GAT TTA CAA GAT CCA AGC AAT Phe Arg Asn Val Phe His Pro Asn Tyr Asp Leu Gln Asp Pro Ser Asn 210 215 220	734
AGC GAT ATG AGC GTA GGG ACT CCC AGT GAA GTC AAT AGC GTT TTA GCT Ser Asp Met Ser Val Gly Thr Pro Ser Glu Val Asn Ser Val Leu Ala 225 230 235	782
AAA ATT AAT GGC TAT ATC AAC GAA ACA GAC AGC ATT AGC GTG AGC TAC Lys Ile Asn Gly Tyr Ile Asn Glu Thr Asp Ser Ile Ser Val Ser Tyr 240 245 250	830
AAC CTC ACA CGA GAC AAT TCT ACA AGG CTT TTA CGC CCT AAC ACC ACT Asn Leu Thr Arg Asp Asn Ser Thr Arg Leu Leu Arg Pro Asn Thr Thr 255 260 265 270	878
TCA GCC CTC TCT AAA GCC AAT GAC CCA GGA AGC CAG CCA GCC CCC TTT Ser Ala Leu Ser Lys Ala Asn Asp Pro Gly Ser Gln Pro Ala Pro Phe 275 280 285	926
GTG ATT GAC TTT GGG AAA GAA TTA GCC CAT ACG ATC AAC TTC AAC CAC Val Ile Asp Phe Gly Lys Glu Leu Ala His Thr Ile Asn Phe Asn His 290 295 300	974
AAT TTG AGC TTG AAA TAC AAG CAT GAA GGC GGC CCT AAT TTT AAC CAG Asn Leu Ser Leu Lys Tyr Lys His Glu Gly Gly Pro Asn Phe Asn Gln 305 310 315	1022
CCG CGC GTT GAA TCC ACC GCC TTT TTA GGG GTA AGG GGG GGC AAT TAT Pro Arg Val Glu Ser Thr Ala Phe Leu Gly Val Arg Gly Gly Asn Tyr 320 325 330	1070
AAC CCT GTG GTG AAT CCT TTC GCT TAC AAT TCT AAC GAG CCG GCT AAC Asn Pro Val Val Asn Pro Phe Ala Tyr Asn Ser Asn Glu Pro Ala Asn	1118

335	340	345	350	
CCA GAT TAT ATC CCT GAA GTG AAA GAG TGG TGT AAT AAC CCA GAT AAT	Pro Asp Tyr Ile Pro Glu Val Lys Glu Trp Cys Asn Asn Pro Asp Asn			1166
	355	360	365	
ATC AGC CAG TGC ACG CAA GGG GCT ATC AGG CCT TCT AAT GGA GGC TAT	Ile Ser Gln Cys Thr Gln Gly Ala Ile Arg Pro Ser Asn Gly Gly Tyr			1214
	370	375	380	
CAA ATA GGC TAT GGC ACG CCT AAT TCT ATT AAT TGG CAA GGG ACT AGC	Gln Ile Gly Tyr Gly Thr Pro Asn Ser Ile Asn Trp Gln Gly Thr Ser			1262
	385	390	395	
GAT TCT AGT GGA GGG GCG CAA GCA GGG TAT GGG CAG CTT AAC GCT ATT	Asp Ser Ser Gly Gly Ala Gln Ala Gly Tyr Gly Gln Leu Asn Ala Ile			1310
	400	405	410	
TCT ACA AGC GCG AAC GTT TAT CAT GGG CTT GTC CCT AAA AAT CCT GAT	Ser Thr Ser Ala Asn Val Tyr His Gly Leu Val Pro Lys Asn Pro Asp			1358
	415	420	425	430
TAT GAC ATG ACC CCC CCT AAC GCT CAA AAC CCT AGC GCA AAC GAT TGG	Tyr Asp Met Thr Pro Pro Asn Ala Gln Asn Pro Ser Ala Asn Asp Trp			1406
	435	440	445	
ACT TTA GGG AAT GCG GAC GCT GAG GGG ACT TTA GCC AGA AGG ATT TTT	Thr Leu Gly Asn Ala Asp Ala Glu Gly Thr Leu Ala Arg Arg Ile Phe			1454
	450	455	460	
TTA ATC AAC TCG GGC GTT AAT TTT AAA GTA ACC CAC CCC ATT AGC GAA	Leu Ile Asn Ser Gly Val Asn Phe Lys Val Thr His Pro Ile Ser Glu			1502
	465	470	475	
GAT TAT GGG AAT GTG TTT GAA TAC GGC ATG ATT TAT CAA AAC CTG AGC	Asp Tyr Gly Asn Val Phe Glu Tyr Gly Met Ile Tyr Gln Asn Leu Ser			1550
	480	485	490	
GTT TTC TCT GGA TTG GAT AAA GGC AAA AAC GGC TAT TAT AAA AAC AAC	Val Phe Ser Gly Leu Asp Lys Gly Lys Asn Gly Tyr Tyr Lys Asn Asn			1598
	495	500	505	510
ATT GAT CCT AAC GAC CCT AAC GGG CCG GGC TTG CCT TAC CGC CAT TAC	Ile Asp Pro Asn Asp Pro Asn Gly Pro Gly Leu Pro Tyr Arg His Tyr			1646
	515	520	525	
TAC ACC GAT CAA AGC TCC CAA TAC CCC CAA AAT CTC AAC ACC CCT AAC	Tyr Thr Asp Gln Ser Ser Gln Tyr Pro Gln Asn Leu Asn Thr Pro Asn			1694
	530	535	540	
CCG CTC TAT CGT AAC ATG CCC CAA AAT TCG CAT GCG ATC GGC AAT ATC	Pro Leu Tyr Arg Asn Met Pro Gln Asn Ser His Ala Ile Gly Asn Ile			1742
	545	550	555	
ATC GGA GGG TTT ATG CAA GCA AAC TAC AAC ATT TTA AGC AAT GTG ATC	Ile Gly Gly Phe Met Gln Ala Asn Tyr Asn Ile Leu Ser Asn Val Ile			1790
	560	565	570	

GTG	GGT	GCG	GGA	ACT	CGT	TAT	GAT	ATT	TAC	ACC	TTG	CTA	GAC	AAA	AAC	1838
Val	Gly	Ala	Gly	Thr	Arg	Tyr	Asp	Ile	Tyr	Thr	Leu	Leu	Asp	Lys	Asn	
575					580					585					590	
GGC	CGC	ACG	CAT	GTA	ACT	TCT	GGT	TTC	TCG	CCT	TCT	GCA	ACC	GTG	CTT	1886
Gly	Arg	Thr	His	Val	Thr	Ser	Gly	Phe	Ser	Pro	Ser	Ala	Thr	Val	Leu	
				595					600					605		
TAT	AAC	CCC	ATT	GAA	AGC	ATT	GGC	TTG	AAA	GTG	AGT	TAT	GCG	TAT	GTA	1934
Tyr	Asn	Pro	Ile	Glu	Ser	Ile	Gly	Leu	Lys	Val	Ser	Tyr	Ala	Tyr	Val	
			610					615					620			
ACT	AAG	GGG	GCT	TTG	CCT	GGC	GAT	GGC	GTT	TTG	ATG	CGC	GAT	CCT	ACG	1982
Thr	Lys	Gly	Ala	Leu	Pro	Gly	Asp	Gly	Val	Leu	Met	Arg	Asp	Pro	Thr	
		625					630					635				
GTG	ATT	TAT	CAA	AGG	AAT	TTG	CGC	CCT	GCG	ATC	GGT	CAA	AAT	GTG	GAA	2030
Val	Ile	Tyr	Gln	Arg	Asn	Leu	Arg	Pro	Ala	Ile	Gly	Gln	Asn	Val	Glu	
	640					645					650					
TTT	AAT	GTG	GAT	TTC	AAC	AGC	AAG	TAT	TTC	AAT	GTG	CGC	GGG	GCA	GCG	2078
Phe	Asn	Val	Asp	Phe	Asn	Ser	Lys	Tyr	Phe	Asn	Val	Arg	Gly	Ala	Ala	
655					660					665					670	
TTC	TAT	CAA	GTC	ATC	AAT	AAT	TTC	ATC	AAC	AGC	TAC	GGG	CAA	GAC	ACT	2126
Phe	Tyr	Gln	Val	Ile	Asn	Asn	Phe	Ile	Asn	Ser	Tyr	Gly	Gln	Asp	Thr	
				675					680					685		
TCT	AAA	AAT	GGA	GGG	GGT	AAC	GCA	ACC	GCA	AAA	AAC	ATG	TCA	GGG	AAT	2174
Ser	Lys	Asn	Gly	Gly	Gly	Asn	Ala	Thr	Ala	Lys	Asn	Met	Ser	Gly	Asn	
			690					695					700			
TTA	CCC	GAA	ACC	ATT	AAC	ATT	TAT	GGT	TAT	GAA	GTT	TCA	GGG	AAT	GTG	2222
Leu	Pro	Glu	Thr	Ile	Asn	Ile	Tyr	Gly	Tyr	Glu	Val	Ser	Gly	Asn	Val	
		705					710					715				
AGG	TAT	AAG	AAT	TTC	TTA	GGG	ACT	TTC	TCA	GTG	GCT	CGC	TCT	TGG	CCA	2270
Arg	Tyr	Lys	Asn	Phe	Leu	Gly	Thr	Phe	Ser	Val	Ala	Arg	Ser	Trp	Pro	
	720					725					730					
ACG	GCT	AGG	GGG	CAT	TTA	TTA	GCG	GAC	ACT	TAC	GCT	CTA	GCT	GCA	ACG	2318
Thr	Ala	Arg	Gly	His	Leu	Leu	Ala	Asp	Thr	Tyr	Ala	Leu	Ala	Ala	Thr	
735					740					745					750	
ACT	GGG	AAT	GTG	TTT	ATT	TTA	AAA	GCC	GAT	TAT	GAT	GTT	CGC	AGG	TGG	2366
Thr	Gly	Asn	Val	Phe	Ile	Leu	Lys	Ala	Asp	Tyr	Asp	Val	Arg	Arg	Trp	
				755					760					765		
GGG	CTT	ACT	TTA	ACC	TGG	CTC	TCG	CGC	TTT	GTA	ACT	AAC	ATG	TAT	TAT	2414
Gly	Leu	Thr	Leu	Thr	Trp	Leu	Ser	Arg	Phe	Val	Thr	Asn	Met	Tyr	Tyr	
			770					775					780			
GAG	GGC	TAT	TCT	ATC	TAT	TAC	CCG	CAA	TAC	GGC	TTG	ATC	AAA	ATC	CAT	2462
Glu	Gly	Tyr	Ser	Ile	Tyr	Tyr	Pro	Gln	Tyr	Gly	Leu	Ile	Lys	Ile	His	
		785					790					795				
AAA	CCC	GGG	TAT	GGC	GTG	CAT	AAT	GTC	TTT	ATC	AAC	TGG	ACT	CCG	CCT	2510
Lys	Pro	Gly	Tyr	Gly	Val	His	Asn	Val	Phe	Ile	Asn	Trp	Thr	Pro	Pro	

800	805	810	
TCT AAA AAA TGG CAG GGT TTA AGG ATT TCA GCC GTG TTT AAT AAT ATC			2558
Ser Lys Lys Trp Gln Gly Leu Arg Ile Ser Ala Val Phe Asn Asn Ile			
815	820	825 830	
TTA AAC AAG CAA TAT GTG GAT CAA ACT TCT GTG TTT CAA GCG AGC GCG			2606
Leu Asn Lys Gln Tyr Val Asp Gln Thr Ser Val Phe Gln Ala Ser Ala			
	835	840 845	
GAC GCT CCA GCG AGC GAT ATG ATC CCT AAA GGT AAG CGC ATG GCG CTC			2654
Asp Ala Pro Ala Ser Asp Met Ile Pro Lys Gly Lys Arg Met Ala Leu			
	850	855 860	
CCG GCT CCT GGA TTT AAC GCG CGT TTT GAG GTA TCC TAT CAG TTC TAAAA			2704
Pro Ala Pro Gly Phe Asn Ala Arg Phe Glu Val Ser Tyr Gln Phe			
	865	870 875	
TGAAAGGAAT CTTAGGATTT CTTTTTGAAT TTTGAACATG GAAACA			2750

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 877 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met	Leu	Arg	Asn	Gln	Phe	Arg	Ile	Val	Phe	Val	Ser	Cys	Ile	Val	Ala
1				5					10					15	
Ser	Asn	Leu	Gln	Ala	Gln	Glu	Thr	Thr	His	Thr	Leu	Gly	Lys	Val	Thr
			20					25					30		
Thr	Lys	Gly	Glu	Arg	Thr	Phe	Glu	Tyr	Asn	Asn	Lys	Met	Tyr	Ile	Asp
		35					40					45			
Arg	Lys	Glu	Leu	Gln	Gln	Arg	Gln	Ser	Asn	Gln	Ile	Arg	Asp	Ile	Phe
	50				55					60					
Arg	Thr	Arg	Ala	Asp	Val	Asn	Val	Ala	Ser	Gly	Gly	Leu	Met	Ala	Gln
65				70					75					80	
Lys	Ile	Tyr	Val	Arg	Gly	Ile	Glu	Ser	Arg	Leu	Leu	Arg	Val	Thr	Ile
			85					90					95		
Asp	Gly	Val	Ala	Gln	Asn	Gly	Asn	Ile	Phe	His	His	Asp	Ala	Asn	Thr
			100					105					110		
Val	Ile	Asp	Pro	Asn	Met	Ile	Lys	Glu	Val	Glu	Val	Ile	Lys	Gly	Ala
		115					120					125			
Ala	Asn	Ala	Ser	Ala	Gly	Pro	Gly	Ala	Val	Ala	Gly	Lys	Leu	Ser	Phe
		130				135					140				
Thr	Thr	Ile	Asp	Ala	Asn	Asp	Phe	Leu	Arg	Lys	Asn	Gln	Thr	Tyr	Gly
145				150					155					160	
Ala	Lys	Ala	Glu	Ala	Phe	Tyr	Thr	Asn	Phe	Gly	Tyr	Arg	Met	Asn	
			165					170					175		
Ala	Thr	Ala	Ala	Tyr	Arg	Gly	Lys	Asn	Trp	Asp	Ile	Leu	Ala	Tyr	Tyr
		180					185					190			
Asn	His	Gln	Asn	Ile	Phe	Tyr	Tyr	Arg	Asp	Gly	Asn	Asn	Ala	Phe	Arg

195	200	205
Asn Val Phe His Pro Asn Tyr Asp Leu Gln Asp Pro Ser Asn Ser Asp		
210	215	220
Met Ser Val Gly Thr Pro Ser Glu Val Asn Ser Val Leu Ala Lys Ile		
225	230	235
Asn Gly Tyr Ile Asn Glu Thr Asp Ser Ile Ser Val Ser Tyr Asn Leu		240
	245	250
Thr Arg Asp Asn Ser Thr Arg Leu Leu Arg Pro Asn Thr Thr Ser Ala		255
	260	265
Leu Ser Lys Ala Asn Asp Pro Gly Ser Gln Pro Ala Pro Phe Val Ile		270
	275	280
Asp Phe Gly Lys Glu Leu Ala His Thr Ile Asn Phe Asn His Asn Leu		285
	290	295
Ser Leu Lys Tyr Lys His Glu Gly Gly Pro Asn Phe Asn Gln Pro Arg		300
305	310	315
Val Glu Ser Thr Ala Phe Leu Gly Val Arg Gly Gly Asn Tyr Asn Pro		320
	325	330
Val Val Asn Pro Phe Ala Tyr Asn Ser Asn Glu Pro Ala Asn Pro Asp		335
	340	345
Tyr Ile Pro Glu Val Lys Glu Trp Cys Asn Asn Pro Asp Asn Ile Ser		350
	355	360
Gln Cys Thr Gln Gly Ala Ile Arg Pro Ser Asn Gly Gly Tyr Gln Ile		365
	370	375
Gly Tyr Gly Thr Pro Asn Ser Ile Asn Trp Gln Gly Thr Ser Asp Ser		380
385	390	395
Ser Gly Gly Ala Gln Ala Gly Tyr Gly Gln Leu Asn Ala Ile Ser Thr		400
	405	410
Ser Ala Asn Val Tyr His Gly Leu Val Pro Lys Asn Pro Asp Tyr Asp		415
	420	425
Met Thr Pro Pro Asn Ala Gln Asn Pro Ser Ala Asn Asp Trp Thr Leu		430
	435	440
Gly Asn Ala Asp Ala Glu Gly Thr Leu Ala Arg Arg Ile Phe Leu Ile		445
	450	455
Asn Ser Gly Val Asn Phe Lys Val Thr His Pro Ile Ser Glu Asp Tyr		460
465	470	475
Gly Asn Val Phe Glu Tyr Gly Met Ile Tyr Gln Asn Leu Ser Val Phe		480
	485	490
Ser Gly Leu Asp Lys Gly Lys Asn Gly Tyr Tyr Lys Asn Asn Ile Asp		495
	500	505
Pro Asn Asp Pro Asn Gly Pro Gly Leu Pro Tyr Arg His Tyr Tyr Thr		510
	515	520
Asp Gln Ser Ser Gln Tyr Pro Gln Asn Leu Asn Thr Pro Asn Pro Leu		525
	530	535
Tyr Arg Asn Met Pro Gln Asn Ser His Ala Ile Gly Asn Ile Ile Gly		540
545	550	555
Gly Phe Met Gln Ala Asn Tyr Asn Ile Leu Ser Asn Val Ile Val Gly		560
	565	570
Ala Gly Thr Arg Tyr Asp Ile Tyr Thr Leu Leu Asp Lys Asn Gly Arg		575
	580	585
Thr His Val Thr Ser Gly Phe Ser Pro Ser Ala Thr Val Leu Tyr Asn		590
	595	600
Pro Ile Glu Ser Ile Gly Leu Lys Val Ser Tyr Ala Tyr Val Thr Lys		605
	610	615
Gly Ala Leu Pro Gly Asp Gly Val Leu Met Arg Asp Pro Thr Val Ile		620
625	630	635
Tyr Gln Arg Asn Leu Arg Pro Ala Ile Gly Gln Asn Val Glu Phe Asn		640
	645	650
Val Asp Phe Asn Ser Lys Tyr Phe Asn Val Arg Gly Ala Ala Phe Tyr		655

										660			665			670		
Gln	Val	Ile	Asn	Asn	Phe	Ile	Asn	Ser	Tyr	Gly	Gln	Asp	Thr	Ser	Lys			
		675					680					685						
Asn	Gly	Gly	Gly	Asn	Ala	Thr	Ala	Lys	Asn	Met	Ser	Gly	Asn	Leu	Pro			
		690					695					700						
Glu	Thr	Ile	Asn	Ile	Tyr	Gly	Tyr	Glu	Val	Ser	Gly	Asn	Val	Arg	Tyr			
705					710					715					720			
Lys	Asn	Phe	Leu	Gly	Thr	Phe	Ser	Val	Ala	Arg	Ser	Trp	Pro	Thr	Ala			
				725					730					735				
Arg	Gly	His	Leu	Leu	Ala	Asp	Thr	Tyr	Ala	Leu	Ala	Ala	Thr	Thr	Gly			
				740					745					750				
Asn	Val	Phe	Ile	Leu	Lys	Ala	Asp	Tyr	Asp	Val	Arg	Arg	Trp	Gly	Leu			
				755					760					765				
Thr	Leu	Thr	Trp	Leu	Ser	Arg	Phe	Val	Thr	Asn	Met	Tyr	Tyr	Glu	Gly			
						775					780							
Tyr	Ser	Ile	Tyr	Tyr	Pro	Gln	Tyr	Gly	Leu	Ile	Lys	Ile	His	Lys	Pro			
785					790					795					800			
Gly	Tyr	Gly	Val	His	Asn	Val	Phe	Ile	Asn	Trp	Thr	Pro	Pro	Ser	Lys			
				805					810					815				
Lys	Trp	Gln	Gly	Leu	Arg	Ile	Ser	Ala	Val	Phe	Asn	Asn	Ile	Leu	Asn			
				820					825					830				
Lys	Gln	Tyr	Val	Asp	Gln	Thr	Ser	Val	Phe	Gln	Ala	Ser	Ala	Asp	Ala			
						840					845							
Pro	Ala	Ser	Asp	Met	Ile	Pro	Lys	Gly	Lys	Arg	Met	Ala	Leu	Pro	Ala			
						855					860							
Pro	Gly	Phe	Asn	Ala	Arg	Phe	Glu	Val	Ser	Tyr	Gln	Phe						
865					870					875								

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...317
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTTAAAATCA	CCCGTTACAG	CATCACTGAA	ATCACTAATA	GGGGTGATTG	ATG CGT		56
					Met Arg		
					1		
AAG GTT TTA TAC GCT CTT GTG GGC TTT TTG TTG GCT TTT AGC GCT TTA							104
Lys Val Leu Tyr Ala Leu Val Gly Phe Leu Leu Ala Phe Ser Ala Leu							
	5					15	
AAA GCC GAT GAT TTT TTA GAA GAA GCG AAC GAA ACA GCC CCG GCG CAT							152
Lys Ala Asp Asp Phe Leu Glu Glu Ala Asn Glu Thr Ala Pro Ala His							
	20				25	30	

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TTA AAC CAC CCT ATG CAG GAT TTA AAC GCC ATT CAA GGG AGC TTT TTT      200
Leu Asn His Pro Met Gln Asp Leu Asn Ala Ile Gln Gly Ser Phe Phe
 35                      40                      45                      50

GAC AAA AAC CGC TCA AAA ATG TCC AAC ACT TTG AAC ATT GAT TAC TTT      248
Asp Lys Asn Arg Ser Lys Met Ser Asn Thr Leu Asn Ile Asp Tyr Phe
                    55                      60                      65

CAA GGG CAA ACT TAT AAA ATC CCG CTT GCG TTA TGC GAT GGC GGC CTT      296
Gln Gly Gln Thr Tyr Lys Ile Pro Leu Ala Leu Cys Asp Gly Xaa Leu
                    70                      75                      80

ATT GTT TTT TTC AAA ACC CAT TAGCGATTTT GTTTTAGGGG ATAAGGTGGG TTTT      351
Ile Val Phe Phe Lys Thr His
                    85

GATGCGAAAA TTTTAGAAA                                              370

```

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

Met Arg Lys Val Leu Tyr Ala Leu Val Gly Phe Leu Leu Ala Phe Ser
 1                      5                      10                      15
Ala Leu Lys Ala Asp Asp Phe Leu Glu Glu Ala Asn Glu Thr Ala Pro
                    20                      25                      30
Ala His Leu Asn His Pro Met Gln Asp Leu Asn Ala Ile Gln Gly Ser
                    35                      40                      45
Phe Phe Asp Lys Asn Arg Ser Lys Met Ser Asn Thr Leu Asn Ile Asp
                    50                      55                      60
Tyr Phe Gln Gly Gln Thr Tyr Lys Ile Pro Leu Ala Leu Cys Asp Gly
                    65                      70                      75                      80
Xaa Leu Ile Val Phe Phe Lys Thr His
                    85

```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...305
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGCAATAAA AAAAGAAATT CTTAGGATTT CTCACATTAA GGAGTTTAA ATG AAA 56
Met Lys
1

AAG GTT TTT TTA GGT ATG GCA TTA GCC TTT AGT GTG TCC ATG GCA GAA 104
Lys Val Phe Leu Gly Met Ala Leu Ala Phe Ser Val Ser Met Ala Glu
5 10 15

AAA AGT GGC GCG TTT TTA GGA GGG GGG TTT CAA TAT TCT AAT TTA GAA 152
Lys Ser Gly Ala Phe Leu Gly Gly Gly Phe Gln Tyr Ser Asn Leu Glu
20 25 30

AAC CAA AAC ACC ACC CGC ACC CCA GGC GCT AAC AAT AAC ACC CCG ATA 200
Asn Gln Asn Thr Thr Arg Thr Pro Gly Ala Asn Asn Asn Thr Pro Ile
35 40 45 50

GAC ACT TCA ATG TTT GGC AGC AAC AAA ACA GCT CCA GCC CAA GAA ACG 248
Asp Thr Ser Met Phe Gly Ser Asn Lys Thr Ala Pro Ala Gln Glu Thr
55 60 65

CAA AGC GCT TCC AAA CCG GAC ACT AAA GTC AAT CCA AGC GCA AGT TGG 296
Gln Ser Ala Ser Lys Pro Asp Thr Lys Val Asn Pro Ser Ala Ser Trp
70 75 80

ATG AAA AAA TAAGAAGGAA GTTATGAAAA AGTCATTCAA AAAATTAGGC TTTGTCTCT 354
Met Lys Lys
85

TTA 357

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Lys Lys Val Phe Leu Gly Met Ala Leu Ala Phe Ser Val Ser Met
1 5 10 15
Ala Glu Lys Ser Gly Ala Phe Leu Gly Gly Gly Phe Gln Tyr Ser Asn
20 25 30
Leu Glu Asn Gln Asn Thr Thr Arg Thr Pro Gly Ala Asn Asn Asn Thr
35 40 45
Pro Ile Asp Thr Ser Met Phe Gly Ser Asn Lys Thr Ala Pro Ala Gln
50 55 60
Glu Thr Gln Ser Ala Ser Lys Pro Asp Thr Lys Val Asn Pro Ser Ala
65 70 75 80
Ser Trp Met Lys Lys

85

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 961 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...908
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GAATGTAGCA TTTAGAACTC AAGTAGAGAA AATGTAGAAG GAAGGAATAC ATG AAG	56
Met Lys	
1	
AAA TCT GTT ATA GTA GGT GCT ATC TCT CTA GCA ATG ACA AGC TTA TTG	104
Lys Ser Val Ile Val Gly Ala Ile Ser Leu Ala Met Thr Ser Leu Leu	
5 10 15	
TCA GCA GAG ACC CCT AAG CAA GAA AAA GCT ATT AAG ACT AGC CCT ACC	152
Ser Ala Glu Thr Pro Lys Gln Glu Lys Ala Ile Lys Thr Ser Pro Thr	
20 25 30	
AAA AAA GGT GAA AGA AAT GCT GCT TTT ATA GGG ATT GAT TAC CAG TTG	200
Lys Lys Gly Glu Arg Asn Ala Ala Phe Ile Gly Ile Asp Tyr Gln Leu	
35 40 45 50	
GGT ATG CTC AGC ACT ACC GCT CAA AAT TGT TCC CAT GGG AAT TGC AAT	248
Gly Met Leu Ser Thr Thr Ala Gln Asn Cys Ser His Gly Asn Cys Asn	
55 60 65	
GGT AAT CAA AGT GGG GCT TAC GGC TCT AAT ACG CCT AAC ATG CCT ACA	296
Gly Asn Gln Ser Gly Ala Tyr Gly Ser Asn Thr Pro Asn Met Pro Thr	
70 75 80	
GCG TCA AAC CCA ACA GGA GGG TTT ACT CAT GGC GCT CTA GGG ACT CGT	344
Ala Ser Asn Pro Thr Gly Gly Phe Thr His Gly Ala Leu Gly Thr Arg	
85 90 95	
GGG TAT AAA GGC TTA AGC AAC CAA CAA TAC GCT ATC AAT GGT TTT GGT	392
Gly Tyr Lys Gly Leu Ser Asn Gln Gln Tyr Ala Ile Asn Gly Phe Gly	
100 105 110	
TTT GTT GTA GGG TAT AAG CAT TTT TTC AAG AAA TCC CCG CAA TTT GGA	440
Phe Val Val Gly Tyr Lys His Phe Phe Lys Lys Ser Pro Gln Phe Gly	
115 120 125 130	
ATG CGT TAT TAC GGA TTC TTT GAT TTT GCA AGC TCT TAT TAT AAG TAT	488

Met	Arg	Tyr	Tyr	Gly	Phe	Phe	Asp	Phe	Ala	Ser	Ser	Tyr	Tyr	Lys	Tyr	
				135					140					145		
TAC	ACT	TAT	AAT	GAT	TAT	GGC	ATG	AGA	GAC	GCT	CGC	AAG	GGT	TCT	CAA	536
Tyr	Thr	Tyr	Asn	Asp	Tyr	Gly	Met	Arg	Asp	Ala	Arg	Lys	Gly	Ser	Gln	
			150					155					160			
AGT	TTC	ATG	TTT	GGC	TAT	GGG	GCT	GGC	ACA	GAT	GTG	TTG	TTT	AAC	CCG	584
Ser	Phe	Met	Phe	Gly	Tyr	Gly	Ala	Gly	Thr	Asp	Val	Leu	Phe	Asn	Pro	
		165					170					175				
GCT	ATT	TTC	AAT	CGT	GAG	AAC	TTG	CAT	TTT	GGG	TTT	TTC	TTG	GGC	GTT	632
Ala	Ile	Phe	Asn	Arg	Glu	Asn	Leu	His	Phe	Gly	Phe	Phe	Leu	Gly	Val	
	180					185				190						
GCG	ATC	GGT	GGC	ACC	TCT	TGG	GGT	CCA	ACA	AAC	TAT	TAT	TTT	AAG	GAC	680
Ala	Ile	Gly	Gly	Thr	Ser	Trp	Gly	Pro	Thr	Asn	Tyr	Tyr	Phe	Lys	Asp	
195					200					205					210	
TTG	GCT	GAT	GAG	TAT	AGA	GGG	AGT	TTC	CAC	CCA	TCA	AAT	TTC	CAG	GTC	728
Leu	Ala	Asp	Glu	Tyr	Arg	Gly	Ser	Phe	His	Pro	Ser	Asn	Phe	Gln	Val	
			215					220						225		
TTA	GTT	AAT	GGT	GGG	ATT	CGC	TTA	GGC	ACT	AAA	CAC	CAA	GGT	TTT	GAA	776
Leu	Val	Asn	Gly	Gly	Ile	Arg	Leu	Gly	Thr	Lys	His	Gln	Gly	Phe	Glu	
		230						235					240			
ATT	GGC	TTG	AAA	ATC	CAA	ACC	ATC	CGC	AAC	AAT	TAC	TAC	ACC	GCT	AGT	824
Ile	Gly	Leu	Lys	Ile	Gln	Thr	Ile	Arg	Asn	Asn	Tyr	Tyr	Thr	Ala	Ser	
		245					250					255				
GCG	GAT	AAT	GTG	CCT	GAA	GGG	ACT	ACT	TAT	AGA	TTC	ACT	TTC	CAC	CGC	872
Ala	Asp	Asn	Val	Pro	Glu	Gly	Thr	Thr	Tyr	Arg	Phe	Thr	Phe	His	Arg	
	260					265					270					
CCC	TAT	GCC	TTT	TAT	TGG	CGT	TAC	ATT	GTA	AGC	TTT	TAAGGTGTTT	TAGGGC			924
Pro	Tyr	Ala	Phe	Tyr	Trp	Arg	Tyr	Ile	Val	Ser	Phe					
275					280					285						
TAATCTTATG	GGGGCATAGA	AAAGGGCTTT	TGCTCTT													961

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met	Lys	Lys	Ser	Val	Ile	Val	Gly	Ala	Ile	Ser	Leu	Ala	Met	Thr	Ser	
1				5				10						15		
Leu	Leu	Ser	Ala	Glu	Thr	Pro	Lys	Gln	Glu	Lys	Ala	Ile	Lys	Thr	Ser	
			20					25					30			

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Pro Thr Lys Lys Gly Glu Arg Asn Ala Ala Phe Ile Gly Ile Asp Tyr
   35                               40                               45
Gln Leu Gly Met Leu Ser Thr Thr Ala Gln Asn Cys Ser His Gly Asn
   50                               55                               60
Cys Asn Gly Asn Gln Ser Gly Ala Tyr Gly Ser Asn Thr Pro Asn Met
   65                               70                               75                               80
Pro Thr Ala Ser Asn Pro Thr Gly Gly Phe Thr His Gly Ala Leu Gly
   85                               90                               95
Thr Arg Gly Tyr Lys Gly Leu Ser Asn Gln Gln Tyr Ala Ile Asn Gly
  100                               105                               110
Phe Gly Phe Val Val Gly Tyr Lys His Phe Phe Lys Lys Ser Pro Gln
  115                               120                               125
Phe Gly Met Arg Tyr Tyr Gly Phe Phe Asp Phe Ala Ser Ser Tyr Tyr
  130                               135                               140
Lys Tyr Tyr Thr Tyr Asn Asp Tyr Gly Met Arg Asp Ala Arg Lys Gly
  145                               150                               155                               160
Ser Gln Ser Phe Met Phe Gly Tyr Gly Ala Gly Thr Asp Val Leu Phe
  165                               170                               175
Asn Pro Ala Ile Phe Asn Arg Glu Asn Leu His Phe Gly Phe Phe Leu
  180                               185                               190
Gly Val Ala Ile Gly Gly Thr Ser Trp Gly Pro Thr Asn Tyr Tyr Phe
  195                               200                               205
Lys Asp Leu Ala Asp Glu Tyr Arg Gly Ser Phe His Pro Ser Asn Phe
  210                               215                               220
Gln Val Leu Val Asn Gly Gly Ile Arg Leu Gly Thr Lys His Gln Gly
  225                               230                               235                               240
Phe Glu Ile Gly Leu Lys Ile Gln Thr Ile Arg Asn Asn Tyr Tyr Thr
  245                               250                               255
Ala Ser Ala Asp Asn Val Pro Glu Gly Thr Thr Tyr Arg Phe Thr Phe
  260                               265                               270
His Arg Pro Tyr Ala Phe Tyr Trp Arg Tyr Ile Val Ser Phe
  275                               280                               285

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(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...236
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

GGGATTTTAT TTCTTATAGC AGAAATTATT TTAAAGTAA AAGACAAATC ATG TTT      56
                                   Met Phe
                                   1

AGA GAT ATA GTA GAT ATT TTA ATA TCT GTT GTT ATT ATT GGA TTA GTA      104
Arg Asp Ile Val Asp Ile Leu Ile Ser Val Val Ile Ile Gly Leu Val

```


5					10					15						
TTA	ACA	GCT	ATT	AGA	GCT	ACT	ATA	ATG	GCG	TTT	AAA	GGC	GAT	ACT	GAT	152
Leu	Thr	Ala	Ile	Arg	Ala	Thr	Ile	Met	Ala	Phe	Lys	Gly	Asp	Thr	Asp	
20					25					30						
GAT	GAT	GAA	GTT	GAG	AGT	GAT	GGG	TTT	TTT	AGT	AGA	ATA	TGG	GAT	AAA	200
Asp	Asp	Glu	Val	Glu	Ser	Asp	Gly	Phe	Phe	Ser	Arg	Ile	Trp	Asp	Lys	
35					40					45					50	
TTC	GTT	GAA	TAT	TTC	GGC	TAT	ACT	CTA	GTT	ACT	ATA	TAATGTTTTT			TCCTTA	252
Phe	Val	Glu	Tyr	Phe	Gly	Tyr	Thr	Leu	Val	Thr	Ile					
55					60											
TATAATTGGA CCAGTTATCG CTTTAATTTT TATATTT															289	

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Phe	Arg	Asp	Ile	Val	Asp	Ile	Leu	Ile	Ser	Val	Val	Ile	Ile	Gly
1				5				10					15		
Leu	Val	Leu	Thr	Ala	Ile	Arg	Ala	Thr	Ile	Met	Ala	Phe	Lys	Gly	Asp
		20					25					30			
Thr	Asp	Asp	Asp	Glu	Val	Glu	Ser	Asp	Gly	Phe	Phe	Ser	Arg	Ile	Trp
	35					40					45				
Asp	Lys	Phe	Val	Glu	Tyr	Phe	Gly	Tyr	Thr	Leu	Val	Thr	Ile		
50						55					60				

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...1491
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GACACACATT	AGTTATAGTT	TCTAAGAGAG	TTCTCCCCCT	ATCTCTTAGA	T	ATG	CCT	57
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Met Pro
1

TTT	TGT	ATT	TTT	ATT	TTA	ATA	TCT	TTG	GGA	GTT	AGG	GTT	TTG	GAA	ATT	105
Phe	Cys	Ile	Phe	Ile	Leu	Ile	Ser	Leu	Gly	Val	Arg	Val	Leu	Glu	Ile	
		5					10					15				
AAG	AAA	TAT	TTT	TCT	TAC	TCT	CTA	TTT	TTT	TTG	CTT	TTT	TCT	AGT	CTC	153
Lys	Lys	Tyr	Phe	Ser	Tyr	Ser	Leu	Phe	Phe	Leu	Leu	Phe	Ser	Ser	Leu	
	20					25					30					
TTT	TTA	TCC	AAA	CTT	CAA	GCT	TAT	AAA	TTC	AAC	ATG	AGC	ATT	GTT	GGA	201
Phe	Leu	Ser	Lys	Leu	Gln	Ala	Tyr	Lys	Phe	Asn	Met	Ser	Ile	Val	Gly	
35					40					45					50	
AAG	GTG	AGC	AGC	TAT	ACC	AAG	TTT	GGC	TTT	AAC	AAC	CAA	AGA	TAC	CAG	249
Lys	Val	Ser	Ser	Tyr	Thr	Lys	Phe	Gly	Phe	Asn	Asn	Gln	Arg	Tyr	Gln	
				55					60					65		
CCT	TCT	AAA	GAC	ATT	TAT	CCT	ACA	GGT	AGC	TAC	ACT	TCT	TTA	CTC	GGC	297
Pro	Ser	Lys	Asp	Ile	Tyr	Pro	Thr	Gly	Ser	Tyr	Thr	Ser	Leu	Leu	Gly	
			70					75					80			
GAA	TTG	AAT	TTG	AGC	ATG	GGT	TTA	TAC	AAG	GGT	TTG	AGA	GCG	GAA	GTG	345
Glu	Leu	Asn	Leu	Ser	Met	Gly	Leu	Tyr	Lys	Gly	Leu	Arg	Ala	Glu	Val	
		85					90					95				
GGG	GCT	ATG	ATG	GCA	GCG	CTC	CCC	TAT	GAC	TCT	ACC	GCC	TAT	CAA	GGC	393
Gly	Ala	Met	Met	Ala	Ala	Leu	Pro	Tyr	Asp	Ser	Thr	Ala	Tyr	Gln	Gly	
	100					105					110					
AAC	AAT	ATC	CCT	AAC	GGC	CAG	CCC	GGC	TCT	AGG	ACC	GAT	CCT	TTT	GGG	441
Asn	Asn	Ile	Pro	Asn	Gly	Gln	Pro	Gly	Ser	Arg	Thr	Asp	Pro	Phe	Gly	
115					120					125					130	
GCG	GGT	ATC	TTT	TGG	CAA	TAT	ATT	GGT	TGG	TAT	GCG	GGG	CAT	AGT	GGT	489
Ala	Gly	Ile	Phe	Trp	Gln	Tyr	Ile	Gly	Trp	Tyr	Ala	Gly	His	Ser	Gly	
				135					140					145		
TTG	CAA	GTG	CAA	AAA	CCT	CGT	TTA	GCC	ATG	GTG	CAT	AAC	GCT	TTT	TTG	537
Leu	Gln	Val	Gln	Lys	Pro	Arg	Leu	Ala	Met	Val	His	Asn	Ala	Phe	Leu	
			150					155					160			
AGC	TAC	AAC	TAC	AAA	AAA	GAC	AAA	TTC	AGT	TTT	GGC	GTG	AAA	GGG	GGG	585
Ser	Tyr	Asn	Tyr	Lys	Lys	Asp	Lys	Phe	Ser	Phe	Gly	Val	Lys	Gly	Gly	
		165					170					175				
CGC	TAT	GAC	GCT	GAA	GAG	TAT	GAT	TGG	TTC	ACT	TCT	TAC	ACT	CAA	GGG	633
Arg	Tyr	Asp	Ala	Glu	Glu	Tyr	Asp	Trp	Phe	Thr	Ser	Tyr	Thr	Gln	Gly	
	180					185					190					
GTT	GAA	GGC	TTT	GTC	AAA	TAT	AAA	GAC	ACC	AGA	TTC	AGG	GTG	ATG	TAT	681
Val	Glu	Gly	Phe	Val	Lys	Tyr	Lys	Asp	Thr	Arg	Phe	Arg	Val	Met	Tyr	
195					200				205					210		
TCA	GAC	GCT	AGG	GCT	TCA	GCG	TCA	AGC	GAC	TGG	TTT	TGG	TAT	TTT	GGG	729
Ser	Asp	Ala	Arg	Ala	Ser	Ala	Ser	Ser	Asp	Trp	Phe	Trp	Tyr	Phe	Gly	
				215					220					225		

CGT	TAC	TAT	ACA	AGC	GGT	AAG	GCT	CTA	ATG	GTA	GCT	GAT	TTG	AAA	TAT	777
Arg	Tyr	Tyr	Thr	Ser	Gly	Lys	Ala	Leu	Met	Val	Ala	Asp	Leu	Lys	Tyr	
			230					235					240			
GAA	AAA	GAC	AAC	CTA	AAA	ATC	AAC	CCT	TAT	TTT	TAT	GCG	ATC	TTT	CAA	825
Glu	Lys	Asp	Asn	Leu	Lys	Ile	Asn	Pro	Tyr	Phe	Tyr	Ala	Ile	Phe	Gln	
		245					250					255				
AGA	ATG	TAT	GCG	CCA	GGC	ATT	AAT	ATC	ACT	TAT	GAC	ACC	AAC	CCT	AAT	873
Arg	Met	Tyr	Ala	Pro	Gly	Ile	Asn	Ile	Thr	Tyr	Asp	Thr	Asn	Pro	Asn	
	260					265					270					
TTC	AAC	AAT	AAG	GGT	TTT	CGT	TTT	GTA	GGC	ACT	TTC	GTA	GGG	TTT	TTC	921
Phe	Asn	Asn	Lys	Gly	Phe	Arg	Phe	Val	Gly	Thr	Phe	Val	Gly	Phe	Phe	
275					280					285					290	
CCC	ATT	TTT	GCC	ACT	CCG	GCT	AAT	CAA	AAT	GAT	ATT	ATC	CTC	TTC	CAA	969
Pro	Ile	Phe	Ala	Thr	Pro	Ala	Asn	Gln	Asn	Asp	Ile	Ile	Leu	Phe	Gln	
				295					300					305		
CAA	GTG	CCA	TTA	GGC	AAG	AGT	GGG	CAA	ACT	TAT	TTC	TTC	CGC	ACT	CGT	1017
Gln	Val	Pro	Leu	Gly	Lys	Ser	Gly	Gln	Thr	Tyr	Phe	Phe	Arg	Thr	Arg	
			310					315					320			
TTT	TAC	TAT	AAT	AAG	TGG	CAA	TTT	GGG	GGC	AGC	GTC	TAT	AAA	AAC	ATC	1065
Phe	Tyr	Tyr	Asn	Lys	Trp	Gln	Phe	Gly	Gly	Ser	Val	Tyr	Lys	Asn	Ile	
		325					330					335				
GGT	AAC	GCT	AAT	GGT	GAT	ATA	GGT	ATT	TAT	GGC	GAC	CCT	TTG	GGG	TAT	1113
Gly	Asn	Ala	Asn	Gly	Asp	Ile	Gly	Ile	Tyr	Gly	Asp	Pro	Leu	Gly	Tyr	
	340					345					350					
AAC	ATT	TGG	ACG	AAT	AGT	ATT	TAT	GAC	GCA	GAA	ATT	AAC	AAT	ATT	GTT	1161
Asn	Ile	Trp	Thr	Asn	Ser	Ile	Tyr	Asp	Ala	Glu	Ile	Asn	Asn	Ile	Val	
355					360					365					370	
GGC	GCT	GAT	GTT	ATT	AAC	GGG	TTT	TTG	TAT	GTA	GGC	TCA	CAA	TAT	AGA	1209
Gly	Ala	Asp	Val	Ile	Asn	Gly	Phe	Leu	Tyr	Val	Gly	Ser	Gln	Tyr	Arg	
				375					380					385		
GGG	TTT	AGT	TGG	AAA	ATT	TTA	GGC	CGT	TGG	ACG	GAT	AGC	CCA	AGG	GCT	1257
Gly	Phe	Ser	Trp	Lys	Ile	Leu	Gly	Arg	Trp	Thr	Asp	Ser	Pro	Arg	Ala	
			390					395					400			
GAT	GAA	AGG	AGT	CTC	GCG	CTC	TTT	TTG	AGT	TAT	TTT	TCT	AAT	AAG	TAT	1305
Asp	Glu	Arg	Ser	Leu	Ala	Leu	Phe	Leu	Ser	Tyr	Phe	Ser	Asn	Lys	Tyr	
		405					410					415				
AAT	ATT	AGA	ATG	GAT	TTA	AAA	CTA	GAA	TAT	TAT	GGC	AAT	ATC	ACC	AAA	1353
Asn	Ile	Arg	Met	Asp	Leu	Lys	Leu	Glu	Tyr	Tyr	Gly	Asn	Ile	Thr	Lys	
		420				425					430					
AAA	GGC	TAT	TGT	ATT	GGG	TAT	TGT	GGC	ATG	TAT	GTT	CCA	GTC	GAT	CCT	1401
Lys	Gly	Tyr	Cys	Ile	Gly	Tyr	Cys	Gly	Met	Tyr	Val	Pro	Val	Asp	Pro	
435					440					445					450	
AAC	GGG	CCT	GGG	ACA	CAG	CCT	TTA	ACG	CAC	AAT	GTG	TAT	TCT	GAC	AGG	1449
Asn	Gly	Pro	Gly	Thr	Gln	Pro	Leu	Thr	His	Asn	Val	Tyr	Ser	Asp	Arg	

455

460

465

AGC CAT ATA ATG TTT AAC ATT GCT TAC GGT TTT AGG ATT TAC TAGCATTTT 1500
 Ser His Ile Met Phe Asn Ile Ala Tyr Gly Phe Arg Ile Tyr
 470 475 480

ATCCTTAATG GATATTTTGT ATTAGCCTTT TTAAATATT GAAA 1544

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Pro Phe Cys Ile Phe Ile Leu Ile Ser Leu Gly Val Arg Val Leu
 1 5 10 15
 Glu Ile Lys Lys Tyr Phe Ser Tyr Ser Leu Phe Phe Leu Leu Phe Ser
 20 25 30
 Ser Leu Phe Leu Ser Lys Leu Gln Ala Tyr Lys Phe Asn Met Ser Ile
 35 40 45
 Val Gly Lys Val Ser Ser Tyr Thr Lys Phe Gly Phe Asn Asn Gln Arg
 50 55 60
 Tyr Gln Pro Ser Lys Asp Ile Tyr Pro Thr Gly Ser Tyr Thr Ser Leu
 65 70 75 80
 Leu Gly Glu Leu Asn Leu Ser Met Gly Leu Tyr Lys Gly Leu Arg Ala
 85 90 95
 Glu Val Gly Ala Met Met Ala Ala Leu Pro Tyr Asp Ser Thr Ala Tyr
 100 105 110
 Gln Gly Asn Asn Ile Pro Asn Gly Gln Pro Gly Ser Arg Thr Asp Pro
 115 120 125
 Phe Gly Ala Gly Ile Phe Trp Gln Tyr Ile Gly Trp Tyr Ala Gly His
 130 135 140
 Ser Gly Leu Gln Val Gln Lys Pro Arg Leu Ala Met Val His Asn Ala
 145 150 155 160
 Phe Leu Ser Tyr Asn Tyr Lys Lys Asp Lys Phe Ser Phe Gly Val Lys
 165 170 175
 Gly Gly Arg Tyr Asp Ala Glu Glu Tyr Asp Trp Phe Thr Ser Tyr Thr
 180 185 190
 Gln Gly Val Glu Gly Phe Val Lys Tyr Lys Asp Thr Arg Phe Arg Val
 195 200 205
 Met Tyr Ser Asp Ala Arg Ala Ser Ala Ser Ser Asp Trp Phe Trp Tyr
 210 215 220
 Phe Gly Arg Tyr Tyr Thr Ser Gly Lys Ala Leu Met Val Ala Asp Leu
 225 230 235 240
 Lys Tyr Glu Lys Asp Asn Leu Lys Ile Asn Pro Tyr Phe Tyr Ala Ile
 245 250 255
 Phe Gln Arg Met Tyr Ala Pro Gly Ile Asn Ile Thr Tyr Asp Thr Asn
 260 265 270
 Pro Asn Phe Asn Asn Lys Gly Phe Arg Phe Val Gly Thr Phe Val Gly
 275 280 285
 Phe Phe Pro Ile Phe Ala Thr Pro Ala Asn Gln Asn Asp Ile Ile Leu

290		295		300
Phe Gln Gln Val Pro Leu Gly Lys Ser Gly Gln Thr Tyr Phe Phe Arg				
305		310		315
Thr Arg Phe Tyr Tyr Asn Lys Trp Gln Phe Gly Gly Ser Val Tyr Lys				320
		325		330
Asn Ile Gly Asn Ala Asn Gly Asp Ile Gly Ile Tyr Gly Asp Pro Leu				335
		340		345
Gly Tyr Asn Ile Trp Thr Asn Ser Ile Tyr Asp Ala Glu Ile Asn Asn				350
		355		360
Ile Val Gly Ala Asp Val Ile Asn Gly Phe Leu Tyr Val Gly Ser Gln				365
		370		375
Tyr Arg Gly Phe Ser Trp Lys Ile Leu Gly Arg Trp Thr Asp Ser Pro				380
385		390		395
Arg Ala Asp Glu Arg Ser Leu Ala Leu Phe Leu Ser Tyr Phe Ser Asn				400
		405		410
Lys Tyr Asn Ile Arg Met Asp Leu Lys Leu Glu Tyr Tyr Gly Asn Ile				415
		420		425
Thr Lys Lys Gly Tyr Cys Ile Gly Tyr Cys Gly Met Tyr Val Pro Val				430
		435		440
Asp Pro Asn Gly Pro Gly Thr Gln Pro Leu Thr His Asn Val Tyr Ser				445
		450		455
Asp Arg Ser His Ile Met Phe Asn Ile Ala Tyr Gly Phe Arg Ile Tyr				460
465		470		475
				480

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 658 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...605
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AATTTTAGGT TATTAGTTAC CATTTTATTA TTCTTAAGGA TGTGTTTATA ATG AGA	56
Met Arg	
1	
ATT AAG GCT TAT TTT TTG CGT TTT ATC GCG CTG GTT TTG ATT GTT TTG	104
Ile Lys Ala Tyr Phe Leu Arg Phe Ile Ala Leu Val Leu Ile Val Leu	
5 10 15	
TTA GGT TTT AGT GCT TGT AAA AAT TCT CAA AAA TCT CAA GAT TCT CAA	152
Leu Gly Phe Ser Ala Cys Lys Asn Ser Gln Lys Ser Gln Asp Ser Gln	
20 25 30	
AAC AAT ACC CCC CAA CAA GAT AGC CCT AAA ACC TAC ACC GCT ATG GAT	200
Asn Asn Thr Pro Gln Gln Asp Ser Pro Lys Thr Tyr Thr Ala Met Asp	
35 40 45 50	

TTG AAT AAC CAA GAA TAC ACC ATC ACA GGC GAT TTA GAT TCT CTC AAT	248
Leu Asn Asn Gln Glu Tyr Thr Ile Thr Gly Asp Leu Asp Ser Leu Asn	
55 60 65	
ATC AGC CCG GAT TCC AAC ACC CCT ACC CTA TTA GTT TTA AGC GCT TTA	296
Ile Ser Pro Asp Ser Asn Thr Pro Thr Leu Leu Val Leu Ser Ala Leu	
70 75 80	
GAT AAT TCT TTA AAA GAT TAC GCC CCC AGC TTT AAC ATC TTA AAA AAA	344
Asp Asn Ser Leu Lys Asp Tyr Ala Pro Ser Phe Asn Ile Leu Lys Lys	
85 90 95	
ACT TTT AAA GAT CGT TTG AGG GTG CTT ATT TTA CTC AAT AAA CCC TAT	392
Thr Phe Lys Asp Arg Leu Arg Val Leu Ile Leu Asn Lys Pro Tyr	
100 105 110	
TCA AGC GAT GCA ATC AAA GAC TTT AGC GCG CAT TTT CAA GCT GAT TTG	440
Ser Ser Asp Ala Ile Lys Asp Phe Ser Ala His Phe Gln Ala Asp Leu	
115 120 125 130	
ATG ATT TTA AAC CCT AAA GAT ACC GCT CTT TTT GAT CAT TTA AAG TAT	488
Met Ile Leu Asn Pro Lys Asp Thr Ala Leu Phe Asp His Leu Lys Tyr	
135 140 145	
GAC GCT TTA AAC CAT TCT TTT AAC ATG CTC TTA TAC CAC AAA CAC CAA	536
Asp Ala Leu Asn His Ser Phe Asn Met Leu Leu Tyr His Lys His Gln	
150 155 160	
TTG ATC AAA ATG TAT CAA GGG ATC GTG CCA ATA GAA ATG CTC CAA TTT	584
Leu Ile Lys Met Tyr Gln Gly Ile Val Pro Ile Glu Met Leu Gln Phe	
165 170 175	
GAT ATT TCC AAT TTA AAG GAT TAAAAAAAC CATGTTTAAT TTTTTCAAAA AAAT	639
Asp Ile Ser Asn Leu Lys Asp	
180 185	
TGTCAATAAA ATTAAGGGT	658

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Arg Ile Lys Ala Tyr Phe Leu Arg Phe Ile Ala Leu Val Leu Ile	
1 5 10 15	
Val Leu Leu Gly Phe Ser Ala Cys Lys Asn Ser Gln Lys Ser Gln Asp	
20 25 30	
Ser Gln Asn Asn Thr Pro Gln Gln Asp Ser Pro Lys Thr Tyr Thr Ala	
35 40 45	
Met Asp Leu Asn Asn Gln Glu Tyr Thr Ile Thr Gly Asp Leu Asp Ser	

50	55	60
Leu Asn Ile Ser Pro Asp Ser Asn Thr Pro Thr Leu Leu Val Leu Ser		
65	70	75
Ala Leu Asp Asn Ser Leu Lys Asp Tyr Ala Pro Ser Phe Asn Ile Leu		80
	85	90
Lys Lys Thr Phe Lys Asp Arg Leu Arg Val Leu Ile Leu Leu Asn Lys		95
	100	105
Pro Tyr Ser Ser Asp Ala Ile Lys Asp Phe Ser Ala His Phe Gln Ala		110
	115	120
Asp Leu Met Ile Leu Asn Pro Lys Asp Thr Ala Leu Phe Asp His Leu		125
	130	135
Lys Tyr Asp Ala Leu Asn His Ser Phe Asn Met Leu Leu Tyr His Lys		140
145	150	155
His Gln Leu Ile Lys Met Tyr Gln Gly Ile Val Pro Ile Glu Met Leu		160
	165	170
Gln Phe Asp Ile Ser Asn Leu Lys Asp		175
	180	185

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...407
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AATCCCTTCA AAAATGATAT AATAGACTTG ATGAATCAT TTTAAGGAAA ATG CCC	56
Met Pro	
1	
ATG CGT TTG CAC ACT GCC TTT TTT GGT ATT AAT TCA TTG CTT GTT GCC	104
Met Arg Leu His Thr Ala Phe Phe Gly Ile Asn Ser Leu Leu Val Ala	
5 10 15	
TCT CTT TTG ATA AGC GGT TGC AGT CTC TTT AAA AAG CGT AAC ACT AAC	152
Ser Leu Leu Ile Ser Gly Cys Ser Leu Phe Lys Lys Arg Asn Thr Asn	
20 25 30	
GCC CAG CTA ATC CCC CCT TCA GCT AAT GGC TTG CAA GCC CCC ATT TAT	200
Ala Gln Leu Ile Pro Pro Ser Ala Asn Gly Leu Gln Ala Pro Ile Tyr	
35 40 45 50	
CCC CCA ACC AAT TTC ACC CCT AGA AAG AGC ATT CAG CCT CTC CCA AGC	248
Pro Pro Thr Asn Phe Thr Pro Arg Lys Ser Ile Gln Pro Leu Pro Ser	
55 60 65	
CCT CGC CTT GAG AAT AAC GAT CAG CCC GTC ATT AGT TCT AAC CCC ACT	296

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Pro Arg Leu Glu Asn Asn Asp Gln Pro Val Ile Ser Ser Asn Pro Thr
      70                                75                                80

AAC GCT ATC CCT AAC ACC CCC ATT CTC ACG CCT AAT AAT GTC ATT GAA      344
Asn Ala Ile Pro Asn Thr Pro Ile Leu Thr Pro Asn Asn Val Ile Glu
      85                                90                                95

TTG AAC GCA TGG GCA TGG GCG TGG CTC CAG AAT CCA CCA TTT CAC CCT      392
Leu Asn Ala Trp Ala Trp Ala Trp Leu Gln Asn Pro Pro Phe His Pro
      100                                105                                110

CTC AAG CCC TGG CTC TAGCCAAGCG GGCGGCTATC GTTGATGGCT ACCGCCAGTT G      448
Leu Lys Pro Trp Leu
115

GGTGAAAAAA TG      460

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(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

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Met Pro Met Arg Leu His Thr Ala Phe Phe Gly Ile Asn Ser Leu Leu
 1          5          10          15
Val Ala Ser Leu Leu Ile Ser Gly Cys Ser Leu Phe Lys Lys Arg Asn
      20          25          30
Thr Asn Ala Gln Leu Ile Pro Pro Ser Ala Asn Gly Leu Gln Ala Pro
      35          40          45
Ile Tyr Pro Pro Thr Asn Phe Thr Pro Arg Lys Ser Ile Gln Pro Leu
      50          55          60
Pro Ser Pro Arg Leu Glu Asn Asn Asp Gln Pro Val Ile Ser Ser Asn
      65          70          75          80
Pro Thr Asn Ala Ile Pro Asn Thr Pro Ile Leu Thr Pro Asn Asn Val
      85          90          95
Ile Glu Leu Asn Ala Trp Ala Trp Ala Trp Leu Gln Asn Pro Pro Phe
      100          105          110
His Pro Leu Lys Pro Trp Leu
115

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(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...1232
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GTTGTGATTT TATTGTGTTT TCATATCAAT TTTCATATCA AGGAGTTTAA ATG AAA	56
Met Lys	
1	
GAA ACA AGA CTT TTA AAA TTG AGA GCG TTG AGC TTA GCA TGT TTA ATG	104
Glu Thr Arg Leu Leu Lys Leu Arg Ala Leu Ser Leu Ala Cys Leu Met	
5 10 15	
GGA TTA GGC GTG AGT GGG TGC GCG TTT TTA GAT AAG CAA ATC TTA AAC	152
Gly Leu Gly Val Ser Gly Cys Ala Phe Leu Asp Lys Gln Ile Leu Asn	
20 25 30	
GAC CAT TTG ACT AAA GCT AAA AAT AAC CCA AAA TAC GAT TGC CAA AAA	200
Asp His Leu Thr Lys Ala Lys Asn Asn Pro Lys Tyr Asp Cys Gln Lys	
35 40 45 50	
GAA ATG TGG TCT TTC CCT AAA AAA TAC GAT GGG ATA AAT CAG TGT TTA	248
Glu Met Trp Ser Phe Pro Lys Lys Tyr Asp Gly Ile Asn Gln Cys Leu	
55 60 65	
AAG GCT CAA GAA GAG CTT ATT GAA CCA ATC ATC ACT AAA AAG ATC GAT	296
Lys Ala Gln Glu Glu Leu Ile Glu Pro Ile Ile Thr Lys Lys Ile Asp	
70 75 80	
CAG TAT CAA TGC GAT GAT TTC ACT AAT GAA GGC TTA AAA GAT AAG TGT	344
Gln Tyr Gln Cys Asp Asp Phe Thr Asn Glu Gly Leu Lys Asp Lys Cys	
85 90 95	
TTC AAA AGA AAC GAT GCC TAC TTA AAC ACC CTT TTA ACG CCC ATC ATT	392
Phe Lys Arg Asn Asp Ala Tyr Leu Asn Thr Leu Leu Thr Pro Ile Ile	
100 105 110	
CAA AAA CAA GAG CGT CGT TTT AGC TGC TCT GAT TTC CAT AAC CCA GAG	440
Gln Lys Gln Glu Arg Arg Phe Ser Cys Ser Asp Phe His Asn Pro Glu	
115 120 125 130	
CTA AAA GAA CAA TGC ATG GAT AAA ACT AAC GCT TAT GAA AAG CAA AAA	488
Leu Lys Glu Gln Cys Met Asp Lys Thr Asn Ala Tyr Glu Lys Gln Lys	
135 140 145	
GAC CGA CAA AAA AGA CTA ATT AAT CTC GTG CAA TTA GAA GCG TTT GAA	536
Asp Arg Gln Lys Arg Leu Ile Asn Leu Val Gln Leu Glu Ala Phe Glu	
150 155 160	
AAA GAA TAC GCG CAA TAT AAA CCA TAC ATT ATC CCT TAC TTC ACC AAA	584
Lys Glu Tyr Ala Gln Tyr Lys Pro Tyr Ile Ile Pro Tyr Phe Thr Lys	
165 170 175	
GAA TGC GTT AAA AAT GCG CCC CAT TTA GCC AAC AAG GAA AGA CTA TGC	632
Glu Cys Val Lys Asn Ala Pro His Leu Ala Asn Lys Glu Arg Leu Cys	

180	185	190	
CAA AAA GAA GTG CAT GAA AAA TTT GAC GAC CCT TAT TCT AGC TCT AAA Gln Lys Glu Val His Glu Lys Phe Asp Asp Pro Tyr Ser Ser Ser Lys 195 200 205 210			680
GAA TTG AGC GTT CAA TCG GCT ATT TCT TTT TGC ATT AAA AAA GTT GAT Glu Leu Ser Val Gln Ser Ala Ile Ser Phe Cys Ile Lys Lys Val Asp 215 220 225			728
GCT AAA TTA GAA AAA GCC GCT CTT ATG AAT GGC GTT TAT ATA AGC CCT Ala Lys Leu Glu Lys Ala Ala Leu Met Asn Gly Val Tyr Ile Ser Pro 230 235 240			776
TAT AAA AAA TCC ACC CAT TGC CAA AGA ACG CAT TTG GAA AAT AAG AGC Tyr Lys Lys Ser Thr His Cys Gln Arg Thr His Leu Glu Asn Lys Ser 245 250 255			824
TTG AAA GAA ATC GCT TTA AAT ATG AAC CCT AAA TTA GAA AAG CAA AGC Leu Lys Glu Ile Ala Leu Asn Met Asn Pro Lys Leu Glu Lys Gln Ser 260 265 270			872
CCT TTT ATT GAT GCG GAT AAA ATG GCT ATG CAA TCT GCG GGG TTA TTG Pro Phe Ile Asp Ala Asp Lys Met Ala Met Gln Ser Ala Gly Leu Leu 275 280 285 290			920
AGA AAG AAT AAA GGT GTC TTG ATT GCT TTT GCT ACA GAT ATT TGC ATG Arg Lys Asn Lys Gly Val Leu Ile Ala Phe Ala Thr Asp Ile Cys Met 295 300 305			968
GAG CGT AAC GAA CAT AAA AAA GAA GAG TTT ATC AGC CTT AAA GAT AGT Glu Arg Asn Glu His Lys Lys Glu Glu Phe Ile Ser Leu Lys Asp Ser 310 315 320			1016
TGC ACC CAA TCG CAA GCC AAA ATC TAT AAC AAC AAG GAG CGC TTT GAC Cys Thr Gln Ser Gln Ala Lys Ile Tyr Asn Asn Lys Glu Arg Phe Asp 325 330 335			1064
AAA TTC ATA CAA GAT TAC CAA AAA GAC TTA AAA ACT TGT CTT TTA GAC Lys Phe Ile Gln Asp Tyr Gln Lys Asp Leu Lys Thr Cys Leu Leu Asp 340 345 350			1112
ACT TCT AAC ACT AAA GAA GAA GTG GAG CAA AAT TTT TCA CAA TGC CAA Thr Ser Asn Thr Lys Glu Glu Val Glu Gln Asn Phe Ser Gln Cys Gln 355 360 365 370			1160
AAA GAG CAA TTG AGA GAT GAT AAC AAA GGC TTG GGT TTC ACT TTA GAA Lys Glu Gln Leu Arg Asp Asp Asn Lys Gly Leu Gly Phe Thr Leu Glu 375 380 385			1208
GAA TTG GTT AAA AAA TAC GCT AAG TAAAGTTATT TAATTTTATG GATGGTTTAA Glu Leu Val Lys Lys Tyr Ala Lys 390			1262
AAAATCCATT CCATAGTTAT TGT			1285

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met	Lys	Glu	Thr	Arg	Leu	Leu	Lys	Leu	Arg	Ala	Leu	Ser	Leu	Ala	Cys	1	5	10	15
Leu	Met	Gly	Leu	Gly	Val	Ser	Gly	Cys	Ala	Phe	Leu	Asp	Lys	Gln	Ile	20	25	30	35
Leu	Asn	Asp	His	Leu	Thr	Lys	Ala	Lys	Asn	Asn	Pro	Lys	Tyr	Asp	Cys	40	45	50	55
Gln	Lys	Glu	Met	Trp	Ser	Phe	Pro	Lys	Lys	Tyr	Asp	Gly	Ile	Asn	Gln	60	65	70	75
Cys	Leu	Lys	Ala	Gln	Glu	Glu	Leu	Ile	Glu	Pro	Ile	Ile	Thr	Lys	Lys	80	85	90	95
Ile	Asp	Gln	Tyr	Gln	Cys	Asp	Asp	Phe	Thr	Asn	Glu	Gly	Leu	Lys	Asp	100	105	110	115
Lys	Cys	Phe	Lys	Arg	Asn	Asp	Ala	Tyr	Leu	Asn	Thr	Leu	Leu	Thr	Pro	120	125	130	135
Ile	Ile	Gln	Lys	Gln	Glu	Arg	Arg	Phe	Ser	Cys	Ser	Asp	Phe	His	Asn	140	145	150	155
Pro	Glu	Leu	Lys	Glu	Gln	Cys	Met	Asp	Lys	Thr	Asn	Ala	Tyr	Glu	Lys	160	165	170	175
Gln	Lys	Asp	Arg	Gln	Lys	Arg	Leu	Ile	Asn	Leu	Val	Gln	Leu	Glu	Ala	180	185	190	195
Phe	Glu	Lys	Glu	Tyr	Ala	Gln	Tyr	Lys	Pro	Tyr	Ile	Ile	Pro	Tyr	Phe	200	205	210	215
Thr	Lys	Glu	Cys	Val	Lys	Asn	Ala	Pro	His	Leu	Ala	Asn	Lys	Glu	Arg	220	225	230	235
Leu	Cys	Gln	Lys	Glu	Val	His	Glu	Lys	Phe	Asp	Asp	Pro	Tyr	Ser	Ser	240	245	250	255
Ser	Lys	Glu	Leu	Ser	Val	Gln	Ser	Ala	Ile	Ser	Phe	Cys	Ile	Lys	Lys	260	265	270	275
Val	Asp	Ala	Lys	Leu	Glu	Lys	Ala	Ala	Leu	Met	Asn	Gly	Val	Tyr	Ile	280	285	290	295
Ser	Pro	Tyr	Lys	Lys	Ser	Thr	His	Cys	Gln	Arg	Thr	His	Leu	Glu	Asn	300	305	310	315
Lys	Ser	Leu	Lys	Glu	Ile	Ala	Leu	Asn	Met	Asn	Pro	Lys	Leu	Glu	Lys	320	325	330	335
Gln	Ser	Pro	Phe	Ile	Asp	Ala	Asp	Lys	Met	Ala	Met	Gln	Ser	Ala	Gly	340	345	350	355
Leu	Leu	Arg	Lys	Asn	Lys	Gly	Val	Leu	Ile	Ala	Phe	Ala	Thr	Asp	Ile	360	365	370	375
Cys	Met	Glu	Arg	Asn	Glu	His	Lys	Lys	Glu	Glu	Phe	Ile	Ser	Leu	Lys	380	385	390	394
Asp	Ser	Cys	Thr	Gln	Ser	Gln	Ala	Lys	Ile	Tyr	Asn	Asn	Lys	Glu	Arg				
Phe	Asp	Lys	Phe	Ile	Gln	Asp	Tyr	Gln	Lys	Asp	Leu	Lys	Thr	Cys	Leu				
Leu	Asp	Thr	Ser	Asn	Thr	Lys	Glu	Glu	Val	Glu	Gln	Asn	Phe	Ser	Gln				
Cys	Gln	Lys	Glu	Gln	Leu	Arg	Asp	Asp	Asn	Lys	Gly	Leu	Gly	Phe	Thr				

370 375 380
Leu Glu Glu Leu Val Lys Lys Tyr Ala Lys
385 390

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic RNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 84...704
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TTGATCATTC	TTATTTTCGCA	CAACCCCAAGC	ACGCTAAAAT	TAGCCACTAA	GCATGTGAAA	60
TTAGAGCATG	GGCGTTTGAC	AGA ATG CTA AGG GTT TTA AGC GTT GGT GTT GCT	113			
		Met Leu Arg Val Leu Ser Val Gly Val Ala				
		1 5 10				
TTT ATT TTA CTA GGG TGT CAG TTT TTC AAC AAA ACG ACG CTG CAT TTA	161					
Phe Ile Leu Leu Gly Cys Gln Phe Phe Asn Lys Thr Thr Leu His Leu						
	15 20 25					
AAA TAT AAA GAT TAC CCC AAA AAT AGC GCT TTA AAA ACC GCT TTC ACT	209					
Lys Tyr Lys Asp Tyr Pro Lys Asn Ser Ala Leu Lys Thr Ala Phe Thr						
	30 35 40					
TTA ACC CCC CCT AAA ATC TTT TTT AAC GCC CGT TTT GTG CCG CCC TTT	257					
Leu Thr Pro Pro Lys Ile Phe Phe Asn Ala Arg Phe Val Pro Pro Phe						
	45 50 55					
TAC CAA AAA GAA TTT AAA AAA GCG ATC ACC CAA CAA ATC GCT TAT TTT	305					
Tyr Gln Lys Glu Phe Lys Lys Ala Ile Thr Gln Gln Ile Ala Tyr Phe						
	60 65 70					
TTA AAA GAT AAA AGT GCT TTT ATT CTC AAT GTT TCA GGC AAT GTT TTT	353					
Leu Lys Asp Lys Ser Ala Phe Ile Leu Asn Val Ser Gly Asn Val Phe						
75 80 85 90						
TTT TCT TTT GAA GAG AAT CCT AAA GAT TTA AAA GCC ATT AAA GAA AGG	401					
Phe Ser Phe Glu Glu Asn Pro Lys Asp Leu Lys Ala Ile Lys Glu Arg						
	95 100 105					
CTT AAA AAG ACG ATT GAG CCT AAC GCT GAC CCA AAA GCC GTC ATG CGT	449					
Leu Lys Lys Thr Ile Glu Pro Asn Ala Asp Pro Lys Ala Val Met Arg						
	110 115 120					
TTT TTA AAC CTT CAA GCG AGC TTG ATT TTA GAA TGC GTC CCG CAA ACC	497					
Phe Leu Asn Leu Gln Ala Ser Leu Ile Leu Glu Cys Val Pro Gln Thr						

125	130	135	
ACT TGC CCG TTT GAC ACC CTT TTA ATC CCC ACC GCT TTC AGC GTG CCT			545
Thr Cys Pro Phe Asp Thr Leu Leu Ile Pro Thr Ala Phe Ser Val Pro			
140	145	150	
GTT TAT TAC GCT AAT CGT TTG GGC GAT AAC CCC TCT CTT TTT TCC CAA			593
Val Tyr Tyr Ala Asn Arg Leu Gly Asp Asn Pro Ser Leu Phe Ser Gln			
155	160	165	170
GAG GAT AAA ACC TAT CAT AAC GCT TTG ATC AAA GCC CTT AAT AAG GCT			641
Glu Asp Lys Thr Tyr His Asn Ala Leu Ile Lys Ala Leu Asn Lys Ala			
175	180	185	
TAC TAT TCT CTT ATG GAG GGT TTA GAA AAG CGT TTG AAC GCT ATA AAA			689
Tyr Tyr Ser Leu Met Glu Gly Leu Glu Lys Arg Leu Asn Ala Ile Lys			
190	195	200	
AAT GCA GAG TGG CTT TAAGGCATGA AAAAGATTGC ATTTTTTATT TTTGTCATTT T			745
Asn Ala Glu Trp Leu			
205			
GTTCGCGTA GGGATTTATT TAATTTGGCA TGT'TTTATTG GAAAAAGCCC TAGAATTGAA			805
ATTAGCAACC TCAGCTAATG ATTTGCTTTT			835

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met	Leu	Arg	Val	Leu	Ser	Val	Gly	Val	Ala	Phe	Ile	Leu	Leu	Gly	Cys
1				5					10					15	
Gln	Phe	Phe	Asn	Lys	Thr	Thr	Leu	His	Leu	Lys	Tyr	Lys	Asp	Tyr	Pro
			20					25					30		
Lys	Asn	Ser	Ala	Leu	Lys	Thr	Ala	Phe	Thr	Leu	Thr	Pro	Pro	Lys	Ile
		35					40					45			
Phe	Phe	Asn	Ala	Arg	Phe	Val	Pro	Pro	Phe	Tyr	Gln	Lys	Glu	Phe	Lys
50					55					60					
Lys	Ala	Ile	Thr	Gln	Gln	Ile	Ala	Tyr	Phe	Leu	Lys	Asp	Lys	Ser	Ala
65				70					75					80	
Phe	Ile	Leu	Asn	Val	Ser	Gly	Asn	Val	Phe	Phe	Ser	Phe	Glu	Glu	Asn
			85					90					95		
Pro	Lys	Asp	Leu	Lys	Ala	Ile	Lys	Glu	Arg	Leu	Lys	Lys	Thr	Ile	Glu
			100				105						110		
Pro	Asn	Ala	Asp	Pro	Lys	Ala	Val	Met	Arg	Phe	Leu	Asn	Leu	Gln	Ala
		115					120					125			
Ser	Leu	Ile	Leu	Glu	Cys	Val	Pro	Gln	Thr	Thr	Cys	Pro	Phe	Asp	Thr
130					135						140				
Leu	Leu	Ile	Pro	Thr	Ala	Phe	Ser	Val	Pro	Val	Tyr	Tyr	Ala	Asn	Arg
145					150					155					160

TTT TTA AAA TTG CAA TCG CAT TAT TAC GCT TTC AAA AAC CAT TCT AAA	440
Phe Leu Lys Leu Gln Ser His Tyr Tyr Ala Phe Lys Asn His Ser Lys	
115 120 125 130	
GAC CAG GAA TTT ATC TCT AAT TCT ATT GTG AGT TTA GGC GAA TTT ATA	488
Asp Gln Glu Phe Ile Ser Asn Ser Ile Val Ser Leu Gly Glu Phe Ile	
135 140 145	
GAA AAA TAC CCT AAC AGC CGT TAC CGC CCC TAT GTA GAA TAC ATG CAA	536
Glu Lys Tyr Pro Asn Ser Arg Tyr Arg Pro Tyr Val Glu Tyr Met Gln	
150 155 160	
ATC AAA TTC ATT TTA GGG CAA AAT GAG CTC AAT CGC GCG ATC GCG AAT	584
Ile Lys Phe Ile Leu Gly Gln Asn Glu Leu Asn Arg Ala Ile Ala Asn	
165 170 175	
GTC TAT AAA AAA CGC CAC AAG CCT GAG GGC GTG AAA CGC TAT TTA GAA	632
Val Tyr Lys Lys Arg His Lys Pro Glu Gly Val Lys Arg Tyr Leu Glu	
180 185 190	
AGG ATA GAT GAG ACT TTA GAA AAA GAG ACT AAA CCC AAA CCA TCG CAC	680
Arg Ile Asp Glu Thr Leu Glu Lys Glu Thr Lys Pro Lys Pro Ser His	
195 200 205 210	
ATG CCT TGG TAT GTG TTA ATT TTT GAT TGG TAGGATATTT CAAAACCATA CAC	733
Met Pro Trp Tyr Val Leu Ile Phe Asp Trp	
215 220	
ATTATAACAG AGAGATGAAA AATGACTGAA	763

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Arg Leu Lys His Phe Lys Thr Phe Leu Phe Ile Thr Met Ala Ile	
1 5 10 15	
Ile Val Ile Gly Thr Gly Cys Ala Asn Lys Lys Lys Lys Asp Glu	
20 25 30	
Tyr Asn Lys Pro Ala Ile Phe Trp Tyr Gln Gly Ile Leu Arg Glu Ile	
35 40 45	
Leu Phe Ala Asn Leu Glu Thr Ala Asp Asn Tyr Tyr Ser Ser Leu Gln	
50 55 60	
Ser Glu His Ile Asn Ser Pro Leu Val Pro Glu Ala Met Leu Ala Leu	
65 70 75 80	
Gly Gln Ala His Met Lys Lys Lys Glu Tyr Val Leu Ala Ser Phe Tyr	
85 90 95	
Phe Asp Glu Tyr Ile Lys Arg Phe Gly Thr Lys Asp Asn Val Asp Tyr	
100 105 110	
Leu Thr Phe Leu Lys Leu Gln Ser His Tyr Tyr Ala Phe Lys Asn His	

115	120	125
Ser Lys Asp Gln Glu Phe Ile	Ser Asn Ser Ile Val	Ser Leu Gly Glu
130	135	140
Phe Ile Glu Lys Tyr Pro Asn	Ser Arg Tyr Arg Pro Tyr	Val Glu Tyr
145	150	155
Met Gln Ile Lys Phe Ile Leu	Gly Gln Asn Glu Leu Asn	Arg Ala Ile
165	170	175
Ala Asn Val Tyr Lys Lys Arg	His Lys Pro Glu Gly Val	Lys Arg Tyr
180	185	190
Leu Glu Arg Ile Asp Glu Thr	Leu Glu Lys Glu Thr Lys	Pro Lys Pro
195	200	205
Ser His Met Pro Trp Tyr Val	Leu Ile Phe Asp Trp	
210	215	220

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 75...749
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GAAAAAGGCT CTGCTTTGAT AGATAAATTT GACGCTAACC CCTATAAAAC GATTTTTTGA	60
GAAAGGAAAT AATC ATG AGA GCT ACG GCG ATA AAA ATC TTT TCA CTC TCA	110
Met Arg Ala Thr Ala Ile Lys Ile Phe Ser Leu Ser	
1 5 10	
TCA GCA TTA GCC CTA TTG CTT CAT GGT TGC TTG AGC ATC AAT TTA AAA	158
Ser Ala Leu Ala Leu Leu Leu His Gly Cys Leu Ser Ile Asn Leu Lys	
15 20 25	
CAA ATG CTA CCA GAG ATC AGA ACT TAC GAT TTG AAT GCG AGT TCT TTT	206
Gln Met Leu Pro Glu Ile Arg Thr Tyr Asp Leu Asn Ala Ser Ser Phe	
30 35 40	
GAA ATC ACG CAA TGC GCT AAA CCT TTG ACT GAA GTG AGG CTC ATT AGT	254
Glu Ile Thr Gln Cys Ala Lys Pro Leu Thr Glu Val Arg Leu Ile Ser	
45 50 55 60	
ATT TTG AGC GCG GAT TTA TTC AAC ACT AAA GAG ATC GTT TTT AAA GCC	302
Ile Leu Ser Ala Asp Leu Phe Asn Thr Lys Glu Ile Val Phe Lys Ala	
65 70 75	
AAA GAC GGG CAG ATC ACG CAT GGG AAG CAC CAA AAA TGG ATA GAC TTG	350
Lys Asp Gly Gln Ile Thr His Gly Lys His Gln Lys Trp Ile Asp Leu	
80 85 90	

CCT CGC AAC ATG CTA AAA ACC ATG TTC ATG CAA GAA GCG CAA AAA GCA	398
Pro Arg Asn Met Leu Lys Thr Met Phe Met Gln Glu Ala Gln Lys Ala	
95 100 105	
TGC TTA GGC GTG GCT TTG CCT CCT TAT GGC GCG GGT GCA CCC ACT TAT	446
Cys Leu Gly Val Ala Leu Pro Pro Tyr Gly Ala Gly Ala Pro Thr Tyr	
110 115 120	
GCG GTT CGT TTT ACG ATT TTA TCG TTT TCT CTT TTA GAA AAA GAA AAT	494
Ala Val Arg Phe Thr Ile Leu Ser Phe Ser Leu Leu Glu Lys Glu Asn	
125 130 135 140	
TCT ACC TAT AGG GCG GAA TTT GCA CTA GGC TAT GAC ATT AGC GTG AAA	542
Ser Thr Tyr Arg Ala Glu Phe Ala Leu Gly Tyr Asp Ile Ser Val Lys	
145 150 155	
GGC GAT TCG CAT TCT GGG GTG ATC ATT AAG CAT GAA AAT ATT TCT AGC	590
Gly Asp Ser His Ser Gly Val Ile Ile Lys His Glu Asn Ile Ser Ser	
160 165 170	
TTG GAA AAT AAA ACG ACC AAA ACG AGT AAA AAT GGC AAT CAA GAT TTT	638
Leu Glu Asn Lys Thr Thr Lys Thr Ser Lys Asn Gly Asn Gln Asp Phe	
175 180 185	
CAA GAA AGC GCG ATA CAA TCT CTC CAA CAT GTA AGC GTG CAA GCG ATT	686
Gln Glu Ser Ala Ile Gln Ser Leu Gln His Val Ser Val Gln Ala Ile	
190 195 200	
CAA GAA GCG GTT TCT TTG ATT AAA AAA GCC ATT GAA GCG CAA AGC GTA	734
Gln Glu Ala Val Ser Leu Ile Lys Lys Ala Ile Glu Ala Gln Ser Val	
205 210 215 220	
AGC CCG TTA AAA AAA TAAAAAATAA GGAGGAATTG TTTGATTTTA CGATTGGCTG G	790
Ser Pro Leu Lys Lys	
225	
AGCAAGCGTT T	801

(2). INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Arg Ala Thr Ala Ile Lys Ile Phe Ser Leu Ser Ser Ala Leu Ala	
1 5 10 15	
Leu Leu Leu His Gly Cys Leu Ser Ile Asn Leu Lys Gln Met Leu Pro	
20 25 30	
Glu Ile Arg Thr Tyr Asp Leu Asn Ala Ser Ser Phe Glu Ile Thr Gln	
35 40 45	
Cys Ala Lys Pro Leu Thr Glu Val Arg Leu Ile Ser Ile Leu Ser Ala	

50		55		60
Asp Leu Phe Asn Thr Lys Glu Ile Val Phe Lys Ala Lys Asp Gly Gln				
65		70		75
Ile Thr His Gly Lys His Gln Lys Trp Ile Asp Leu Pro Arg Asn Met				80
	85		90	
Leu Lys Thr Met Phe Met Gln Glu Ala Gln Lys Ala Cys Leu Gly Val				95
	100		105	
Ala Leu Pro Tyr Gly Ala Gly Ala Pro Thr Tyr Ala Val Arg Phe				110
	115		120	
Thr Ile Leu Ser Phe Ser Leu Leu Glu Lys Glu Asn Ser Thr Tyr Arg				125
	130		135	
Ala Glu Phe Ala Leu Gly Tyr Asp Ile Ser Val Lys Gly Asp Ser His				140
	145		150	
Ser Gly Val Ile Ile Lys His Glu Asn Ile Ser Ser Leu Glu Asn Lys				155
	165		170	
Thr Thr Lys Thr Ser Lys Asn Gly Asn Gln Asp Phe Gln Glu Ser Ala				175
	180		185	
Ile Gln Ser Leu Gln His Val Ser Val Gln Ala Ile Gln Glu Ala Val				190
	195		200	
Ser Leu Ile Lys Lys Ala Ile Glu Ala Gln Ser Val Ser Pro Leu Lys				205
	210		215	
				220
Lys				
225				

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...395
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTTTATGATA AGATAGTCAA ATTATACATT GACTTAAGGA AATTTAATTG ATG AAA	56
Met Lys	
1	
TCT AAA ATC ACT CAT TTT ATC GCT ATC TCT TTT GTT TTA AGC CTG TTT	104
Ser Lys Ile Thr His Phe Ile Ala Ile Ser Phe Val Leu Ser Leu Phe	
5 10 15	
AGC GCA TGC AAA GAC GAG CCT AAA AAA TCG TCT CAA TCG CAC CAA AAC	152
Ser Ala Cys Lys Asp Glu Pro Lys Lys Ser Ser Gln Ser His Gln Asn	
20 25 30	
AAC ACT AAA ATC ACT AAA AAC AAT CCA ATC AAT CAA GCG AAT AAT GAT	200
Asn Thr Lys Ile Thr Lys Asn Asn Pro Ile Asn Gln Ala Asn Asn Asp	
35 40 45 50	

ATA AGA AAA ATT GAG CAT GAA GAA GAA GAT GAA AAA GCC ACC AAA GAA 248
 Ile Arg Lys Ile Glu His Glu Glu Glu Asp Glu Lys Ala Thr Lys Glu
 55 60 65
 GTG AAC GAT TTG ATC AAT AAC GAA AAT AAA ATT GAT GAA ATC AAT AAT 296
 Val Asn Asp Leu Ile Asn Asn Glu Asn Lys Ile Asp Glu Ile Asn Asn
 70 75 80
 GAA GAA AAC GCT GAT CCT TCG CAA AAA AGA ACG AAC AAC GTT TTG CAA 344
 Glu Glu Asn Ala Asp Pro Ser Gln Lys Arg Thr Asn Asn Val Leu Gln
 85 90 95
 CGA GCC ACT AAC CAC CAA GAC AAT CTC AAT TCC CCA CTC AAC AGG AAG 392
 Arg Ala Thr Asn His Gln Asp Asn Leu Asn Ser Pro Leu Asn Arg Lys
 100 105 110
 TAT TAAAGTGTGA AACTTTTTTC AAAGGATTTA TTTAAAAAAG TAACCCCTTT ATT 448
 Tyr
 115

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Lys Ser Lys Ile Thr His Phe Ile Ala Ile Ser Phe Val Leu Ser
 1 5 10 15
 Leu Phe Ser Ala Cys Lys Asp Glu Pro Lys Lys Ser Ser Gln Ser His
 20 25 30
 Gln Asn Asn Thr Lys Ile Thr Lys Asn Asn Pro Ile Asn Gln Ala Asn
 35 40 45
 Asn Asp Ile Arg Lys Ile Glu His Glu Glu Glu Asp Glu Lys Ala Thr
 50 55 60
 Lys Glu Val Asn Asp Leu Ile Asn Asn Glu Asn Lys Ile Asp Glu Ile
 65 70 75 80
 Asn Asn Glu Glu Asn Ala Asp Pro Ser Gln Lys Arg Thr Asn Asn Val
 85 90 95
 Leu Gln Arg Ala Thr Asn His Gln Asp Asn Leu Asn Ser Pro Leu Asn
 100 105 110
 Arg Lys Tyr
 115

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 121...1065
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CTATCAAGTC AGTATTTCCA ATATCCAATT AGCCAATGAT CTCAAAGATT CTAATATTTT	60
TATCCACCAG CGTTTAATCA TCCCCACCAA CAAAAATTA CTCGCTACAA GGAATTTTA	120
ATG GGT TTG GCG TTG GAA AAA GTT TGT TTT TTA GGC GTT ATT TTT TTG	168
Met Gly Leu Ala Leu Glu Lys Val Cys Phe Leu Gly Val Ile Phe Leu	
1 5 10 15	
ATT AGC GCT TGC ACG GTT AAA AAA GAG GGG GTA AAG AAT TTG TCT TAC	216
Ile Ser Ala Cys Thr Val Lys Lys Glu Gly Val Lys Asn Leu Ser Tyr	
20 25 30	
AAG CAT GAA AGC TTG CGC GCT TAT GAA AAC GCT AAA GAT TAT GAT CCG	264
Lys His Glu Ser Leu Arg Ala Tyr Glu Asn Ala Lys Asp Tyr Asp Pro	
35 40 45	
ACA ACC AAA AAA GCC GCC TAT AAA CGC AAT TTT TTT GAA CGC CAT TTC	312
Thr Thr Lys Lys Ala Ala Tyr Lys Arg Asn Phe Phe Glu Arg His Phe	
50 55 60	
AAA CGC TAC TCC GAT TCG CAA GAT AGC AAC ACA AAA GAT CAG CCA CTA	360
Lys Arg Tyr Ser Asp Ser Gln Asp Ser Asn Thr Lys Asp Gln Pro Leu	
65 70 75 80	
GAT AAC GGC ATG CGC GAT TCT AGC TCG ATC CAA AGA GCC ACC ATG CGC	408
Asp Asn Gly Met Arg Asp Ser Ser Ser Ile Gln Arg Ala Thr Met Arg	
85 90 95	
CCT TAT CAA GTG GGG GGC AAG TGG TAT TAC CCC ACT AAA GTG GAT TTA	456
Pro Tyr Gln Val Gly Gly Lys Trp Tyr Tyr Pro Thr Lys Val Asp Leu	
100 105 110	
GGC GAA AAA TTT GAT GGC GTT GCG AGT TGG TAT GGC CCT AAC TTC CAT	504
Gly Glu Lys Phe Asp Gly Val Ala Ser Trp Tyr Gly Pro Asn Phe His	
115 120 125	
GCC AAA AAA ACC AGT AAT GGG GAA ATT TAT AAC ATG TAT GCC CAC ACC	552
Ala Lys Lys Thr Ser Asn Gly Glu Ile Tyr Asn Met Tyr Ala His Thr	
130 135 140	
GCC GCG CAC AAA ACT TTA CCC ATG AAC ACC GTG GTG AAA GTC ATC AAT	600
Ala Ala His Lys Thr Leu Pro Met Asn Thr Val Val Lys Val Ile Asn	
145 150 155 160	
GTT GAT AAT AAC TTA AGC ACC ATT GTG CGC ATC AAC GAT AGA GGG CCT	648
Val Asp Asn Asn Leu Ser Thr Ile Val Arg Ile Asn Asp Arg Gly Pro	
165 170 175	
TTT GTG AGC GAT CGC ATC ATT GAT TTG TCT AAT GCG GCC GCT AGG GAT	696

Phe	Val	Ser	Asp	Arg	Ile	Ile	Asp	Leu	Ser	Asn	Ala	Ala	Ala	Arg	Asp	
			180					185						190		
ATT	GAC	ATG	GTT	AAA	AAA	GGC	ACA	GCC	AGC	GTG	CGT	CTC	ATT	GTT	TTG	744
Ile	Asp	Met	Val	Lys	Lys	Gly	Thr	Ala	Ser	Val	Arg	Leu	Ile	Val	Leu	
		195					200					205				
GGC	TTT	GGT	GGG	GTT	ATC	TCC	ACG	CAA	TAC	GAA	CAA	TCC	TTT	AAC	GCC	792
Gly	Phe	Gly	Gly	Val	Ile	Ser	Thr	Gln	Tyr	Glu	Gln	Ser	Phe	Asn	Ala	
	210					215				220						
AGC	TCT	TCA	AAG	ATC	TTG	CAC	AAG	GAA	TTT	AAA	GTC	GGC	GAG	AGC	GAA	840
Ser	Ser	Ser	Lys	Ile	Leu	His	Lys	Glu	Phe	Lys	Val	Gly	Glu	Ser	Glu	
225					230				235					240		
AAA	AGC	GTG	AGC	GGA	GGG	AAA	TTT	TCT	TTG	CAA	ATG	GGG	GCT	TTT	AGA	888
Lys	Ser	Val	Ser	Gly	Gly	Lys	Phe	Ser	Leu	Gln	Met	Gly	Ala	Phe	Arg	
				245				250						255		
AAC	CAA	ATA	GGT	GCT	CAA	ACT	TTA	GCG	GAT	AAA	TTG	CAA	GCA	GAA	AAT	936
Asn	Gln	Ile	Gly	Ala	Gln	Thr	Leu	Ala	Asp	Lys	Leu	Gln	Ala	Glu	Asn	
			260				265					270				
CCA	AAT	TAC	AGC	GTC	AAG	GTT	GCT	TTT	AAA	GAC	GAT	TTG	TAT	AAA	GTT	984
Pro	Asn	Tyr	Ser	Val	Lys	Val	Ala	Phe	Lys	Asp	Asp	Leu	Tyr	Lys	Val	
		275					280					285				
TTA	GTT	CAA	GGG	TTT	CAA	AGC	GAA	GAA	GAG	GCT	AGG	GAT	TTT	ATG	AAA	1032
Leu	Val	Gln	Gly	Phe	Gln	Ser	Glu	Glu	Glu	Ala	Arg	Asp	Phe	Met	Lys	
	290					295				300						
AAA	TAC	AAC	CAG	AAT	GCG	GTT	TTA	ACG	AGA	GAA	TGATTAAGTT	ATTGCTTTTA				1085
Lys	Tyr	Asn	Gln	Asn	Ala	Val	Leu	Thr	Arg	Glu						
305					310					315						
GATGTGGATG	GCACGCTCAC	AGACGGATCG	TTGTAT													1121

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Gly	Leu	Ala	Leu	Glu	Lys	Val	Cys	Phe	Leu	Gly	Val	Ile	Phe	Leu
1				5					10					15	
Ile	Ser	Ala	Cys	Thr	Val	Lys	Lys	Glu	Gly	Val	Lys	Asn	Leu	Ser	Tyr
		20						25				30			
Lys	His	Glu	Ser	Leu	Arg	Ala	Tyr	Glu	Asn	Ala	Lys	Asp	Tyr	Asp	Pro
		35				40					45				
Thr	Thr	Lys	Lys	Ala	Ala	Tyr	Lys	Arg	Asn	Phe	Phe	Glu	Arg	His	Phe
50						55					60				

Lys	Arg	Tyr	Ser	Asp	Ser	Gln	Asp	Ser	Asn	Thr	Lys	Asp	Gln	Pro	Leu	
65					70					75					80	
Asp	Asn	Gly	Met	Arg	Asp	Ser	Ser	Ser	Ile	Gln	Arg	Ala	Thr	Met	Arg	
				85					90					95		
Pro	Tyr	Gln	Val	Gly	Gly	Lys	Trp	Tyr	Tyr	Pro	Thr	Lys	Val	Asp	Leu	
			100					105					110			
Gly	Glu	Lys	Phe	Asp	Gly	Val	Ala	Ser	Trp	Tyr	Gly	Pro	Asn	Phe	His	
		115					120					125				
Ala	Lys	Lys	Thr	Ser	Asn	Gly	Glu	Ile	Tyr	Asn	Met	Tyr	Ala	His	Thr	
	130					135					140					
Ala	Ala	His	Lys	Thr	Leu	Pro	Met	Asn	Thr	Val	Val	Lys	Val	Ile	Asn	
145					150					155					160	
Val	Asp	Asn	Asn	Leu	Ser	Thr	Ile	Val	Arg	Ile	Asn	Asp	Arg	Gly	Pro	
			165						170					175		
Phe	Val	Ser	Asp	Arg	Ile	Ile	Asp	Leu	Ser	Asn	Ala	Ala	Ala	Arg	Asp	
			180					185					190			
Ile	Asp	Met	Val	Lys	Lys	Gly	Thr	Ala	Ser	Val	Arg	Leu	Ile	Val	Leu	
	195						200					205				
Gly	Phe	Gly	Gly	Val	Ile	Ser	Thr	Gln	Tyr	Glu	Gln	Ser	Phe	Asn	Ala	
	210					215					220					
Ser	Ser	Ser	Lys	Ile	Leu	His	Lys	Glu	Phe	Lys	Val	Gly	Glu	Ser	Glu	
225					230					235					240	
Lys	Ser	Val	Ser	Gly	Gly	Lys	Phe	Ser	Leu	Gln	Met	Gly	Ala	Phe	Arg	
				245					250					255		
Asn	Gln	Ile	Gly	Ala	Gln	Thr	Leu	Ala	Asp	Lys	Leu	Gln	Ala	Glu	Asn	
			260					265					270			
Pro	Asn	Tyr	Ser	Val	Lys	Val	Ala	Phe	Lys	Asp	Asp	Leu	Tyr	Lys	Val	
		275					280					285				
Leu	Val	Gln	Gly	Phe	Gln	Ser	Glu	Glu	Glu	Ala	Arg	Asp	Phe	Met	Lys	
	290					295				300						
Lys	Tyr	Asn	Gln	Asn	Ala	Val	Leu	Thr	Arg	Glu						
305					310					315						

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...761
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TATAATAAGG	AAATTCTAAA	CGAAAATTAA	ACTGAATGAA	AGGAGTTTGA	ATG	AAA	56
					Met	Lys	
					1		
AAA	ATC	GTT	TTA	GTA	GCG	ATA	
Lys	Ile	Val	Leu	Val	Ala	Ile	
					Ala	Leu	
					Leu	Met	
					Ser	Ala	
					Cys	Ala	
					Ser		104

5					10					15						
TAT	AAG	ATC	ACG	CCT	GAA	CAT	GTT	ACT	TCC	TAT	AAT	AAT	GGG	ATT	CAA	152
Tyr	Lys	Ile	Thr	Pro	Glu	His	Val	Thr	Ser	Tyr	Asn	Asn	Gly	Ile	Gln	
20						25					30					
GTG	ATG	ACT	TCC	ACG	CAA	GCC	AAA	TCT	AAA	GTC	CAG	CTA	GAA	ATC	GCT	200
Val	Met	Thr	Ser	Thr	Gln	Ala	Lys	Ser	Lys	Val	Gln	Leu	Glu	Ile	Ala	
35					40					45					50	
CAA	AGC	AAG	TTG	AAA	GGC	TTG	AAC	GAG	TCC	CCC	TTA	GTG	CTG	TAT	GTA	248
Gln	Ser	Lys	Leu	Lys	Gly	Leu	Asn	Glu	Ser	Pro	Leu	Val	Leu	Tyr	Val	
				55					60					65		
GCG	GCG	CAA	GTT	ATA	GAG	GGA	AGT	CCT	GTG	GTG	TTT	AGC	CGT	AAA	GCC	296
Ala	Ala	Gln	Val	Ile	Glu	Gly	Ser	Pro	Val	Val	Phe	Ser	Arg	Lys	Ala	
			70					75					80			
ATT	TCA	GTG	TCT	ATC	AAC	CAA	ACG	AAT	TTA	CCG	GTC	TTA	AGC	CTG	AGA	344
Ile	Ser	Val	Ser	Ile	Asn	Gln	Thr	Asn	Leu	Pro	Val	Leu	Ser	Leu	Arg	
		85					90					95				
CAG	GTG	ATG	AAA	TCC	AGT	TTT	GAT	TTT	GAG	GGT	ATT	TTA	CAA	AGT	TTT	392
Gln	Val	Met	Lys	Ser	Ser	Phe	Asp	Phe	Glu	Gly	Ile	Leu	Gln	Ser	Phe	
100						105					110					
AAT	ATC	GCC	GTG	CCG	ACC	ACC	CCT	ATT	GAT	AAT	GTC	AAT	ATG	ATC	ACC	440
Asn	Ile	Ala	Val	Pro	Thr	Thr	Pro	Ile	Asp	Asn	Val	Asn	Met	Ile	Thr	
115					120					125					130	
CCG	CCT	ATG	TTT	TAT	TAC	GGG	CAA	GGG	GGA	TTT	TTA	GCT	TAT	AAC	GGC	488
Pro	Pro	Met	Phe	Tyr	Tyr	Gly	Gln	Gly	Gly	Phe	Leu	Ala	Tyr	Asn	Gly	
				135					140					145		
ATG	ATG	TAT	GGG	GGA	ATG	GGC	ATG	TAT	GGG	CCA	GGC	TTT	GGC	ATG	ATG	536
Met	Met	Tyr	Gly	Gly	Met	Gly	Met	Tyr	Gly	Pro	Gly	Phe	Gly	Met	Met	
			150					155					160			
ATG	ATG	GAT	GAT	GTA	GAA	GAG	CAA	GAA	GTC	ATG	CAA	GAA	AGC	CGC	CAA	584
Met	Met	Asp	Asp	Val	Glu	Glu	Gln	Glu	Val	Met	Gln	Glu	Ser	Arg	Gln	
		165					170					175				
GCT	TTA	AAA	ATC	CTA	GCG	ATC	AAT	TAC	CTT	AAA	AAC	AAC	ACC	CTT	AAT	632
Ala	Leu	Lys	Ile	Leu	Ala	Ile	Asn	Tyr	Leu	Lys	Asn	Asn	Thr	Leu	Asn	
180						185					190					
GTT	GAG	AGT	AAG	GCT	AAG	GGA	GGG	TTT	GTG	GTG	GTG	GAT	ACC	AAA	AAC	680
Val	Glu	Ser	Lys	Ala	Lys	Gly	Gly	Phe	Val	Val	Val	Asp	Thr	Lys	Asn	
195					200					205					210	
CTT	AAA	ACC	CCG	GGT	GTG	GTG	GTG	GTT	AAA	GTC	TTT	TTA	GAA	GAT	GAA	728
Leu	Lys	Thr	Pro	Gly	Val	Val	Val	Val	Lys	Val	Phe	Leu	Glu	Asp	Glu	
				215					220					225		
ATC	CAC	ACC	TTT	AAA	ATT	GAT	ATT	TCT	AAG	ATG	TAATCGCCCC	CTTTAATAAAA				781
Ile	His	Thr	Phe	Lys	Ile	Asp	Ile	Ser	Lys	Met						
			230					235								

AGCCTTTGGG CCATCCACCT AAAGGTTTTT

811

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met	Lys	Lys	Ile	Val	Leu	Val	Ala	Ile	Ala	Leu	Leu	Met	Ser	Ala	Cys	1	5	10	15
Ala	Ser	Tyr	Lys	Ile	Thr	Pro	Glu	His	Val	Thr	Ser	Tyr	Asn	Asn	Gly	20	25	30	
Ile	Gln	Val	Met	Thr	Ser	Thr	Gln	Ala	Lys	Ser	Lys	Val	Gln	Leu	Glu	35	40	45	
Ile	Ala	Gln	Ser	Lys	Leu	Lys	Gly	Leu	Asn	Glu	Ser	Pro	Leu	Val	Leu	50	55	60	
Tyr	Val	Ala	Ala	Gln	Val	Ile	Glu	Gly	Ser	Pro	Val	Val	Phe	Ser	Arg	65	70	75	80
Lys	Ala	Ile	Ser	Val	Ser	Ile	Asn	Gln	Thr	Asn	Leu	Pro	Val	Leu	Ser	85	90	95	
Leu	Arg	Gln	Val	Met	Lys	Ser	Ser	Phe	Asp	Phe	Glu	Gly	Ile	Leu	Gln	100	105	110	
Ser	Phe	Asn	Ile	Ala	Val	Pro	Thr	Thr	Pro	Ile	Asp	Asn	Val	Asn	Met	115	120	125	
Ile	Thr	Pro	Pro	Met	Phe	Tyr	Tyr	Gly	Gln	Gly	Gly	Phe	Leu	Ala	Tyr	130	135	140	
Asn	Gly	Met	Met	Tyr	Gly	Gly	Met	Gly	Met	Tyr	Gly	Pro	Gly	Phe	Gly	145	150	155	160
Met	Met	Met	Met	Asp	Asp	Val	Glu	Glu	Gln	Glu	Val	Met	Gln	Glu	Ser	165	170	175	
Arg	Gln	Ala	Leu	Lys	Ile	Leu	Ala	Ile	Asn	Tyr	Leu	Lys	Asn	Asn	Thr	180	185	190	
Leu	Asn	Val	Glu	Ser	Lys	Ala	Lys	Gly	Gly	Phe	Val	Val	Val	Asp	Thr	195	200	205	
Lys	Asn	Leu	Lys	Thr	Pro	Gly	Val	Val	Val	Val	Lys	Val	Phe	Leu	Glu	210	215	220	
Asp	Glu	Ile	His	Thr	Phe	Lys	Ile	Asp	Ile	Ser	Lys	Met				225	230	235	

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

(B) LOCATION: 97...1371
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TAAAAAAAAAC	TACCCCTTAAA	AAAATCAATC	TAAAATTCTT	AAATTAAAAT	ATAGCTATAA	60
TACACTAAAA	CAATCTCAAG	GTTTCAAAT	TTAGCC	ATG	CGT CTT CTT CTG TTC	114
				Met	Arg Leu Leu Leu Phe	
				1	5	
AAT CAA AAC	GCT TTT TTA	TTA GCG TGC	ATG TTT GTT	TCA AGC GTG	TAT	162
Asn Gln Asn	Ala Phe Leu	Leu Ala Cys	Met Phe Val	Ser Ser Val	Tyr	
	10	15		20		
GTG AAC GCT	GTC TTA GAC	GCT TAT GCA	ATT GAA AAC	CCC TAT ATT	TCT	210
Val Asn Ala	Val Leu Asp	Ala Tyr Ala	Ile Glu Asn	Pro Tyr Ile	Ser	
	25	30		35		
ATC ACA CTC	ACA AGC CTA	TTA GCC CCT	TTA AGC ATG	CTA GCG TTT	TTA	258
Ile Thr Leu	Thr Ser Leu	Leu Ala Pro	Leu Ser Met	Leu Ala Phe	Leu	
	40	45		50		
AAA ACC CCT	AGA AAT AGT	GCT TTT GCT	TTG GGG TTT	TTT GTG GGG	GCG	306
Lys Thr Pro	Arg Asn Ser	Ala Phe Ala	Leu Gly Phe	Phe Val Gly	Ala	
	60		65	70		
TTA TTG TTT	TAT TGG TGC	GCT TTA AGC	TTT CGC TAC	TCG GAT TTC	ACT	354
Leu Leu Phe	Tyr Trp Cys	Ala Leu Ser	Phe Arg Tyr	Ser Asp Phe	Thr	
	75		80	85		
TAT TTA TTG	CCC TTA ATC	ATT GTT TTA	ATA GCG TTA	GTT TAT GGG	GTT	402
Tyr Leu Leu	Pro Leu Ile	Ile Val Leu	Ile Ala Leu	Val Tyr Gly	Val	
	90		95	100		
TTA TTT TAT	TTG TTG CTC	TAT TTT GAA	AAC CCC TAT	TTC AGG CTT	TTG	450
Leu Phe Tyr	Leu Leu Leu	Tyr Phe Glu	Asn Pro Tyr	Phe Arg Leu	Leu	
	105		110	115		
AGT TTT TTA	GGC TCT AGT	TTT ATC CAC	CCC TTT GGA	TTT GAT TGG	TTA	498
Ser Phe Leu	Gly Ser Ser	Phe Ile His	Pro Phe Gly	Phe Asp Trp	Leu	
	120		130			
GTC CCA GAT	AGC TTT TTT	TCT TAT AGC	GTG TTT AGA	GTG GAT AAA	TTA	546
Val Pro Asp	Ser Phe Phe	Ser Tyr Ser	Val Phe Arg	Val Asp Lys	Leu	
	135		145	150		
TCG CTA GGG	CTT GTT TTT	TTG GCT TGC	ATT TTT TTG	AGC ACT AAA	CCA	594
Ser Leu Gly	Leu Val Phe	Leu Ala Cys	Ile Phe Leu	Ser Thr Lys	Pro	
	155		160	165		
TTG AAA AAA	TAT AGG ATC	ATA GGG GTT	TTA TTG TTA	CTT GGC GCG	TTG	642
Leu Lys Lys	Tyr Arg Ile	Ile Gly Val	Leu Leu Leu	Leu Gly Ala	Leu	
	170		175	180		
GAT TTT AAT	GGT TTC AAA	ACA AGC GAT	TTA AAA AAG	GTT GGA AAT	ATT	690
Asp Phe Asn	Gly Phe Lys	Thr Ser Asp	Leu Lys Lys	Val Gly Asn	Ile	

185					190					195						
GAA	TTA	GTC	TCT	ACA	AAA	ACG	CCC	CAA	GAT	TTG	AAA	TTT	GAC	TCA	AGT	738
Glu	Leu	Val	Ser	Thr	Lys	Thr	Pro	Gln	Asp	Leu	Lys	Phe	Asp	Ser	Ser	
	200					205					210					
TAC	CTT	AAT	GAT	ATT	GAA	AAC	AAC	ATT	CTT	AAA	GAA	ATC	AAG	CTC	GCT	786
Tyr	Leu	Asn	Asp	Ile	Glu	Asn	Asn	Ile	Leu	Lys	Glu	Ile	Lys	Leu	Ala	
215					220					225					230	
CAA	AGC	AAG	CAA	AAA	ACC	TTG	ATT	GTT	TTT	CCA	GAA	ACC	GCC	TAC	CCC	834
Gln	Ser	Lys	Gln	Lys	Thr	Leu	Ile	Val	Phe	Pro	Glu	Thr	Ala	Tyr	Pro	
				235					240					245		
ATC	GCT	TTA	GAA	AAC	TCC	CCC	TTT	AAA	GCG	AAG	CTA	GAA	GAT	TTA	AGC	882
Ile	Ala	Leu	Glu	Asn	Ser	Pro	Phe	Lys	Ala	Lys	Leu	Glu	Asp	Leu	Ser	
			250					255					260			
GAT	AAT	ATT	GCT	ATT	TTA	ATA	GGG	ACA	TTA	CGG	ACT	CAA	GGC	TAT	AAT	930
Asp	Asn	Ile	Ala	Ile	Leu	Ile	Gly	Thr	Leu	Arg	Thr	Gln	Gly	Tyr	Asn	
		265					270					275				
CTT	TAT	AAC	AGC	TCG	TTT	TTA	TTT	TCT	AAA	GAA	AGC	GTT	CAG	ATC	GCT	978
Leu	Tyr	Asn	Ser	Ser	Phe	Leu	Phe	Ser	Lys	Glu	Ser	Val	Gln	Ile	Ala	
	280					285					290					
GAT	AAA	GTA	ATT	TTA	GCC	CCC	TTT	GGC	GAG	ACC	ATG	CCT	TTA	CCG	GAA	1026
Asp	Lys	Val	Ile	Leu	Ala	Pro	Phe	Gly	Glu	Thr	Met	Pro	Leu	Pro	Glu	
295					300					305					310	
TTT	CTT	CAA	AAA	CCC	CTT	GAA	AAG	CTC	TTT	TTT	GGC	GAG	AGC	ACT	TAT	1074
Phe	Leu	Gln	Lys	Pro	Leu	Glu	Lys	Leu	Phe	Phe	Gly	Glu	Ser	Thr	Tyr	
				315					320					325		
TTA	TAC	CGC	AAT	GCT	CCT	CAT	TTC	AGC	GAT	TTT	ACA	TTA	GAC	GAT	TTT	1122
Leu	Tyr	Arg	Asn	Ala	Pro	His	Phe	Ser	Asp	Phe	Thr	Leu	Asp	Asp	Phe	
			330					335					340			
ACT	TTT	CGC	CCC	CTG	ATT	TGC	TAT	GAA	GGC	ACT	TCC	AAA	CCC	GCT	TAT	1170
Thr	Phe	Arg	Pro	Leu	Ile	Cys	Tyr	Glu	Gly	Thr	Ser	Lys	Pro	Ala	Tyr	
		345				350						355				
TCA	AAC	AGC	CCT	TCA	AAA	ATT	TTT	ATC	GTG	ATG	AGC	AAT	AAC	GCA	TGG	1218
Ser	Asn	Ser	Pro	Ser	Lys	Ile	Phe	Ile	Val	Met	Ser	Asn	Asn	Ala	Trp	
	360					365					370					
TTT	AGC	CCA	AGC	ATT	GAA	CCC	ACC	TTA	CAA	AGA	ACG	CTT	TTA	AAA	TAC	1266
Phe	Ser	Pro	Ser	Ile	Glu	Pro	Thr	Leu	Gln	Arg	Thr	Leu	Leu	Lys	Tyr	
375					380					385					390	
TAC	GCA	AGG	CGT	TAT	GAT	AAG	ATC	ATC	TTG	CAC	AGC	GCG	AAC	TTT	TCA	1314
Tyr	Ala	Arg	Arg	Tyr	Asp	Lys	Ile	Ile	Leu	His	Ser	Ala	Asn	Phe	Ser	
				395					400					405		
ACT	TCT	TAC	ATC	TTA	AGC	CCT	AGT	TTA	TTA	GGC	GAT	ATT	CTT	TTT	AGG	1362
Thr	Ser	Tyr	Ile	Leu	Ser	Pro	Ser	Leu	Leu	Gly	Asp	Ile	Leu	Phe	Arg	
			410					415					420			

AAA CGA TCA TGATTAAAGC GATTAATATT TCTCATGCTT TTGAAAAGCC TCTTTATAA 1420
 Lys Arg Ser
 425

TGGCG

1425

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met	Arg	Leu	Leu	Leu	Phe	Asn	Gln	Asn	Ala	Phe	Leu	Leu	Ala	Cys	Met
1				5					10					15	
Phe	Val	Ser	Ser	Val	Tyr	Val	Asn	Ala	Val	Leu	Asp	Ala	Tyr	Ala	Ile
		20						25					30		
Glu	Asn	Pro	Tyr	Ile	Ser	Ile	Thr	Leu	Thr	Ser	Leu	Leu	Ala	Pro	Leu
		35					40					45			
Ser	Met	Leu	Ala	Phe	Leu	Lys	Thr	Pro	Arg	Asn	Ser	Ala	Phe	Ala	Leu
	50					55					60				
Gly	Phe	Phe	Val	Gly	Ala	Leu	Leu	Phe	Tyr	Trp	Cys	Ala	Leu	Ser	Phe
65				70					75					80	
Arg	Tyr	Ser	Asp	Phe	Thr	Tyr	Leu	Leu	Pro	Leu	Ile	Ile	Val	Leu	Ile
			85						90					95	
Ala	Leu	Val	Tyr	Gly	Val	Leu	Phe	Tyr	Leu	Leu	Leu	Tyr	Phe	Glu	Asn
		100						105					110		
Pro	Tyr	Phe	Arg	Leu	Leu	Ser	Phe	Leu	Gly	Ser	Ser	Phe	Ile	His	Pro
		115					120					125			
Phe	Gly	Phe	Asp	Trp	Leu	Val	Pro	Asp	Ser	Phe	Phe	Ser	Tyr	Ser	Val
	130					135					140				
Phe	Arg	Val	Asp	Lys	Leu	Ser	Leu	Gly	Leu	Val	Phe	Leu	Ala	Cys	Ile
145				150					155					160	
Phe	Leu	Ser	Thr	Lys	Pro	Leu	Lys	Lys	Tyr	Arg	Ile	Ile	Gly	Val	Leu
			165						170					175	
Leu	Leu	Leu	Gly	Ala	Leu	Asp	Phe	Asn	Gly	Phe	Lys	Thr	Ser	Asp	Leu
		180						185					190		
Lys	Lys	Val	Gly	Asn	Ile	Glu	Leu	Val	Ser	Thr	Lys	Thr	Pro	Gln	Asp
		195					200					205			
Leu	Lys	Phe	Asp	Ser	Ser	Tyr	Leu	Asn	Asp	Ile	Glu	Asn	Asn	Ile	Leu
	210					215					220				
Lys	Glu	Ile	Lys	Leu	Ala	Gln	Ser	Lys	Gln	Lys	Thr	Leu	Ile	Val	Phe
225				230					235					240	
Pro	Glu	Thr	Ala	Tyr	Pro	Ile	Ala	Leu	Glu	Asn	Ser	Pro	Phe	Lys	Ala
			245						250					255	
Lys	Leu	Glu	Asp	Leu	Ser	Asp	Asn	Ile	Ala	Ile	Leu	Ile	Gly	Thr	Leu
		260					265						270		
Arg	Thr	Gln	Gly	Tyr	Asn	Leu	Tyr	Asn	Ser	Ser	Phe	Leu	Phe	Ser	Lys
		275					280					285			
Glu	Ser	Val	Gln	Ile	Ala	Asp	Lys	Val	Ile	Leu	Ala	Pro	Phe	Gly	Glu
	290					295					300				
Thr	Met	Pro	Leu	Pro	Glu	Phe	Leu	Gln	Lys	Pro	Leu	Glu	Lys	Leu	Phe

305		310		315		320									
Phe	Gly	Glu	Ser	Thr	Tyr	Leu	Tyr	Arg	Asn	Ala	Pro	His	Phe	Ser	Asp
				325					330					335	
Phe	Thr	Leu	Asp	Asp	Phe	Thr	Phe	Arg	Pro	Leu	Ile	Cys	Tyr	Glu	Gly
			340					345					350		
Thr	Ser	Lys	Pro	Ala	Tyr	Ser	Asn	Ser	Pro	Ser	Lys	Ile	Phe	Ile	Val
		355					360					365			
Met	Ser	Asn	Asn	Ala	Trp	Phe	Ser	Pro	Ser	Ile	Glu	Pro	Thr	Leu	Gln
	370					375					380				
Arg	Thr	Leu	Leu	Lys	Tyr	Tyr	Ala	Arg	Arg	Tyr	Asp	Lys	Ile	Ile	Leu
385					390					395					400
His	Ser	Ala	Asn	Phe	Ser	Thr	Ser	Tyr	Ile	Leu	Ser	Pro	Ser	Leu	Leu
			405						410					415	
Gly	Asp	Ile	Leu	Phe	Arg	Lys	Arg	Ser							
			420					425							

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...713
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TGTAGTAAGA	TACCTAGTTT	TCAAATCTAT	TAAAAGATAA	AGGTTATTAC	ATG TTT	56
					Met Phe	
					1	
TCA CTT TCT TAT GTT TCC AAG AAA TTT TTA AGC GTT TTA TTA TTG ATT	104					
Ser Leu Ser Tyr Val Ser Lys Lys Phe Leu Ser Val Leu Leu Leu Ile						
5 10 15						
TCG CTG TTT TTA AGC GCT TGC AAA TCC AAC AAT AAA GAC AAG TTA GAC	152					
Ser Leu Phe Leu Ser Ala Cys Lys Ser Asn Asn Lys Asp Lys Leu Asp						
20 25 30						
GAA AAT CTT TTA AGC TCT GGC TCT CAA AGC TCC AAA GAA TTA AAC GAT	200					
Glu Asn Leu Leu Ser Ser Gly Ser Gln Ser Ser Lys Glu Leu Asn Asp						
35 40 45 50						
GAG CGA GAC AAT ATA GAC AAA AAG AGT TAC GCT GGT TTA GAA GAT GTT	248					
Glu Arg Asp Asn Ile Asp Lys Lys Ser Tyr Ala Gly Leu Glu Asp Val						
55 60 65						
TTT TCA GAC AAT AAG TCC ATT AGT CCT AAC GAT AAA TAC ATG CTT TTA	296					
Phe Ser Asp Asn Lys Ser Ile Ser Pro Asn Asp Lys Tyr Met Leu Leu						
70 75 80						

GTT TTT GGC CGT AAT GGT TGC TCC TAT TGC GAA AGG TTT AAA AAA GAT	344
Val Phe Gly Arg Asn Gly Cys Ser Tyr Cys Glu Arg Phe Lys Lys Asp	
85 90 95	
CTC AAA AAT GTC AAA GAA TTG CGC GAC TAC ATT AAA GAG CAT TTT AGC	392
Leu Lys Asn Val Lys Glu Leu Arg Asp Tyr Ile Lys Glu His Phe Ser	
100 105 110	
GCT TAC TAT GTC AAT ATC AGC TAC TCC AAA GAG CAT GAT TTT AAA GTC	440
Ala Tyr Tyr Val Asn Ile Ser Tyr Ser Lys Glu His Asp Phe Lys Val	
115 120 125 130	
GGC GAT AAA AAT AAT GAA AAA GAA ATC AAA ATG TCC ACA GAA GAA TTA	488
Gly Asp Lys Asn Asn Glu Lys Glu Ile Lys Met Ser Thr Glu Glu Leu	
135 140 145	
GCG CAA ATT TAT GCC GTC CAA TCC ACC CCT ACG ATT GTT TTA TCC GAT	536
Ala Gln Ile Tyr Ala Val Gln Ser Thr Pro Thr Ile Val Leu Ser Asp	
150 155 160	
AAA ACC GGC AAA ACC ATC TAT GAA TTG CCC GGC TAT ATG CCC TCT ACG	584
Lys Thr Gly Lys Thr Ile Tyr Glu Leu Pro Gly Tyr Met Pro Ser Thr	
165 170 175	
CAA TTT TTA GCC GTG TTA GAA TTT ATC GGC GAT GGG AAG TAT CAA GAC	632
Gln Phe Leu Ala Val Leu Glu Phe Ile Gly Asp Gly Lys Tyr Gln Asp	
180 185 190	
ACA AAA GAC GAT GAG GAT CTC ACT AAA AAA TTA AAG GCT TAC ATC AAG	680
Thr Lys Asp Asp Glu Asp Leu Thr Lys Lys Leu Lys Ala Tyr Ile Lys	
195 200 205 210	
TAT AAA ACC AAC CTT TCT AAA AGC AAG TCT AAC TAGGAAAGCC TAATGAAGAA	733
Tyr Lys Thr Asn Leu Ser Lys Ser Lys Ser Asn	
215 220	
TCTCAAAAAGC CTGCTTTCTT TTTTGCTGGC TTC	766

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met Phe Ser Leu Ser Tyr Val Ser Lys Lys Phe Leu Ser Val Leu Leu	
1 5 10 15	
Leu Ile Ser Leu Phe Leu Ser Ala Cys Lys Ser Asn Asn Lys Asp Lys	
20 25 30	
Leu Asp Glu Asn Leu Leu Ser Ser Gly Ser Gln Ser Ser Lys Glu Leu	
35 40 45	
Asn Asp Glu Arg Asp Asn Ile Asp Lys Lys Ser Tyr Ala Gly Leu Glu	

50	55	60
Asp Val Phe Ser Asp Asn Lys Ser Ile Ser Pro Asn Asp Lys Tyr Met		
65	70	75
Leu Leu Val Phe Gly Arg Asn Gly Cys Ser Tyr Cys Glu Arg Phe Lys		80
	85	90
Lys Asp Leu Lys Asn Val Lys Glu Leu Arg Asp Tyr Ile Lys Glu His		95
	100	105
Phe Ser Ala Tyr Tyr Val Asn Ile Ser Tyr Ser Lys Glu His Asp Phe		110
	115	120
Lys Val Gly Asp Lys Asn Asn Glu Lys Glu Ile Lys Met Ser Thr Glu		125
	130	135
Glu Leu Ala Gln Ile Tyr Ala Val Gln Ser Thr Pro Thr Ile Val Leu		140
145	150	155
Ser Asp Lys Thr Gly Lys Thr Ile Tyr Glu Leu Pro Gly Tyr Met Pro		160
	165	170
Ser Thr Gln Phe Leu Ala Val Leu Glu Phe Ile Gly Asp Gly Lys Tyr		175
	180	185
Gln Asp Thr Lys Asp Asp Glu Asp Leu Thr Lys Lys Leu Lys Ala Tyr		190
	195	200
Ile Lys Tyr Lys Thr Asn Leu Ser Lys Ser Lys Ser Asn		205
210	215	220

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 980 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 53...931
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TGAATGAAAT CCTAGATTCT AACGCCATTG TATATTATCT CGCTAAAAAT TC ATG AGA	58
Met Arg	
1	
TTG TTA TTC TTG TTA TTG AGT GCT GCT TTT ATG TTA CTG GCT GAA GAA	106
Leu Leu Phe Leu Leu Leu Ser Ala Ala Phe Met Leu Leu Ala Glu Glu	
5 10 15	
AAA ATA TCT TTA AAC GAT GAC GCC CCC ATT AAA CTA GTG CAT TGG CAA	154
Lys Ile Ser Leu Asn Asp Asp Ala Pro Ile Lys Leu Val His Trp Gln	
20 25 30	
AAT GCA TTA AAA GAA GTC CAA CCT GAT TCA AAC GCT CCA GCA ACA CCA	202
Asn Ala Leu Lys Glu Val Gln Pro Asp Ser Asn Ala Pro Ala Thr Pro	
35 40 45 50	
CCT ATA AAA GCC GTG CAA ACC ACG CTC ACT TTT GAA ACG CCT TTT AAC	250
Pro Ile Lys Ala Val Gln Thr Thr Leu Thr Phe Glu Thr Pro Phe Asn	

55										60					65					
AAA Lys	ACG Thr	CCT Pro	AAA Lys 70	ATC Ile	ATG Met	GAA Glu	GTT Val	GAA Glu 75	GGG Gly	CAA Gln	AAG Lys	GTG Val	ATC Ile 80	GTC Val	TTA Leu	298				
AAA Lys	AAC Asn	GCT Ala 85	AAA Lys	CTG Leu	GAT Asp	TCT Ser	AAA Lys 90	AAA Lys	ACC Thr	ATG Met	GAT Asp	TTT Phe 95	AAA Lys	GAA Glu	GCC Ala	346				
TCT Ser	TTG Leu 100	AAT Asn	GCT Ala	TTA Leu	GAA Glu	ATG Met 105	TTT Phe	TCC Ser	TAC Tyr	CAA Gln	AAT Asn 110	GAC Asp	ATC Ile	TAC Tyr	CTC Leu	394				
TTG Leu 115	TCT Ser	AAA Lys	AAA Lys	GCT Ala	AAA Lys 120	GTG Val	GAA Glu	TTA Leu	GAA Glu	ATC Ile 125	CAA Gln	GCT Ala	TCA Ser	AAC Asn	AGC Ser 130	442				
AAG Lys	GAT Asp	AAA Lys	AAA Lys	CGG Arg 135	CTC Leu	CGC Arg	TTT Phe	CTC Leu	TTT Phe 140	TTA Leu	CCC Pro	AAA Lys	GGT Gly	TTT Phe 145	CAT His	490				
TTA Leu	GCC Ala	CCA Pro	CCG Pro 150	CCT Pro	AAC Asn	CTG Leu	AAA Lys	GAA Glu 155	AAA Lys	TCT Ser	CAG Gln	CAA Gln	ACT Thr 160	AAC Asn	CTT Leu	538				
GCA Ala	CAA Gln	AAA Lys 165	GAC Asp	ACC Thr	AAC Asn	GAG Glu	CAA Gln 170	CCC Pro	CAA Gln	AGC Ser	CCT Pro	TTA Leu 175	AAC Asn	ACT Thr	CTA Leu	586				
GAG Glu	TTA Leu 180	AAA Lys	CCC Pro	CCA Pro	CTA Leu	AAT Asn 185	TTA Leu	AGC Ser	CAT His	GCT Ala	TAT Tyr 190	AAG Lys	GCG Ala	CTA Leu	GCG Ala	634				
GTT Val 195	ATT Ile	GCT Ala	GCC Ala	TTA Leu 200	CTC Leu	TTA Leu	ATA Ile	TTG Leu	TAT Tyr	GTC Val 205	ATC Ile	AAA Lys	AAA Lys	AAA Lys	ATT Ile 210	682				
GTT Val	CCC Pro	ACA Thr	CAA Gln	GGG Gly 215	TCT Ser	TTT Phe	TCT Ser	GCA Ala	AAA Lys 220	GAT Asp	TTT Phe	AAG Lys	TTA Leu	GAA Glu 225	ATT Ile	730				
AGC Ser	GTT Val	TTG Leu	GGT Gly 230	CGT Arg	GTT Val	GAT Asp	GCG Ala	AAC Asn 235	CAT His	AAA Lys	ATC Ile	ATT Ile	TCA Ser 240	ATA Ile	GAA Glu	778				
ACC Thr	AAT Asn	AAG Lys 245	GAG Glu	CGT Arg	TAC Tyr	TTG Leu	GTC Val 250	TTA Leu	CTA Leu	AGC Ser	GAT Asp	AAA Lys 255	TAC Tyr	GGC Gly	CTG Leu	826				
CTT Leu	TTA Leu 260	GAC Asp	AAA Lys	ATA Ile	AGC Ser	CCA Pro 265	AAA Lys	ACA Thr	TCT Ser	AAA Lys	GAA Glu 270	GAA Glu	CTG Leu	ATT Ile	AAA Lys	874				
GAA Glu 275	GCT Ala	GAA Glu	AAT Asn	AAT Asn	ATA Ile 280	AAG Lys	AAT Asn	TCA Ser	AAA Lys	TTA Leu 285	GGA Gly	AAT Asn	TTA Leu	TAT Tyr	GCC Ala 290	922				

GGA AAA TTC TAAACTACAA CCTGCTAAGT TAGGGAAAAA TTTTGACCCT GTGGATCAT 980
Gly Lys Phe

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met	Arg	Leu	Leu	Phe	Leu	Leu	Leu	Ser	Ala	Ala	Phe	Met	Leu	Leu	Ala	1	5	10	15
Glu	Glu	Lys	Ile	Ser	Leu	Asn	Asp	Asp	Ala	Pro	Ile	Lys	Leu	Val	His	20	25	30	
Trp	Gln	Asn	Ala	Leu	Lys	Glu	Val	Gln	Pro	Asp	Ser	Asn	Ala	Pro	Ala	35	40	45	
Thr	Pro	Pro	Ile	Lys	Ala	Val	Gln	Thr	Thr	Leu	Thr	Phe	Glu	Thr	Pro	50	55	60	
Phe	Asn	Lys	Thr	Pro	Lys	Ile	Met	Glu	Val	Glu	Gly	Gln	Lys	Val	Ile	65	70	75	80
Val	Leu	Lys	Asn	Ala	Lys	Leu	Asp	Ser	Lys	Lys	Thr	Met	Asp	Phe	Lys	85	90	95	
Glu	Ala	Ser	Leu	Asn	Ala	Leu	Glu	Met	Phe	Ser	Tyr	Gln	Asn	Asp	Ile	100	105	110	
Tyr	Leu	Leu	Ser	Lys	Lys	Ala	Lys	Val	Glu	Leu	Glu	Ile	Gln	Ala	Ser	115	120	125	
Asn	Ser	Lys	Asp	Lys	Lys	Arg	Leu	Arg	Phe	Leu	Phe	Leu	Pro	Lys	Gly	130	135	140	
Phe	His	Leu	Ala	Pro	Pro	Asn	Leu	Lys	Glu	Lys	Ser	Gln	Gln	Thr		145	150	155	160
Asn	Leu	Ala	Gln	Lys	Asp	Thr	Asn	Glu	Gln	Pro	Gln	Ser	Pro	Leu	Asn	165	170	175	
Thr	Leu	Glu	Leu	Lys	Pro	Pro	Leu	Asn	Leu	Ser	His	Ala	Tyr	Lys	Ala	180	185	190	
Leu	Ala	Val	Ile	Ala	Ala	Leu	Leu	Leu	Ile	Leu	Tyr	Val	Ile	Lys	Lys	195	200	205	
Lys	Ile	Val	Pro	Thr	Gln	Gly	Ser	Phe	Ser	Ala	Lys	Asp	Phe	Lys	Leu	210	215	220	
Glu	Ile	Ser	Val	Leu	Gly	Arg	Val	Asp	Ala	Asn	His	Lys	Ile	Ile	Ser	225	230	235	240
Ile	Glu	Thr	Asn	Lys	Glu	Arg	Tyr	Leu	Val	Leu	Leu	Ser	Asp	Lys	Tyr	245	250	255	
Gly	Leu	Leu	Leu	Asp	Lys	Ile	Ser	Pro	Lys	Thr	Ser	Lys	Glu	Glu	Leu	260	265	270	
Ile	Lys	Glu	Ala	Glu	Asn	Asn	Ile	Lys	Asn	Ser	Lys	Leu	Gly	Asn	Leu	275	280	285	
Tyr	Ala	Gly	Lys	Phe												290			

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 70...567
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

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CTAGCGCGAT CTTTGGTCTC ACACAAGCTA TAACAAGCTT GAGAATCGCA TAATATATTC      60
TTGTTCTAC ATG CTA TCA CCA GCA ACT TTC AAA CAA ATA ACT CTA GCA TTA      111
      Met Leu Ser Pro Ala Thr Phe Lys Gln Ile Thr Leu Ala Leu
        1             5             10

ATC GCT TCA AGA CTA ATC GTT GTA ATC CTA TAT GCT TTT ATC TTT ATT      159
Ile Ala Ser Arg Leu Ile Val Val Ile Leu Tyr Ala Phe Ile Phe Ile
15             20             25             30

GTT CTC TCT TTT TAT ATG CTC AAT ATC ATC ACT ATT CTT AAT TTT AAA      207
Val Leu Ser Phe Tyr Met Leu Asn Ile Ile Thr Ile Leu Asn Phe Lys
              35             40             45

GCG CTT ATT TTG GGG TTT GTT AGT GTT TTT TCA AGC GCA TTG TTT TGT      255
Ala Leu Ile Leu Gly Phe Val Ser Val Phe Ser Ser Ala Leu Phe Cys
              50             55             60

TTT TGC TTG GCA ATT TTT GTA GCT AGA ATT TTT CAA AAC GAA CAA AGC      303
Phe Cys Leu Ala Ile Phe Val Ala Arg Ile Phe Gln Asn Glu Gln Ser
              65             70             75

ATC TTA GGA TTT TGT AAT ATC ATC AAT CTC TAT GCG CTA ATG TCT TGT      351
Ile Leu Gly Phe Cys Asn Ile Ile Asn Leu Tyr Ala Leu Met Ser Cys
              80             85             90

AAT GTT TTT GTT CCT TTA GAA TAC CTA CCT AGT ATT GGT CAA TTA TTT      399
Asn Val Phe Val Pro Leu Glu Tyr Leu Pro Ser Ile Gly Gln Leu Phe
              95             100             105             110

ATC AAA ACA TCT ATT TTT TAC TAC CTT AAT CAA CTT CTA ATC AAA GCT      447
Ile Lys Thr Ser Ile Phe Tyr Tyr Leu Asn Gln Leu Leu Ile Lys Ala
              115             120             125

TTT CAA GGG ATT GAT ACT ATA CTG GTT TTA GCA ACT TCA ACA TTT TTC      495
Phe Gln Gly Ile Asp Thr Ile Leu Val Leu Ala Thr Ser Thr Phe Phe
              130             135             140

ATT ATT GGT GGC ATT ATT TTA TTT TTA CTA AGC GCT AAT CGC ATG TTA      543
Ile Ile Gly Gly Ile Ile Leu Phe Leu Leu Ser Ala Asn Arg Met Leu
              145             150             155

CTA ACA CCA AAA GAA CGC ATG CGT TAAAGGCTTA GTCCCACCAT TGATTTATTT      597

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Leu Thr Pro Lys Glu Arg Met Arg
160 165

AATGGCTCAA AAAAGGGGTA AGC

620

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met	Leu	Ser	Pro	Ala	Thr	Phe	Lys	Gln	Ile	Thr	Leu	Ala	Leu	Ile	Ala
1				5				10						15	
Ser	Arg	Leu	Ile	Val	Val	Ile	Leu	Tyr	Ala	Phe	Ile	Phe	Ile	Val	Leu
			20					25					30		
Ser	Phe	Tyr	Met	Leu	Asn	Ile	Ile	Thr	Ile	Leu	Asn	Phe	Lys	Ala	Leu
		35					40					45			
Ile	Leu	Gly	Phe	Val	Ser	Val	Phe	Ser	Ser	Ala	Leu	Phe	Cys	Phe	Cys
	50					55					60				
Leu	Ala	Ile	Phe	Val	Ala	Arg	Ile	Phe	Gln	Asn	Glu	Gln	Ser	Ile	Leu
65					70				75					80	
Gly	Phe	Cys	Asn	Ile	Ile	Asn	Leu	Tyr	Ala	Leu	Met	Ser	Cys	Asn	Val
			85					90						95	
Phe	Val	Pro	Leu	Glu	Tyr	Leu	Pro	Ser	Ile	Gly	Gln	Leu	Phe	Ile	Lys
			100					105					110		
Thr	Ser	Ile	Phe	Tyr	Tyr	Leu	Asn	Gln	Leu	Leu	Ile	Lys	Ala	Phe	Gln
		115				120						125			
Gly	Ile	Asp	Thr	Ile	Leu	Val	Leu	Ala	Thr	Ser	Thr	Phe	Phe	Ile	Ile
	130					135					140				
Gly	Gly	Ile	Ile	Leu	Phe	Leu	Leu	Ser	Ala	Asn	Arg	Met	Leu	Leu	Thr
145				150					155						160
Pro	Lys	Glu	Arg	Met	Arg										
				165											

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 50...1366
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ATTGATTTCT TTTGGGAAGT GGATTTGAAA AACTTAAAAA GCCATTAAC ATG CAA GTT	58
Met Gln Val	
1	
AAA GAA AAC AAA CAA CTC TGC TTA ATT TCA TTA GGT TGC TCT AAA AAT	106
Lys Glu Asn Lys Gln Leu Cys Leu Ile Ser Leu Gly Cys Ser Lys Asn	
5 10 15	
TTG GTG GAT TCA GAG GTG ATG TTA GGC AAG CTT TAT AAT TAC ACG CTC	154
Leu Val Asp Ser Glu Val Met Leu Gly Lys Leu Tyr Asn Tyr Thr Leu	
20 25 30 35	
ACT AAT GAC GCT AAG AGC GCT GAT GTG ATT TTG ATC AAC ACT TGC GGG	202
Thr Asn Asp Ala Lys Ser Ala Asp Val Ile Leu Ile Asn Thr Cys Gly	
40 45 50	
TTT ATT GAA AGC GCT AAA CAA GAG AGT ATC CAA ACC ATT CTC AAC GCC	250
Phe Ile Glu Ser Ala Lys Gln Glu Ser Ile Gln Thr Ile Leu Asn Ala	
55 60 65	
GCC AAA GAC AAA AAA GAG GGA GCG ATT TTG ATT GCG AGC GGG TGC TTG	298
Ala Lys Asp Lys Lys Glu Gly Ala Ile Leu Ile Ala Ser Gly Cys Leu	
70 75 80	
AGC GAA CGC TAT AAA GAT GAA ATC AAA GAA TTG ATC CCT GAA GTG GAT	346
Ser Glu Arg Tyr Lys Asp Glu Ile Lys Glu Leu Ile Pro Glu Val Asp	
85 90 95	
ATT TTT ACC GGC GTG GGG GAT TAT GAC AAG ATC GAT ATA ATG ATT GCT	394
Ile Phe Thr Gly Val Gly Asp Tyr Asp Lys Ile Asp Ile Met Ile Ala	
100 105 110 115	
AAA AAA CAA AAC CAG TTC AGC GAG CAA GTG TTT TTA AGC GAG CAT TAC	442
Lys Lys Gln Asn Gln Phe Ser Glu Gln Val Phe Leu Ser Glu His Tyr	
120 125 130	
AAC GCA CGC ATC ATC ACG GGA TCG AGC GTG CAT GCG TAT GTG AAA ATT	490
Asn Ala Arg Ile Ile Thr Gly Ser Ser Val His Ala Tyr Val Lys Ile	
135 140 145	
TCT GAG GGT TGC AAT CAA AAA TGT TCT TTT TGC GCT ATC CCT AGC TTT	538
Ser Glu Gly Cys Asn Gln Lys Cys Ser Phe Cys Ala Ile Pro Ser Phe	
150 155 160	
AAG GGG AAA TTG CAA AGC AGG GAA TTG GAC TCC ATT TTA AAA GAA GTG	586
Lys Gly Lys Leu Gln Ser Arg Glu Leu Asp Ser Ile Leu Lys Glu Val	
165 170 175	
GAA AAT CTC GCG CTT AAA GGC TAT ACG GAT ATG ACT TTT ATC GCT CAA	634
Glu Asn Leu Ala Leu Lys Gly Tyr Thr Asp Met Thr Phe Ile Ala Gln	
180 185 190 195	
GAC TCT AGC TCC TTT TTA TAC GAT AAG GGG CAA AAA GAC GGC TTG ATC	682
Asp Ser Ser Ser Phe Leu Tyr Asp Lys Gly Gln Lys Asp Gly Leu Ile	
200 205 210	
CAG CTC ATT AGA GCG ATT GAT AAA CAG CAA GCC TTA AAG AGC GCG CGT	730
Gln Leu Ile Arg Ala Ile Asp Lys Gln Gln Ala Leu Lys Ser Ala Arg	

215					220					225							
ATT	TTA	TAT	CTC	TAC	CCC	TCT	AGC	ACC	ACG	CTA	GAG	CTT	ATT	GGC	GCG	778	
Ile	Leu	Tyr	Leu	Tyr	Pro	Ser	Ser	Thr	Thr	Leu	Glu	Leu	Ile	Gly	Ala		
		230					235					240					
ATT	GAA	AGT	TCG	CCC	ATT	TTT	CAA	AAT	TAT	TTT	GAC	ATG	CCC	ATC	CAG	826	
Ile	Glu	Ser	Ser	Pro	Ile	Phe	Gln	Asn	Tyr	Phe	Asp	Met	Pro	Ile	Gln		
	245					250					255						
CAC	ATC	AGC	GAC	TCC	ATG	CTC	AAA	AAG	ATG	CGG	CGC	AAC	TCT	AGC	CAA	874	
His	Ile	Ser	Asp	Ser	Met	Leu	Lys	Lys	Met	Arg	Arg	Asn	Ser	Ser	Gln		
260					265					270					275		
GCG	CAC	CAT	TTA	AAG	CTT	TTA	GAT	GCC	ATG	AAG	CAG	GTT	AAA	GAA	AGC	922	
Ala	His	His	Leu	Lys	Leu	Leu	Asp	Ala	Met	Lys	Gln	Val	Lys	Glu	Ser		
				280					285					290			
TTT	ATC	AGA	AGC	ACG	ATC	ATT	GTA	GGG	CAT	CCG	GAA	GAA	AAT	GAG	AGC	970	
Phe	Ile	Arg	Ser	Thr	Ile	Ile	Val	Gly	His	Pro	Glu	Glu	Asn	Glu	Ser		
			295					300					305				
GAA	TTT	GAA	GAA	TTG	AGC	GCG	TTT	TTA	GAC	GAG	TTC	CAG	TTT	GAT	AGA	1018	
Glu	Phe	Glu	Glu	Leu	Ser	Ala	Phe	Leu	Asp	Glu	Phe	Gln	Phe	Asp	Arg		
		310					315					320					
TTG	AAT	ATT	TTT	GCT	TTC	AGC	GCT	GAA	GAA	AAC	ACG	CAT	GCC	TAT	TCT	1066	
Leu	Asn	Ile	Phe	Ala	Phe	Ser	Ala	Glu	Glu	Asn	Thr	His	Ala	Tyr	Ser		
	325					330					335						
TTA	GAA	AAA	GTG	CCT	AAA	AAA	ACC	ATC	AAC	GCT	CGC	ATC	AAA	GCC	TTG	1114	
Leu	Glu	Lys	Val	Pro	Lys	Lys	Thr	Ile	Asn	Ala	Arg	Ile	Lys	Ala	Leu		
340					345					350					355		
AAT	AAA	ATC	GCT	TTA	AAG	CAC	CAA	AAC	CAT	TCC	TTT	AAG	GCT	TTG	TTG	1162	
Asn	Lys	Ile	Ala	Leu	Lys	His	Gln	Asn	His	Ser	Phe	Lys	Ala	Leu	Leu		
				360					365					370			
AAT	AAG	CCC	ATT	AAG	GCG	TTA	GTG	GAA	AAT	AAA	GAG	GGC	GAG	TAT	TTT	1210	
Asn	Lys	Pro	Ile	Lys	Ala	Leu	Val	Glu	Asn	Lys	Glu	Gly	Glu	Tyr	Phe		
			375					380					385				
TAC	AAA	GCA	AGG	GAT	CTC	AGA	TGG	GCG	CCT	GAA	GTG	GAT	GGG	GAA	ATC	1258	
Tyr	Lys	Ala	Arg	Asp	Leu	Arg	Trp	Ala	Pro	Glu	Val	Asp	Gly	Glu	Ile		
		390					395					400					
TTG	ATC	AAT	GAT	AGC	GAA	CTA	ACC	ACC	CCC	TTA	AAA	CCC	GGG	CAT	TAT	1306	
Leu	Ile	Asn	Asp	Ser	Glu	Leu	Thr	Thr	Pro	Leu	Lys	Pro	Gly	His	Tyr		
	405					410					415						
ACG	ATT	GCA	CCT	AGC	GAA	TTT	AAA	GAT	AAT	ATC	CTA	CTC	GCT	AAG	GTT	1354	
Thr	Ile	Ala	Pro	Ser	Glu	Phe	Lys	Asp	Asn	Ile	Leu	Leu	Ala	Lys	Val		
420					425					430					435		
TTA	AGC	CCT	TTT	TAAAGTTAG			CCATAAGGCT			AAAAGCACGG			CTAAAGCGT			1405	
Leu	Ser	Pro	Phe														

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met	Gln	Val	Lys	Glu	Asn	Lys	Gln	Leu	Cys	Leu	Ile	Ser	Leu	Gly	Cys
1				5					10					15	
Ser	Lys	Asn	Leu	Val	Asp	Ser	Glu	Val	Met	Leu	Gly	Lys	Leu	Tyr	Asn
			20					25					30		
Tyr	Thr	Leu	Thr	Asn	Asp	Ala	Lys	Ser	Ala	Asp	Val	Ile	Leu	Ile	Asn
		35					40					45			
Thr	Cys	Gly	Phe	Ile	Glu	Ser	Ala	Lys	Gln	Glu	Ser	Ile	Gln	Thr	Ile
	50					55				60					
Leu	Asn	Ala	Ala	Lys	Asp	Lys	Lys	Glu	Gly	Ala	Ile	Leu	Ile	Ala	Ser
65					70				75					80	
Gly	Cys	Leu	Ser	Glu	Arg	Tyr	Lys	Asp	Glu	Ile	Lys	Glu	Leu	Ile	Pro
				85					90				95		
Glu	Val	Asp	Ile	Phe	Thr	Gly	Val	Gly	Asp	Tyr	Asp	Lys	Ile	Asp	Ile
			100					105					110		
Met	Ile	Ala	Lys	Lys	Gln	Asn	Gln	Phe	Ser	Glu	Gln	Val	Phe	Leu	Ser
		115					120					125			
Glu	His	Tyr	Asn	Ala	Arg	Ile	Ile	Thr	Gly	Ser	Ser	Val	His	Ala	Tyr
	130					135					140				
Val	Lys	Ile	Ser	Glu	Gly	Cys	Asn	Gln	Lys	Cys	Ser	Phe	Cys	Ala	Ile
145					150					155				160	
Pro	Ser	Phe	Lys	Gly	Lys	Leu	Gln	Ser	Arg	Glu	Leu	Asp	Ser	Ile	Leu
				165					170					175	
Lys	Glu	Val	Glu	Asn	Leu	Ala	Leu	Lys	Gly	Tyr	Thr	Asp	Met	Thr	Phe
			180					185					190		
Ile	Ala	Gln	Asp	Ser	Ser	Ser	Phe	Leu	Tyr	Asp	Lys	Gly	Gln	Lys	Asp
		195					200					205			
Gly	Leu	Ile	Gln	Leu	Ile	Arg	Ala	Ile	Asp	Lys	Gln	Gln	Ala	Leu	Lys
	210					215					220				
Ser	Ala	Arg	Ile	Leu	Tyr	Leu	Tyr	Pro	Ser	Ser	Thr	Thr	Leu	Glu	Leu
225					230					235				240	
Ile	Gly	Ala	Ile	Glu	Ser	Ser	Pro	Ile	Phe	Gln	Asn	Tyr	Phe	Asp	Met
				245					250					255	
Pro	Ile	Gln	His	Ile	Ser	Asp	Ser	Met	Leu	Lys	Lys	Met	Arg	Arg	Asn
			260					265					270		
Ser	Ser	Gln	Ala	His	His	Leu	Lys	Leu	Leu	Asp	Ala	Met	Lys	Gln	Val
		275					280					285			
Lys	Glu	Ser	Phe	Ile	Arg	Ser	Thr	Ile	Ile	Val	Gly	His	Pro	Glu	Glu
	290					295					300				
Asn	Glu	Ser	Glu	Phe	Glu	Glu	Leu	Ser	Ala	Phe	Leu	Asp	Glu	Phe	Gln
305					310					315				320	
Phe	Asp	Arg	Leu	Asn	Ile	Phe	Ala	Phe	Ser	Ala	Glu	Glu	Asn	Thr	His
				325					330					335	
Ala	Tyr	Ser	Leu	Glu	Lys	Val	Pro	Lys	Lys	Thr	Ile	Asn	Ala	Arg	Ile
			340					345					350		
Lys	Ala	Leu	Asn	Lys	Ile	Ala	Leu	Lys	His	Gln	Asn	His	Ser	Phe	Lys

355	360	365
Ala Leu Leu Asn Lys Pro Ile Lys Ala Leu Val Glu Asn Lys Glu Gly		
370	375	380
Glu Tyr Phe Tyr Lys Ala Arg Asp Leu Arg Trp Ala Pro Glu Val Asp		
385	390	395
Gly Glu Ile Leu Ile Asn Asp Ser Glu Leu Thr Thr Pro Leu Lys Pro		400
	405	410
Gly His Tyr Thr Ile Ala Pro Ser Glu Phe Lys Asp Asn Ile Leu Leu		415
	420	425
Ala Lys Val Leu Ser Pro Phe		430
435		

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 200...1366
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

TGCGCGTTAT RTGGTTTTGA TTGAAAAGTT AGGCATTAAA GACAGATAAT TTTTATCGGT	60
TTTAGGGTGT GGCGAGTTTG TGTTGAAAGA GCGTTTGAAG GCCTTTTTTA GTGCGGACTC	120
TGTTTTCAC TTAATTTTTG CCCTTTTCTT TCTCACTTCG TTTAAAAAAC CTTTAACTCA	180
AGTCTTGTTG ATTGTTTTA ATG GTT TTT TTG TTT TTT AGG TGT TAT TTC CAA	232
Met Val Phe Leu Phe Phe Arg Cys Tyr Phe Gln	
1 5 10	
GCG TCT TTG AAA GAA ACT TTC GCA ATT AAT CAT TTA AAA ACA ATG TCT	280
Ala Ser Leu Lys Glu Thr Phe Ala Ile Asn His Leu Lys Thr Met Ser	
15 20 25	
TTT AAA TGG CTC ACT CTG GCT TTT TTG GGC GTG TTT TTA AGC ATC TTC	328
Phe Lys Trp Leu Thr Leu Ala Phe Leu Gly Val Phe Leu Ser Ile Phe	
30 35 40	
CCT AAC ATG TTT AAC ATG CAT GAT AGC CAA ACT TTC CGC TAC AAT TTA	376
Pro Asn Met Phe Asn Met His Asp Ser Gln Thr Phe Arg Tyr Asn Leu	
45 50 55	
TTC GCT CTA AAC ATG TCC TTA ACT TAT GCT TGC GGG GCG TTA TGC TTG	424
Phe Ala Leu Asn Met Ser Leu Thr Tyr Ala Cys Gly Ala Leu Cys Leu	
60 65 70 75	
CTT TTT GCC AGT TGC TTA AGA ATC AAA TTG AAT CAA AAA ATC CTT TTT	472
Leu Phe Ala Ser Cys Leu Arg Ile Lys Leu Asn Gln Lys Ile Leu Phe	
80 85 90	

TAC	AGC	ATG	GCT	GTT	GCA	AAT	TTC	ATC	AAC	GGC	TTG	CTC	TCA	TTG	GTG	520
Tyr	Ser	Met	Ala	Val	Ala	Asn	Phe	Ile	Asn	Gly	Leu	Leu	Ser	Leu	Val	
			95					100						105		
CAA	AAA	ATT	TAT	TTT	AAC	ATG	CCC	AGA	GCG	CAA	GGG	TTT	AGC	ACG	GTT	568
Gln	Lys	Ile	Tyr	Phe	Asn	Met	Pro	Arg	Ala	Gln	Gly	Phe	Ser	Thr	Val	
		110					115					120				
AAG	GAG	TAT	GTG	GTT	TTA	GTG	AGC	GTG	TCC	ATT	TTA	GGC	TGT	TAT	ATT	616
Lys	Glu	Tyr	Val	Val	Leu	Val	Ser	Val	Ser	Ile	Leu	Gly	Cys	Tyr	Ile	
	125					130					135					
TAT	GCG	CTT	TAT	TCG	CAC	AAT	CAA	AAA	GAA	AAA	CTT	TTT	TTC	ACG	CTT	664
Tyr	Ala	Leu	Tyr	Ser	His	Asn	Gln	Lys	Glu	Lys	Leu	Phe	Phe	Thr	Leu	
140					145					150					155	
TCT	GTT	TTT	GTG	GGG	TTT	TTA	GTC	GTT	ATT	TTA	AGC	GCC	ACA	AGG	AGC	712
Ser	Val	Phe	Val	Gly	Phe	Leu	Val	Val	Ile	Leu	Ser	Ala	Thr	Arg	Ser	
				160					165					170		
GCG	ACA	ATC	GCT	TTT	GTT	ATT	ACT	TTT	TTA	ATC	CTT	TCT	TGC	TTT	ATT	760
Ala	Thr	Ile	Ala	Phe	Val	Ile	Thr	Phe	Leu	Ile	Leu	Ser	Cys	Phe	Ile	
			175					180					185			
TTA	TAC	GCC	AAA	AAA	TCG	CTC	AAA	CCA	TTG	GGT	TAT	ATG	GTG	GTC	GTG	808
Leu	Tyr	Ala	Lys	Lys	Ser	Leu	Lys	Pro	Leu	Gly	Tyr	Met	Val	Val	Val	
		190					195					200				
AGT	CTT	ATT	TTG	AGC	GCT	TTG	TAT	GTG	GGG	AGT	AAC	GCT	TTA	GAA	AAA	856
Ser	Leu	Ile	Leu	Ser	Ala	Leu	Tyr	Val	Gly	Ser	Asn	Ala	Leu	Glu	Lys	
	205					210					215					
AAG	GGG	GCA	ATA	GAG	CAA	TCT	AGA	GTT	CAA	AAT	CAA	AGC	TTT	GAA	GAA	904
Lys	Gly	Ala	Ile	Glu	Gln	Ser	Arg	Val	Gln	Asn	Gln	Ser	Phe	Glu	Glu	
220					225				230					235		
GAT	CTG	AAA	CGC	TAC	GCT	AAA	AAG	GAC	GCT	GAT	AGC	AGT	ATC	GGA	TGG	952
Asp	Leu	Lys	Arg	Tyr	Ala	Lys	Lys	Asp	Ala	Asp	Ser	Ser	Ile	Gly	Trp	
				240				245						250		
CGT	TTG	GAG	CGT	TGG	AAA	GAA	GCC	CTA	ACG	GTT	TTG	CGT	TTA	AGG	CCC	1000
Arg	Leu	Glu	Arg	Trp	Lys	Glu	Ala	Leu	Thr	Val	Leu	Arg	Leu	Arg	Pro	
			255					260					265			
TTT	TTT	GGT	ATG	GCC	GCT	AGC	GAG	AAA	TGC	CAG	AGG	TTA	GAA	GAG	ATT	1048
Phe	Phe	Gly	Met	Ala	Ala	Ser	Glu	Lys	Cys	Gln	Arg	Leu	Glu	Glu	Ile	
		270					275					280				
TTA	TCC	TTA	TCA	AAG	TCT	TAT	AGG	GCC	AAA	GAT	TTG	ATT	CTC	TGT	TAT	1096
Leu	Ser	Leu	Ser	Lys	Ser	Tyr	Arg	Ala	Lys	Asp	Leu	Ile	Leu	Cys	Tyr	
	285					290					295					
GAA	AGA	TAC	GAC	AAT	CAA	ATC	ATT	CAC	ATT	TTA	GCC	ACT	AGG	GGG	ATC	1144
Glu	Arg	Tyr	Asp	Asn	Gln	Ile	Ile	His	Ile	Leu	Ala	Thr	Arg	Gly	Ile	
300					305					310				315		
ATA	GGC	TTT	TTG	ATC	TGG	CTC	TTT	TTT	TTA	TTA	GTT	ATT	GTA	AAG	ATT	1192
Ile	Gly	Phe	Leu	Ile	Trp	Leu	Phe	Phe	Leu	Leu	Val	Ile	Val	Lys	Ile	

320	325	330	
TTT TGG AGC GGG ATA AAG CAA AAC TCT TTA ATA TCG TTT TTT ATA CTA			1240
Phe Trp Ser Gly Ile Lys Gln Asn Ser Leu Ile Ser Phe Phe Ile Leu			
335	340	345	
ATG ACA CTC GCC TTT TAC CTC ATT TTT GGC ATT GGG TTT GAC CCC TTT			1288
Met Thr Leu Ala Phe Tyr Leu Ile Phe Gly Ile Gly Phe Asp Pro Phe			
350	355	360	
GAT TTC TTC ATT ACG GGA AGT TTT TTT GTA GGA ATG ATC ATG ATG GCT			1336
Asp Phe Phe Ile Thr Gly Ser Phe Phe Val Gly Met Ile Met Met Ala			
365	370	375	
GTT TTT TTA AAA AAA GAT AAA AGT GCT TTT TAGCATCAAG GGGTTTGACA TTA			1389
Val Phe Leu Lys Lys Asp Lys Ser Ala Phe			
380	385		
GTCAAGCGGT AGTTTCTTGT GATTCGTTCT T			1420

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met	Val	Phe	Leu	Phe	Phe	Arg	Cys	Tyr	Phe	Gln	Ala	Ser	Leu	Lys	Glu
1				5				10						15	
Thr	Phe	Ala	Ile	Asn	His	Leu	Lys	Thr	Met	Ser	Phe	Lys	Trp	Leu	Thr
			20					25					30		
Leu	Ala	Phe	Leu	Gly	Val	Phe	Leu	Ser	Ile	Phe	Pro	Asn	Met	Phe	Asn
			35					40				45			
Met	His	Asp	Ser	Gln	Thr	Phe	Arg	Tyr	Asn	Leu	Phe	Ala	Leu	Asn	Met
			50				55				60				
Ser	Leu	Thr	Tyr	Ala	Cys	Gly	Ala	Leu	Cys	Leu	Leu	Phe	Ala	Ser	Cys
65					70				75					80	
Leu	Arg	Ile	Lys	Leu	Asn	Gln	Lys	Ile	Leu	Phe	Tyr	Ser	Met	Ala	Val
				85				90						95	
Ala	Asn	Phe	Ile	Asn	Gly	Leu	Leu	Ser	Leu	Val	Gln	Lys	Ile	Tyr	Phe
			100					105					110		
Asn	Met	Pro	Arg	Ala	Gln	Gly	Phe	Ser	Thr	Val	Lys	Glu	Tyr	Val	Val
			115				120					125			
Leu	Val	Ser	Val	Ser	Ile	Leu	Gly	Cys	Tyr	Ile	Tyr	Ala	Leu	Tyr	Ser
			130				135				140				
His	Asn	Gln	Lys	Glu	Lys	Leu	Phe	Phe	Thr	Leu	Ser	Val	Phe	Val	Gly
145					150				155						160
Phe	Leu	Val	Val	Ile	Leu	Ser	Ala	Thr	Arg	Ser	Ala	Thr	Ile	Ala	Phe
				165				170						175	
Val	Ile	Thr	Phe	Leu	Ile	Leu	Ser	Cys	Phe	Ile	Leu	Tyr	Ala	Lys	Lys
			180					185				190			
Ser	Leu	Lys	Pro	Leu	Gly	Tyr	Met	Val	Val	Val	Ser	Leu	Ile	Leu	Ser

195	200	205
Ala Leu Tyr Val Gly Ser Asn	Ala Leu Glu Lys Lys	Gly Ala Ile Glu
210	215	220
Gln Ser Arg Val Gln Asn Gln Ser Phe Glu Glu Asp	Leu Lys Arg Tyr	
225	230	235
Ala Lys Lys Asp Ala Asp Ser Ser Ile Gly Trp Arg	Leu Glu Arg Trp	
245	250	255
Lys Glu Ala Leu Thr Val Leu Arg Leu Arg Pro Phe Phe Gly Met Ala		
260	265	270
Ala Ser Glu Lys Cys Gln Arg Leu Glu Glu Ile Leu Ser Leu Ser Lys		
275	280	285
Ser Tyr Arg Ala Lys Asp Leu Ile Leu Cys Tyr Glu Arg Tyr Asp Asn		
290	295	300
Gln Ile Ile His Ile Leu Ala Thr Arg Gly Ile Ile Gly Phe Leu Ile		
305	310	315
Trp Leu Phe Phe Leu Val Ile Val Lys Ile Phe Trp Ser Gly Ile		
325	330	335
Lys Gln Asn Ser Leu Ile Ser Phe Phe Ile Leu Met Thr Leu Ala Phe		
340	345	350
Tyr Leu Ile Phe Gly Ile Gly Phe Asp Pro Phe Asp Phe Phe Ile Thr		
355	360	365
Gly Ser Phe Phe Val Gly Met Ile Met Met Ala Val Phe Leu Lys Lys		
370	375	380
Asp Lys Ser Ala Phe		
385		

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 89...1198
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

AAAAAGGAAA TAGCACGATG AAACCTAAAG GGGATATTAG CGTTAATATG CTAATATAGT	60
AGAACATTAT GACTACAAAA AGGGTGAT ATG CTG ATC TCC ATA GCG TTT TTA	112
Met Leu Ile Ser Ile Ala Phe Leu	
1 5	
TTG GTT TTA TAT CTT TTG AAT TAT AGT TCT TTC AGG ATG TTG AAA TCG	160
Leu Val Leu Tyr Leu Leu Asn Tyr Ser Ser Phe Arg Met Leu Lys Ser	
10 15 20	
TTT TTA ACC TTA AAG AAA ATC TCT CAA TAC GCT TAT TTA TGG TTT TTT	208
Phe Leu Thr Leu Lys Lys Ile Ser Gln Tyr Ala Tyr Leu Trp Phe Phe	
25 30 35 40	
ATC CTT TTG AGC ATA GGC GAG GCG GCT TTT GTT TTT TAT AGA AAT ATT	256

Ile	Leu	Leu	Ser	Ile	Gly	Glu	Ala	Ala	Phe	Val	Phe	Tyr	Arg	Asn	Ile	
				45					50					55		
ATG	CCT	AGC	CAT	TTG	TTT	GTT	TTG	ACT	TCA	GCG	TGT	TCG	TTT	GTG	TCT	304
Met	Pro	Ser	His	Leu	Phe	Val	Leu	Thr	Ser	Ala	Cys	Ser	Phe	Val	Ser	
			60					65					70			
TTT	ATT	ATT	TTT	ATC	CTT	TCT	TTA	AGT	TTT	TAC	GGG	TTT	TCC	TAT	TCC	352
Phe	Ile	Ile	Phe	Ile	Leu	Ser	Leu	Ser	Phe	Tyr	Gly	Phe	Ser	Tyr	Ser	
			75				80					85				
ATA	GAA	AAA	ATA	GAT	TTT	TTG	CAT	TCA	AGG	CGT	AAA	AGT	TTA	AAA	AAC	400
Ile	Glu	Lys	Ile	Asp	Phe	Leu	His	Ser	Arg	Arg	Lys	Ser	Leu	Lys	Asn	
	90					95					100					
TTT	TTA	AAA	TTG	GGG	TTT	TAT	CTG	GCG	TTA	TTA	GGG	TAT	TTT	TGG	CGT	448
Phe	Leu	Lys	Leu	Gly	Phe	Tyr	Leu	Ala	Leu	Leu	Gly	Tyr	Phe	Trp	Arg	
105					110					115					120	
GGG	TTT	TAT	GAA	GGG	TTG	GCC	CGC	CCT	AAA	ATC	AAA	GAA	ACC	CCT	ATT	496
Gly	Phe	Tyr	Glu	Gly	Leu	Ala	Arg	Pro	Lys	Ile	Lys	Glu	Thr	Pro	Ile	
				125				130						135		
TAT	TTG	GAT	AAG	CTG	GAT	AAA	GAA	TTA	AAG	ATT	ATT	TTA	CTC	ACA	GAC	544
Tyr	Leu	Asp	Lys	Leu	Asp	Lys	Glu	Leu	Lys	Ile	Ile	Leu	Leu	Thr	Asp	
			140					145						150		
ATG	CAT	GTG	GGG	AGT	TTG	TTG	CAA	AAA	GAT	TTT	GTT	GAT	TAC	ATT	GTA	592
Met	His	Val	Gly	Ser	Leu	Leu	Gln	Lys	Asp	Phe	Val	Asp	Tyr	Ile	Val	
			155				160					165				
GAA	GAA	GTC	AAT	CAA	AAA	GAA	GTG	GAT	ATG	GTG	CTG	ATT	GGG	GGG	GAT	640
Glu	Glu	Val	Asn	Gln	Lys	Glu	Val	Asp	Met	Val	Leu	Ile	Gly	Gly	Asp	
	170					175					180					
TTA	GTG	GAT	GAA	AGC	ATT	GAA	AAA	GTC	AAA	TCT	TTT	TTA	CTG	CCT	TTA	688
Leu	Val	Asp	Glu	Ser	Ile	Glu	Lys	Val	Lys	Ser	Phe	Leu	Leu	Pro	Leu	
185					190					195					200	
AAC	AAC	CTT	AAA	AGC	ACG	CAT	GGC	ACT	TTT	TAT	GTG	CCA	GGA	AAT	CAT	736
Asn	Asn	Leu	Lys	Ser	Thr	His	Gly	Thr	Phe	Tyr	Val	Pro	Gly	Asn	His	
				205				210						215		
GAG	TAT	TAT	CAT	GGC	ATA	GAG	CCG	ATT	TTA	TCG	TTT	CTT	GAC	ACG	CTT	784
Glu	Tyr	Tyr	His	Gly	Ile	Glu	Pro	Ile	Leu	Ser	Phe	Leu	Asp	Thr	Leu	
			220					225					230			
AAT	TTG	ACG	ATT	TTA	GGG	AAT	GAG	TGC	GTG	CAT	TTA	GGG	GGG	ATC	AAT	832
Asn	Leu	Thr	Ile	Leu	Gly	Asn	Glu	Cys	Val	His	Leu	Gly	Gly	Ile	Asn	
			235				240					245				
TTG	TGC	GGC	GTG	TAT	GAT	TAT	TTC	GCA	AGG	AAG	CGT	CAA	AAT	TTT	GCC	880
Leu	Cys	Gly	Val	Tyr	Asp	Tyr	Phe	Ala	Arg	Lys	Arg	Gln	Asn	Phe	Ala	
	250					255					260					
CCT	GAT	ATT	GAC	AAA	GCT	TTA	AAA	AAG	CGC	AAT	GAG	AGT	AAG	CCC	ACG	928
Pro	Asp	Ile	Asp	Lys	Ala	Leu	Lys	Lys	Arg	Asn	Glu	Ser	Lys	Pro	Thr	
265					270					275					280	

ATC CTT TTG GCC CAC CAA CCT AAA CAA ATT AGA AGC CTC AAA GAA AGC 976
 Ile Leu Leu Ala His Gln Pro Lys Gln Ile Arg Ser Leu Lys Glu Ser
 285 290 295
 CAC TCT GTA GAT TTA GTC CTT TCA GGG CAT ACC CAT GCA GGG CAA ATC 1024
 His Ser Val Asp Leu Val Leu Ser Gly His Thr His Ala Gly Gln Ile
 300 305 310
 TTT CCC TTT AGC CTT TTA GTC AAG TTG GCG CAA ACC TAT TTA CAT GGT 1072
 Phe Pro Phe Ser Leu Leu Val Lys Leu Ala Gln Thr Tyr Leu His Gly
 315 320 325
 TTA TAC AAG CAC AGC CCC ACC ACT CAA ATT TAT GTG AGC AGT GGG GCA 1120
 Leu Tyr Lys His Ser Pro Thr Thr Gln Ile Tyr Val Ser Ser Gly Ala
 330 335 340
 GGG TAT TGG GGG ATT CCT TTA AGG TTT TTA GCC CCT AGC GAG ATC GCA 1168
 Gly Tyr Trp Gly Ile Pro Leu Arg Phe Leu Ala Pro Ser Glu Ile Ala
 345 350 355 360
 TAC CTT AGG CTT TTA CCT AAA AAT CAA GCT TAGTTAAACA AAATCTTAAA ATC 1221
 Tyr Leu Arg Leu Leu Pro Lys Asn Gln Ala
 365 370
 TTAATCGTAA TCAAGCGGTT AAAAATAAGA A 1252

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Leu Ile Ser Ile Ala Phe Leu Leu Val Leu Tyr Leu Leu Asn Tyr
 1 5 10 15
 Ser Ser Phe Arg Met Leu Lys Ser Phe Leu Thr Leu Lys Lys Ile Ser
 20 25 30
 Gln Tyr Ala Tyr Leu Trp Phe Phe Ile Leu Leu Ser Ile Gly Glu Ala
 35 40 45
 Ala Phe Val Phe Tyr Arg Asn Ile Met Pro Ser His Leu Phe Val Leu
 50 55 60
 Thr Ser Ala Cys Ser Phe Val Ser Phe Ile Ile Phe Ile Leu Ser Leu
 65 70 75 80
 Ser Phe Tyr Gly Phe Ser Tyr Ser Ile Glu Lys Ile Asp Phe Leu His
 85 90 95
 Ser Arg Arg Lys Ser Leu Lys Asn Phe Leu Lys Leu Gly Phe Tyr Leu
 100 105 110
 Ala Leu Leu Gly Tyr Phe Trp Arg Gly Phe Tyr Glu Gly Leu Ala Arg
 115 120 125
 Pro Lys Ile Lys Glu Thr Pro Ile Tyr Leu Asp Lys Leu Asp Lys Glu
 130 135 140
 Leu Lys Ile Ile Leu Leu Thr Asp Met His Val Gly Ser Leu Leu Gln

145		150		155		160									
Lys	Asp	Phe	Val	Asp	Tyr	Ile	Val	Glu	Glu	Val	Asn	Gln	Lys	Glu	Val
				165				170						175	
Asp	Met	Val	Leu	Ile	Gly	Gly	Asp	Leu	Val	Asp	Glu	Ser	Ile	Glu	Lys
			180					185						190	
Val	Lys	Ser	Phe	Leu	Leu	Pro	Leu	Asn	Asn	Leu	Lys	Ser	Thr	His	Gly
		195						200					205		
Thr	Phe	Tyr	Val	Pro	Gly	Asn	His	Glu	Tyr	Tyr	His	Gly	Ile	Glu	Pro
	210					215					220				
Ile	Leu	Ser	Phe	Leu	Asp	Thr	Leu	Asn	Leu	Thr	Ile	Leu	Gly	Asn	Glu
225					230					235				240	
Cys	Val	His	Leu	Gly	Gly	Ile	Asn	Leu	Cys	Gly	Val	Tyr	Asp	Tyr	Phe
			245						250					255	
Ala	Arg	Lys	Arg	Gln	Asn	Phe	Ala	Pro	Asp	Ile	Asp	Lys	Ala	Leu	Lys
			260					265					270		
Lys	Arg	Asn	Glu	Ser	Lys	Pro	Thr	Ile	Leu	Leu	Ala	His	Gln	Pro	Lys
		275					280					285			
Gln	Ile	Arg	Ser	Leu	Lys	Glu	Ser	His	Ser	Val	Asp	Leu	Val	Leu	Ser
	290					295					300				
Gly	His	Thr	His	Ala	Gly	Gln	Ile	Phe	Pro	Phe	Ser	Leu	Leu	Val	Lys
305					310					315				320	
Leu	Ala	Gln	Thr	Tyr	Leu	His	Gly	Leu	Tyr	Lys	His	Ser	Pro	Thr	Thr
			325						330					335	
Gln	Ile	Tyr	Val	Ser	Ser	Gly	Ala	Gly	Tyr	Trp	Gly	Ile	Pro	Leu	Arg
		340						345					350		
Phe	Leu	Ala	Pro	Ser	Glu	Ile	Ala	Tyr	Leu	Arg	Leu	Leu	Pro	Lys	Asn
		355					360					365			
Gln	Ala														
370															

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 103...381
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AGTCTTTGCC	CGCTATCAAA	AAAGAGATTT	TTTGCAATAT	TTTCATAAGC	ACCGAAGAAA	60
GCTTGCTTTA	GCGAGTTTGT	GGGTGAAACG	TACGCCTTGC	TC ATG ATT TTT GTC		114
				Met Ile Phe Val		
				1		
AAT AAA TAT CTC TAT GGG ATT AAA AGC GTT GTG CCT TTG GCG GTT GGT						162
Asn Lys Tyr Leu Tyr Gly Ile Lys Ser Val Val Pro Leu Ala Val Gly						
5	10		15		20	

TTT AGC AAA TAC CCT TTA AAA AAG TTT TTA TGG CTT AAT GTT TTT TCC 210
Phe Ser Lys Tyr Pro Leu Lys Lys Phe Leu Trp Leu Asn Val Phe Ser
25 30 35

AGT TTT TTG TGG GCG CTC ATC GTG GGG AGC GTT TCT TTT CAA GCG AGC 258
Ser Phe Leu Trp Ala Leu Ile Val Gly Ser Val Ser Phe Gln Ala Ser
40 45 50

GAT TGG GTG AAA ACG CTG TAT GAA AGG CTT TCT CAT TAC ACT TCG TTT 306
Asp Trp Val Lys Thr Leu Tyr Glu Arg Leu Ser His Tyr Thr Ser Phe
55 60 65

TTT ATC ATA AGT TTT GTT CTT ATA GCG CTT TTA ATA TGG TTT TTA TTG 354
Phe Ile Ile Ser Phe Val Leu Ile Ala Leu Leu Ile Trp Phe Leu Leu
70 75 80

AAA CGA TAT TCG CGC AAA ATG GGT TTT TAAGCAAGAT GTTTAATTAA ATGCGCT 408
Lys Arg Tyr Ser Arg Lys Met Gly Phe
85 90

AGACTACGCC CACAAGCATT CGC 431

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met Ile Phe Val Asn Lys Tyr Leu Tyr Gly Ile Lys Ser Val Val Pro
1 5 10 15
Leu Ala Val Gly Phe Ser Lys Tyr Pro Leu Lys Lys Phe Leu Trp Leu
20 25 30
Asn Val Phe Ser Ser Phe Leu Trp Ala Leu Ile Val Gly Ser Val Ser
35 40 45
Phe Gln Ala Ser Asp Trp Val Lys Thr Leu Tyr Glu Arg Leu Ser His
50 55 60
Tyr Thr Ser Phe Phe Ile Ile Ser Phe Val Leu Ile Ala Leu Leu Ile
65 70 75 80
Trp Phe Leu Leu Lys Arg Tyr Ser Arg Lys Met Gly Phe
85 90

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 70...1227
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

TAGCATCAAT ACCCCTTAAA TAAAAGATAT AATGCTGTAT TATAAGCTAG TTTTAATTAC	60
AATTTTCAA ATG TTA AGG AAA AAC ATT TTA GCT TAC TAT GGG GCG AAT TTT	111
Met Leu Arg Lys Asn Ile Leu Ala Tyr Tyr Gly Ala Asn Phe	
1 5 10	
CTC TTA ATC ATC GCT CAA AGC TTA CCC CAT GCG ATT TTA ACC CCC TTG	159
Leu Leu Ile Ile Ala Gln Ser Leu Pro His Ala Ile Leu Thr Pro Leu	
15 20 25 30	
TTG CTT TCT AAA GGG CTT AGT TTG AGT GAA ATC TTG CTC GTG CAA ACC	207
Leu Leu Ser Lys Gly Leu Ser Leu Ser Glu Ile Leu Leu Val Gln Thr	
35 40 45	
TTT TTT AGC TTT TGC GTG CTA GTG GCT GAA TAC CCA AGC GGC GTT TTA	255
Phe Phe Ser Phe Cys Val Leu Val Ala Glu Tyr Pro Ser Gly Val Leu	
50 55 60	
GCG GAT TTG ATG AGC CGA AAA AAT TTA TTC CTG GTT TCT AAT GCC TTT	303
Ala Asp Leu Met Ser Arg Lys Asn Leu Phe Leu Val Ser Asn Ala Phe	
65 70 75	
TTA ATC GCT AGT TTT TCG TTT GTG CTG TTT TTT GAT AGC TTT ATT TTC	351
Leu Ile Ala Ser Phe Ser Phe Val Leu Phe Phe Asp Ser Phe Ile Phe	
80 85 90	
ATG CTT TTA GCG TGG GGG TTG TAT GGT TTG TAT AGC GCA TGC TCT AGC	399
Met Leu Leu Ala Trp Gly Leu Tyr Gly Leu Tyr Ser Ala Cys Ser Ser	
95 100 105 110	
GGC ACG ATT GAA GCT TCA CTC ATC ACA GAC ATT AAG GAA AAC AAA AAA	447
Gly Thr Ile Glu Ala Ser Leu Ile Thr Asp Ile Lys Glu Asn Lys Lys	
115 120 125	
GAT TTA TCC AAG TTT TTA GCC AAA AAC AAT CAA ATT ACT TAT TTA GGC	495
Asp Leu Ser Lys Phe Leu Ala Lys Asn Asn Gln Ile Thr Tyr Leu Gly	
130 135 140	
ATG ATT ATA GGG AGT TCT TTG GGA TCG TTT TTG TAT CTC AAA GTC CAT	543
Met Ile Ile Gly Ser Ser Leu Gly Ser Phe Leu Tyr Leu Lys Val His	
145 150 155	
GCG ATG CTG TAT ATT GTG GGG ATT TTT TTA ATC ATG CTC TGT GTG CTA	591
Ala Met Leu Tyr Ile Val Gly Ile Phe Leu Ile Met Leu Cys Val Leu	
160 165 170	
ACG ATC ATT TTT TAT TTT AAA GAG AAA GAA GGG GAT TTT AAA AGC CAA	639
Thr Ile Ile Phe Tyr Phe Lys Glu Lys Glu Gly Asp Phe Lys Ser Gln	
175 180 185 190	
AAA AGC CTG AAA CTC CTT AAA GAG CAA GTC AAA GGC AGT CTT AAA GAG	687

Lys	Ser	Leu	Lys	Leu	Leu	Lys	Glu	Gln	Val	Lys	Gly	Ser	Leu	Lys	Glu	
				195					200						205	
CTT	AAA	GAT	AAC	CCC	AAA	CTT	AAA	ATT	CTG	TTA	GTG	GGG	CAT	TTG	ATT	735
Leu	Lys	Asp	Asn	Pro	Lys	Leu	Lys	Ile	Leu	Leu	Val	Gly	His	Leu	Ile	
			210					215					220			
ACG	CCC	GTC	TTT	TTT	ATG	AGC	CAT	TTT	CAA	ATG	TGG	CAA	GCG	TAT	TTT	783
Thr	Pro	Val	Phe	Phe	Met	Ser	His	Phe	Gln	Met	Trp	Gln	Ala	Tyr	Phe	
		225					230					235				
TTA	AAA	CAA	GGC	GTT	AAA	GAG	CAA	TAC	CTT	TTT	GTG	TTT	TAT	ATC	GCT	831
Leu	Lys	Gln	Gly	Val	Lys	Glu	Gln	Tyr	Leu	Phe	Val	Phe	Tyr	Ile	Ala	
	240					245					250					
TTT	CAA	GTG	ATT	TCT	ATT	CTC	ATT	CAT	TTT	TTA	AAA	GCC	TCT	AGT	TAT	879
Phe	Gln	Val	Ile	Ser	Ile	Leu	Ile	His	Phe	Leu	Lys	Ala	Ser	Ser	Tyr	
255					260					265					270	
AGC	CAA	AAA	ATC	GCC	TTG	AGT	TCG	CTT	GTG	GTG	TTG	TTA	GGC	GTT	AGC	927
Ser	Gln	Lys	Ile	Ala	Leu	Ser	Ser	Leu	Val	Val	Leu	Leu	Gly	Val	Ser	
				275					280					285		
CCC	TTA	TTG	CTT	AGC	AAT	ATC	CCT	TAT	TGT	TTC	ATA	GGG	GTG	TAT	GCG	975
Pro	Leu	Leu	Leu	Ser	Asn	Ile	Pro	Tyr	Cys	Phe	Ile	Gly	Val	Tyr	Ala	
			290					295					300			
CTC	ATG	GTG	GCG	TTT	TTC	ACT	TAC	ATG	AGC	TAT	TGC	TTA	AAC	TAT	CAA	1023
Leu	Met	Val	Ala	Phe	Phe	Thr	Tyr	Met	Ser	Tyr	Cys	Leu	Asn	Tyr	Gln	
		305					310					315				
TTC	TCC	AAA	TTC	GTT	TCT	AAA	AAC	AAC	ATT	TCC	TCG	CTC	TCA	TCG	CTT	1071
Phe	Ser	Lys	Phe	Val	Ser	Lys	Asn	Asn	Ile	Ser	Ser	Leu	Ser	Ser	Leu	
		320				325					330					
TTA	TCA	AGC	TGT	GTG	CGC	GTG	GTC	TCT	GTG	CTA	ATC	TTA	TCG	CTC	AGC	1119
Leu	Ser	Ser	Cys	Val	Arg	Val	Val	Ser	Val	Leu	Ile	Leu	Ser	Leu	Ser	
335					340					345					350	
AGT	CTG	GAA	CTG	CGT	TAC	TTC	TCA	CCC	CTA	ACT	ATC	ATA	ACC	ATG	CAT	1167
Ser	Leu	Glu	Leu	Arg	Tyr	Phe	Ser	Pro	Leu	Thr	Ile	Ile	Thr	Met	His	
				355					360					365		
TTT	GCC	TTG	ACG	CTT	ATC	ATC	CTC	TTT	TTC	TTT	TTG	TAT	AAG	GCT	AAG	1215
Phe	Ala	Leu	Thr	Leu	Ile	Ile	Leu	Phe	Phe	Phe	Leu	Tyr	Lys	Ala	Lys	
			370					375					380			
CCG	TTT	GAT	GAG	TGAGCGGCTT	TAAGAGTGCA	ACCTTTTAGC	GATTTCTATA	GCAAC								1272
Pro	Phe	Asp	Glu													
			385													
ATCATAGCC																1281

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 386 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Met	Leu	Arg	Lys	Asn	Ile	Leu	Ala	Tyr	Tyr	Gly	Ala	Asn	Phe	Leu	Leu	1	5	10	15
Ile	Ile	Ala	Gln	Ser	Leu	Pro	His	Ala	Ile	Leu	Thr	Pro	Leu	Leu	Leu	20	25	30	
Ser	Lys	Gly	Leu	Ser	Leu	Ser	Glu	Ile	Leu	Leu	Val	Gln	Thr	Phe	Phe	35	40	45	
Ser	Phe	Cys	Val	Leu	Val	Ala	Glu	Tyr	Pro	Ser	Gly	Val	Leu	Ala	Asp	50	55	60	
Leu	Met	Ser	Arg	Lys	Asn	Leu	Phe	Leu	Val	Ser	Asn	Ala	Phe	Leu	Ile	65	70	75	80
Ala	Ser	Phe	Ser	Phe	Val	Leu	Phe	Phe	Asp	Ser	Phe	Ile	Phe	Met	Leu	85	90	95	
Leu	Ala	Trp	Gly	Leu	Tyr	Gly	Leu	Tyr	Ser	Ala	Cys	Ser	Ser	Gly	Thr	100	105	110	
Ile	Glu	Ala	Ser	Leu	Ile	Thr	Asp	Ile	Lys	Glu	Asn	Lys	Lys	Asp	Leu	115	120	125	
Ser	Lys	Phe	Leu	Ala	Lys	Asn	Gln	Ile	Thr	Tyr	Leu	Gly	Met	Ile		130	135	140	
Ile	Gly	Ser	Ser	Leu	Gly	Ser	Phe	Leu	Tyr	Leu	Lys	Val	His	Ala	Met	145	150	155	160
Leu	Tyr	Ile	Val	Gly	Ile	Phe	Leu	Ile	Met	Leu	Cys	Val	Leu	Thr	Ile	165	170	175	
Ile	Phe	Tyr	Phe	Lys	Glu	Lys	Glu	Gly	Asp	Phe	Lys	Ser	Gln	Lys	Ser	180	185	190	
Leu	Lys	Leu	Leu	Lys	Glu	Gln	Val	Lys	Gly	Ser	Leu	Lys	Glu	Leu	Lys	195	200	205	
Asp	Asn	Pro	Lys	Leu	Lys	Ile	Leu	Leu	Val	Gly	His	Leu	Ile	Thr	Pro	210	215	220	
Val	Phe	Phe	Met	Ser	His	Phe	Gln	Met	Trp	Gln	Ala	Tyr	Phe	Leu	Lys	225	230	235	240
Gln	Gly	Val	Lys	Glu	Gln	Tyr	Leu	Phe	Val	Phe	Tyr	Ile	Ala	Phe	Gln	245	250	255	
Val	Ile	Ser	Ile	Leu	Ile	His	Phe	Leu	Lys	Ala	Ser	Ser	Tyr	Ser	Gln	260	265	270	
Lys	Ile	Ala	Leu	Ser	Ser	Leu	Val	Val	Leu	Leu	Gly	Val	Ser	Pro	Leu	275	280	285	
Leu	Leu	Ser	Asn	Ile	Pro	Tyr	Cys	Phe	Ile	Gly	Val	Tyr	Ala	Leu	Met	290	295	300	
Val	Ala	Phe	Phe	Thr	Tyr	Met	Ser	Tyr	Cys	Leu	Asn	Tyr	Gln	Phe	Ser	305	310	315	320
Lys	Phe	Val	Ser	Lys	Asn	Asn	Ile	Ser	Ser	Leu	Ser	Ser	Leu	Leu	Ser	325	330	335	
Ser	Cys	Val	Arg	Val	Val	Ser	Val	Leu	Ile	Leu	Ser	Leu	Ser	Ser	Leu	340	345	350	
Glu	Leu	Arg	Tyr	Phe	Ser	Pro	Leu	Thr	Ile	Ile	Thr	Met	His	Phe	Ala	355	360	365	
Leu	Thr	Leu	Ile	Ile	Leu	Phe	Phe	Phe	Leu	Tyr	Lys	Ala	Lys	Pro	Phe	370	375	380	
Asp	Glu															385			

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 77...2167
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

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GAAGTTTATG AGCCGTTTTG CCACTATTCA AAGAAATTTT GGATTATAAT AAAAAAATG      60
GCTGAAATTA ACAACA ATG ATT AAA CAA TCA TTA AAT GGA GAG GAC ATG CAA      112
      Met Ile Lys Gln Ser Leu Asn Gly Glu Asp Met Gln
              1              5              10

AAA AGT TTA GTT TCT TTG GCT TGG GTT TTT GTA GCT ATT TTA GGG GCG      160
Lys Ser Leu Val Ser Leu Ala Trp Val Phe Val Ala Ile Leu Gly Ala
      15              20              25

ATC TGT TTA GGG GTG TTA GCC TTA CAC AAG GGT GAG AGC ATT AAC ACG      208
Ile Cys Leu Gly Val Leu Ala Leu His Lys Gly Glu Ser Ile Asn Thr
      30              35              40

CTA TGG CTT GTA GTA GCG AGC GCT TGT ATT TAT AGC ATA GGC TAT CGT      256
Leu Trp Leu Val Val Ala Ser Ala Cys Ile Tyr Ser Ile Gly Tyr Arg
      45              50              55              60

TTT TAT AGC CAT TTT ATC GCT TAT AAG GTG TTA AAG CTA GAT GAT AGC      304
Phe Tyr Ser His Phe Ile Ala Tyr Lys Val Leu Lys Leu Asp Asp Ser
      65              70              75

AGA GCC ACG CCC GCA TGC GTA AGG AAT GAT GGC AAG GAT TTT GTG CCA      352
Arg Ala Thr Pro Ala Cys Val Arg Asn Asp Gly Lys Asp Phe Val Pro
      80              85              90

ACC GAT AAA GCG ATC ACT TTT GGG CAC CAT TTC GCC GCT ATT GCT GGG      400
Thr Asp Lys Ala Ile Thr Phe Gly His His Phe Ala Ala Ile Ala Gly
      95              100              105

GCT GGC CCT TTA GTA GGC CCG ATA CTA GCC GCT CAA ATG GGT TAC TTG      448
Ala Gly Pro Leu Val Gly Pro Ile Leu Ala Ala Gln Met Gly Tyr Leu
      110              115              120

CCC TCT ATC TTA TGG ATT TTG ATA GGC TCG GTT TTA GGG GGT TGC GTG      496
Pro Ser Ile Leu Trp Ile Leu Ile Gly Ser Val Leu Gly Gly Cys Val
      125              130              135              140

CAT GAT TTT GTG GTG CTT TTT GCT TCT ATT AGG CGC GAT GGC AAG TCT      544
His Asp Phe Val Val Leu Phe Ala Ser Ile Arg Arg Asp Gly Lys Ser

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145										150										155									
TTA	GGC	GAA	ATG	ATC	AAA	CTT	GAA	ATG	GGC	CAA	TTT	GTA	GGC	ATG	ATC														
Leu	Gly	Glu	Met	Ile	Lys	Leu	Glu	Met	Gly	Gln	Phe	Val	Gly	Met	Ile														
			160						165					170															
GCA	AGT	CTG	GGC	ATT	TTA	GGG	ATC	ATG	CTC	ATT	ATC	ATT	GCG	ATT	TTA														
Ala	Ser	Leu	Gly	Ile	Leu	Gly	Ile	Met	Leu	Ile	Ile	Ile	Ala	Ile	Leu														
			175						180					185															
GCG	ATG	GTG	GTG	GTG	AAG	GCT	TTA	GCG	CAT	TCG	CCT	TGG	GCG	TTT	TTT														
Ala	Met	Val	Val	Val	Lys	Ala	Leu	Ala	His	Ser	Pro	Trp	Gly	Phe	Phe														
			190						195					200															
ACG	ATC	GCA	ATG	ACT	ATT	CCC	ATT	GCG	ATT	CTT	ATG	GGG	CTT	TAC	ATG														
Thr	Ile	Ala	Met	Thr	Ile	Pro	Ile	Ala	Ile	Leu	Met	Gly	Leu	Tyr	Met														
						210				215					220														
CGG	TTT	TTC	AGG	CCA	CAC	AAG	ATT	TTA	GAG	GTT	TCT	GTT	ATT	GGC	TTT														
Arg	Phe	Phe	Arg	Pro	His	Lys	Ile	Leu	Glu	Val	Ser	Val	Ile	Gly	Phe														
						225				230					235														
ATC	CTA	TTG	ATT	ATA	GCG	ATT	TAT	GCG	GGT	AAA	TAC	GTT	TCT	TTA	GAT														
Ile	Leu	Leu	Ile	Ile	Ala	Ile	Tyr	Ala	Gly	Lys	Tyr	Val	Ser	Leu	Asp														
						240				245					250														
CCT	AAA	TTA	GCG	TCA	ATA	TTC	ACT	TTT	GAG	GCC	AGT	TCT	TTA	GCG	TGG														
Pro	Lys	Leu	Ala	Ser	Ile	Phe	Thr	Phe	Glu	Ala	Ser	Ser	Leu	Ala	Trp														
						255				260					265														
ATG	ATC	ATG	GGC	TAT	GGG	TTT	GTG	GCT	TCT	ATT	TTA	CCG	GTA	TGG	TTT														
Met	Ile	Met	Gly	Tyr	Gly	Phe	Val	Ala	Ser	Ile	Leu	Pro	Val	Trp	Phe														
						275								280															
TTA	CTC	GCT	CCA	CGA	GAT	TAT	CTA	AGC	ACT	TTT	TTA	AAA	ATT	GGC	GTT														
Leu	Leu	Ala	Pro	Arg	Asp	Tyr	Leu	Ser	Thr	Phe	Leu	Lys	Ile	Gly	Val														
						290								300															
ATA	GGG	GTG	TTG	GTT	GTG	GCC	ATT	ATT	TTT	GTC	GCT	CCG	CCT	TTA	CAA														
Ile	Gly	Val	Leu	Val	Val	Ala	Ile	Ile	Phe	Val	Ala	Pro	Pro	Leu	Gln														
						305				310					315														
ATC	CCT	AAA	ATC	ACG	CCC	TTT	GTA	GAT	GGC	AGT	GGG	CCT	GTG	TTT	GCA														
Ile	Pro	Lys	Ile	Thr	Pro	Phe	Val	Asp	Gly	Ser	Gly	Pro	Val	Phe	Ala														
						320				325					330														
GGA	AGC	GTG	TTC	CCT	TTC	TTG	TTT	ATC	ACG	GTG	GCT	TGC	GGG	ACG	ATT														
Gly	Ser	Val	Phe	Pro	Phe	Leu	Phe	Ile	Thr	Val	Ala	Cys	Gly	Thr	Ile														
						335				340				345															
AGC	GGA	TTC	CAT	GCT	TTA	ATT	TCT	TCA	GGC	ACG	ACC	CCT	AAA	ATG	CTC														
Ser	Gly	Phe	His	Ala	Leu	Ile	Ser	Ser	Gly	Thr	Thr	Pro	Lys	Met	Leu														
						355								360															
GCT	AAA	GAA	AGC	GAC	GCA	AGG	CTA	GTG	GGC	TAT	GGC	TCT	ATG	GTG	ATG														
Ala	Lys	Glu	Ser	Asp	Ala	Arg	Leu	Val	Gly	Tyr	Gly	Ser	Met	Val	Met														
						370								380															

GAG	AGC	GTT	GTG	GCT	CTT	ATG	GCG	TTG	GTG	TGC	GCA	GGG	ATC	TTG	CAC	1264
Glu	Ser	Val	Val	Ala	Leu	Met	Ala	Leu	Val	Cys	Ala	Gly	Ile	Leu	His	
				385					390					395		
CCA	GGG	CTT	TAT	TTC	GCT	ATC	AAT	TCG	CCA	GAA	GTG	AGC	ATC	GGT	AAA	1312
Pro	Gly	Leu	Tyr	Phe	Ala	Ile	Asn	Ser	Pro	Glu	Val	Ser	Ile	Gly	Lys	
		400						405					410			
GAT	ATA	GCT	GAT	GCG	GCT	TCA	GTG	ATT	AGC	TCA	TGG	GGG	TTT	AAT	ATC	1360
Asp	Ile	Ala	Asp	Ala	Ala	Ser	Val	Ile	Ser	Ser	Trp	Gly	Phe	Asn	Ile	
		415					420					425				
AGC	GCT	GAA	GAA	ATT	CGT	GAG	ATG	ACT	AAA	AAC	ATC	GGC	GAA	AGC	TCC	1408
Ser	Ala	Glu	Glu	Ile	Arg	Glu	Met	Thr	Lys	Asn	Ile	Gly	Glu	Ser	Ser	
	430					435					440					
ATT	TTG	AGC	CGC	ACC	GGT	GGG	GCG	CCC	ACT	TTT	GCG	ATC	GGT	TTA	GCG	1456
Ile	Leu	Ser	Arg	Thr	Gly	Gly	Ala	Pro	Thr	Phe	Ala	Ile	Gly	Leu	Ala	
	445				450					455					460	
ATG	ATT	GTG	TAT	CAC	ATT	TTA	GGG	GAT	CCA	AGC	GTG	ATG	GCG	TTT	TGG	1504
Met	Ile	Val	Tyr	His	Ile	Leu	Gly	Asp	Pro	Ser	Val	Met	Ala	Phe	Trp	
				465				470					475			
TAT	CAT	TTT	GCG	ATT	TTG	TTT	GAA	GCT	TTG	TTC	ATT	TTA	ACC	GCT	GTG	1552
Tyr	His	Phe	Ala	Ile	Leu	Phe	Glu	Ala	Leu	Phe	Ile	Leu	Thr	Ala	Val	
		480					485						490			
GAT	GCT	GGC	ACA	CGA	ACC	GCT	CGT	TTC	ATG	ATT	CAA	GAT	TTG	CTC	GGT	1600
Asp	Ala	Gly	Thr	Arg	Thr	Ala	Arg	Phe	Met	Ile	Gln	Asp	Leu	Leu	Gly	
		495				500					505					
AAT	GTT	TAT	AAG	CCT	TTG	GGC	GAT	CTT	AGC	TCT	TAT	AAG	GCT	GGG	ATT	1648
Asn	Val	Tyr	Lys	Pro	Leu	Gly	Asp	Leu	Ser	Ser	Tyr	Lys	Ala	Gly	Ile	
	510					515					520					
TTT	GCC	ACT	CTT	TTG	TGC	GTG	GCA	GGG	TGG	GGG	TAT	TTC	TTG	TAT	CAA	1696
Phe	Ala	Thr	Leu	Leu	Cys	Val	Ala	Gly	Trp	Gly	Tyr	Phe	Leu	Tyr	Gln	
	525				530					535					540	
GGC	ACG	ATT	GAT	CCT	AAA	GGG	GGG	ATT	TAT	ACG	CTA	TGG	CCT	TTA	TTT	1744
Gly	Thr	Ile	Asp	Pro	Lys	Gly	Gly	Ile	Tyr	Thr	Leu	Trp	Pro	Leu	Phe	
			545						550					555		
GGC	GTG	AGC	AAT	CAG	ATG	TTA	GCG	GGC	ATG	GCG	TTG	TTG	TTG	GTC	ACG	1792
Gly	Val	Ser	Asn	Gln	Met	Leu	Ala	Gly	Met	Ala	Leu	Leu	Leu	Val	Thr	
			560					565					570			
GTG	GTG	TTG	TTT	AAA	ATG	GGG	CGT	TTT	AAG	GGG	GCG	ATG	ATA	AGC	GCC	1840
Val	Val	Leu	Phe	Lys	Met	Gly	Arg	Phe	Lys	Gly	Ala	Met	Ile	Ser	Ala	
		575				580						585				
TTA	CCG	GCA	GTT	TTG	ATT	TTA	TCC	ATC	ACT	TTT	TAT	AGC	GGT	ATT	TTA	1888
Leu	Pro	Ala	Val	Leu	Ile	Leu	Ser	Ile	Thr	Phe	Tyr	Ser	Gly	Ile	Leu	
	590					595					600					
AAG	GTG	GTG	CCA	AAG	AGC	GAT	AAC	AGC	GTG	CTG	AAT	AAT	GTT	TCC	CAT	1936
Lys	Val	Val	Pro	Lys	Ser	Asp	Asn	Ser	Val	Leu	Asn	Asn	Val	Ser	His	

605	610	615	620	
GTG GCG CAA ATG CAA ATC ATC AAA GAA AAA ATG GCT ACC ACT ACC GAT				1984
Val Ala Gln Met Gln Ile Ile Lys Glu Lys Met Ala Thr Thr Thr Asp	625	630	635	
GAA AAA GCG CTC AAA ACG CTC CAA AAA TCC TTT TTT AAC CAC GCT ATT				2032
Glu Lys Ala Leu Lys Thr Leu Gln Lys Ser Phe Phe Asn His Ala Ile	640	645	650	
GAT GCG ATT TTG TGC GTG TTT TTC ATG CTT GTG GCG CTA TTG GTT TTA				2080
Asp Ala Ile Leu Cys Val Phe Phe Met Leu Val Ala Leu Leu Val Leu	655	660	665	
ATC GTG AGC GTT AGG ATT TGC TCA AAC GCT TAT TTT AAA AAC AAA ATT				2128
Ile Val Ser Val Arg Ile Cys Ser Asn Ala Tyr Phe Lys Asn Lys Ile	670	675	680	
TAC CCA CCG CTG GCT GAA ACG CCC TAC ATC AAA GCC TCT TGAATAAAAA AG				2179
Tyr Pro Pro Leu Ala Glu Thr Pro Tyr Ile Lys Ala Ser	685	690	695	
GGGTTTAAAC CCCCTTTAAA TCCATAGAAA AAAGTTTGA				2218

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 697 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met	Ile	Lys	Gln	Ser	Leu	Asn	Gly	Glu	Asp	Met	Gln	Lys	Ser	Leu	Val
1				5				10						15	
Ser	Leu	Ala	Trp	Val	Phe	Val	Ala	Ile	Leu	Gly	Ala	Ile	Cys	Leu	Gly
		20						25					30		
Val	Leu	Ala	Leu	His	Lys	Gly	Glu	Ser	Ile	Asn	Thr	Leu	Trp	Leu	Val
		35					40					45			
Val	Ala	Ser	Ala	Cys	Ile	Tyr	Ser	Ile	Gly	Tyr	Arg	Phe	Tyr	Ser	His
		50				55					60				
Phe	Ile	Ala	Tyr	Lys	Val	Leu	Lys	Leu	Asp	Asp	Ser	Arg	Ala	Thr	Pro
65					70				75						80
Ala	Cys	Val	Arg	Asn	Asp	Gly	Lys	Asp	Phe	Val	Pro	Thr	Asp	Lys	Ala
				85					90					95	
Ile	Thr	Phe	Gly	His	His	Phe	Ala	Ala	Ile	Ala	Gly	Ala	Gly	Pro	Leu
			100					105					110		
Val	Gly	Pro	Ile	Leu	Ala	Ala	Gln	Met	Gly	Tyr	Leu	Pro	Ser	Ile	Leu
		115					120					125			
Trp	Ile	Leu	Ile	Gly	Ser	Val	Leu	Gly	Gly	Cys	Val	His	Asp	Phe	Val
		130				135					140				
Val	Leu	Phe	Ala	Ser	Ile	Arg	Arg	Asp	Gly	Lys	Ser	Leu	Gly	Glu	Met
145					150					155					160
Ile	Lys	Leu	Glu	Met	Gly	Gln	Phe	Val	Gly	Met	Ile	Ala	Ser	Leu	Gly

				165					170					175			
Ile	Leu	Gly	Ile	Met	Leu	Ile	Ile	Ile	Ala	Ile	Leu	Ala	Met	Val	Val		
			180					185					190				
Val	Lys	Ala	Leu	Ala	His	Ser	Pro	Trp	Gly	Phe	Phe	Thr	Ile	Ala	Met		
		195					200					205					
Thr	Ile	Pro	Ile	Ala	Ile	Leu	Met	Gly	Leu	Tyr	Met	Arg	Phe	Phe	Arg		
	210					215					220						
Pro	His	Lys	Ile	Leu	Glu	Val	Ser	Val	Ile	Gly	Phe	Ile	Leu	Leu	Ile		
225				230						235					240		
Ile	Ala	Ile	Tyr	Ala	Gly	Lys	Tyr	Val	Ser	Leu	Asp	Pro	Lys	Leu	Ala		
			245					250					255				
Ser	Ile	Phe	Thr	Phe	Glu	Ala	Ser	Ser	Leu	Ala	Trp	Met	Ile	Met	Gly		
		260					265					270					
Tyr	Gly	Phe	Val	Ala	Ser	Ile	Leu	Pro	Val	Trp	Phe	Leu	Ala	Pro			
	275						280				285						
Arg	Asp	Tyr	Leu	Ser	Thr	Phe	Leu	Lys	Ile	Gly	Val	Ile	Gly	Val	Leu		
	290					295					300						
Val	Val	Ala	Ile	Ile	Phe	Val	Ala	Pro	Pro	Leu	Gln	Ile	Pro	Lys	Ile		
305				310						315					320		
Thr	Pro	Phe	Val	Asp	Gly	Ser	Gly	Pro	Val	Phe	Ala	Gly	Ser	Val	Phe		
			325					330					335				
Pro	Phe	Leu	Phe	Ile	Thr	Val	Ala	Cys	Gly	Thr	Ile	Ser	Gly	Phe	His		
		340					345				350						
Ala	Leu	Ile	Ser	Ser	Gly	Thr	Thr	Pro	Lys	Met	Leu	Ala	Lys	Glu	Ser		
	355						360				365						
Asp	Ala	Arg	Leu	Val	Gly	Tyr	Gly	Ser	Met	Val	Met	Glu	Ser	Val	Val		
	370				375					380							
Ala	Leu	Met	Ala	Leu	Val	Cys	Ala	Gly	Ile	Leu	His	Pro	Gly	Leu	Tyr		
385				390					395						400		
Phe	Ala	Ile	Asn	Ser	Pro	Glu	Val	Ser	Ile	Gly	Lys	Asp	Ile	Ala	Asp		
			405					410					415				
Ala	Ala	Ser	Val	Ile	Ser	Ser	Trp	Gly	Phe	Asn	Ile	Ser	Ala	Glu	Glu		
		420					425					430					
Ile	Arg	Glu	Met	Thr	Lys	Asn	Ile	Gly	Glu	Ser	Ser	Ile	Leu	Ser	Arg		
	435					440					445						
Thr	Gly	Gly	Ala	Pro	Thr	Phe	Ala	Ile	Gly	Leu	Ala	Met	Ile	Val	Tyr		
	450				455					460							
His	Ile	Leu	Gly	Asp	Pro	Ser	Val	Met	Ala	Phe	Trp	Tyr	His	Phe	Ala		
465				470					475						480		
Ile	Leu	Phe	Glu	Ala	Leu	Phe	Ile	Leu	Thr	Ala	Val	Asp	Ala	Gly	Thr		
			485					490					495				
Arg	Thr	Ala	Arg	Phe	Met	Ile	Gln	Asp	Leu	Leu	Gly	Asn	Val	Tyr	Lys		
		500					505					510					
Pro	Leu	Gly	Asp	Leu	Ser	Ser	Tyr	Lys	Ala	Gly	Ile	Phe	Ala	Thr	Leu		
	515						520				525						
Leu	Cys	Val	Ala	Gly	Trp	Gly	Tyr	Phe	Leu	Tyr	Gln	Gly	Thr	Ile	Asp		
	530				535					540							
Pro	Lys	Gly	Gly	Ile	Tyr	Thr	Leu	Trp	Pro	Leu	Phe	Gly	Val	Ser	Asn		
545				550					555						560		
Gln	Met	Leu	Ala	Gly	Met	Ala	Leu	Leu	Leu	Val	Thr	Val	Val	Leu	Phe		
			565					570					575				
Lys	Met	Gly	Arg	Phe	Lys	Gly	Ala	Met	Ile	Ser	Ala	Leu	Pro	Ala	Val		
		580					585				590						
Leu	Ile	Leu	Ser	Ile	Thr	Phe	Tyr	Ser	Gly	Ile	Leu	Lys	Val	Val	Pro		
	595					600					605						
Lys	Ser	Asp	Asn	Ser	Val	Leu	Asn	Asn	Val	Ser	His	Val	Ala	Gln	Met		
	610				615				620								
Gln	Ile	Ile	Lys	Glu	Lys	Met	Ala	Thr	Thr	Thr	Asp	Glu	Lys	Ala	Leu		

625		630		635		640
Lys Thr Leu Gln Lys Ser Phe Phe Asn His Ala Ile Asp Ala Ile Leu						
	645		650		655	
Cys Val Phe Phe Met Leu Val Ala Leu Leu Val Leu Ile Val Ser Val						
	660		665		670	
Arg Ile Cys Ser Asn Ala Tyr Phe Lys Asn Lys Ile Tyr Pro Pro Leu						
	675		680		685	
Ala Glu Thr Pro Tyr Ile Lys Ala Ser						
690		695				

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 911 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 121...861
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TAAGGGGCTT TGCATTTTTC ACTCATTTCA TGCCTCTTTT TCCTTTATTTA GACAGATTAT	60
TATCTTAAAA TAATTGTAAT ATCATTATTA TTATATCAAC TCAATAAAAA AGGAGAAGGT	120
ATG CAA AAA ACT TCT AAC ACT CTG GCG CTG GGG AGT TTG ACA GCG CTA	168
Met Gln Lys Thr Ser Asn Thr Leu Ala Leu Gly Ser Leu Thr Ala Leu	
1 5 10 15	
TTC TTT CTA ATG GGT TTT ATC ACG GTT TTA AAC GAT ATT TTA ATC CCA	216
Phe Phe Leu Met Gly Phe Ile Thr Val Leu Asn Asp Ile Leu Ile Pro	
20 25 30	
CAC TTA AAG CCC ATT TTT GAC TTG ACC TAT TTT GAA GCT TCA CTC ATT	264
His Leu Lys Pro Ile Phe Asp Leu Thr Tyr Phe Glu Ala Ser Leu Ile	
35 40 45	
CAA TTT TGC TTT TTT GGG GCG TAT TTC ATC ATG GGA GGA GTT TTT GGG	312
Gln Phe Cys Phe Phe Gly Ala Tyr Phe Ile Met Gly Gly Val Phe Gly	
50 55 60	
AAT GTG ATC AGT AAA ATC GGC TAC CCT TTT GGC GTG GTG CTT GGT TTT	360
Asn Val Ile Ser Lys Ile Gly Tyr Pro Phe Gly Val Val Leu Gly Phe	
65 70 75 80	
GTG ATC ACA GCG ACG GGG TGC GCG TTG TTT TAT CCG GCG GCG CAT TTT	408
Val Ile Thr Ala Thr Gly Cys Ala Leu Phe Tyr Pro Ala Ala His Phe	
85 90 95	
GGA TCC TAT GGG TTT TTT TTA GGA GCG TTG TTT ATT TTA GCG AGC GGG	456
Gly Ser Tyr Gly Phe Phe Leu Gly Ala Leu Phe Ile Leu Ala Ser Gly	
100 105 110	

ATT GTG TGC TTG CAA ACC GCT GGT AAT CCC TTT GTA ACC TTG CTT TCT	504
Ile Val Cys Leu Gln Thr Ala Gly Asn Pro Phe Val Thr Leu Leu Ser	
115 120 125	
AAA GGT AAA GAA GCC AGA AAT TTG GTT TTA GTC CAG GCG TTC AAT TCG	552
Lys Gly Lys Lys Glu Ala Arg Asn Leu Val Leu Val Gln Ala Phe Asn Ser	
130 135 140	
CTT GGC ACA ACT TTA GGG CCT ATT TTT GGG AGC TTG TTG ATT TTT AGC	600
Leu Gly Thr Thr Leu Gly Pro Ile Phe Gly Ser Leu Leu Ile Phe Ser	
145 150 155 160	
ACG ACT AAA ATG GGC GAT AAT GCA AGT TTG ATA GAT AAA TTA GCG GAC	648
Thr Thr Lys Met Gly Asp Asn Ala Ser Leu Ile Asp Lys Leu Ala Asp	
165 170 175	
GCT AAA AGC GTT CAA ATG CCT TAT TTG GGC TTG GCG GTG TTT TCG CTT	696
Ala Lys Ser Val Gln Met Pro Tyr Leu Gly Leu Ala Val Phe Ser Leu	
180 185 190	
CTT TTA GCG CTC ATC ATG TAT CTT TTG AAA TTG CCT GAT GTG GAA AAA	744
Leu Leu Ala Leu Ile Met Tyr Leu Leu Lys Leu Pro Asp Val Glu Lys	
195 200 205	
GAA ATG CCC AAA GAG ACG ACT CAA AAA AGC TTG TTT TCG CAC AAA CAC	792
Glu Met Pro Lys Glu Thr Thr Gln Lys Ser Leu Phe Ser His Lys His	
210 215 220	
TTT GTT TTT GGG GCT TGG GGA TCT TTT TTT ATG TGG GGG GAG AAN TGG	840
Phe Val Phe Gly Ala Trp Gly Ser Phe Phe Met Trp Gly Glu Xaa Trp	
225 230 235 240	
CGA TTG GCT CAT TCT TGG TGC TAAGCTTTGA AAAGCTTTTG AATTTAGACT CTCA	895
Arg Leu Ala His Ser Trp Cys	
245	
ATCAAGCGCG CATTAC	911

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met	Gln	Lys	Thr	Ser	Asn	Thr	Leu	Ala	Leu	Gly	Ser	Leu	Thr	Ala	Leu
1				5					10					15	
Phe	Phe	Leu	Met	Gly	Phe	Ile	Thr	Val	Leu	Asn	Asp	Ile	Leu	Ile	Pro
			20					25					30		
His	Leu	Lys	Pro	Ile	Phe	Asp	Leu	Thr	Tyr	Phe	Glu	Ala	Ser	Leu	Ile
		35					40					45			
Gln	Phe	Cys	Phe	Phe	Gly	Ala	Tyr	Phe	Ile	Met	Gly	Gly	Val	Phe	Gly

50	Asn Val Ile Ser Lys	55	Ile Gly Tyr Pro Phe Gly	60	Val Val Leu Gly Phe
65	Val Ile Thr Ala Thr	70	Gly Cys Ala Leu Phe Tyr	75	Pro Ala Ala His Phe
		85		90	
	Gly Ser Tyr Gly Phe		Phe Leu Gly Ala Leu Phe		Ile Leu Ala Ser Gly
		100		105	
	Ile Val Cys Leu Gln Thr		Ala Gly Asn Pro Phe Val		Thr Leu Leu Ser
		115		120	
	Lys Gly Lys Glu Ala Arg		Asn Leu Val Leu Val Gln		Ala Phe Asn Ser
		130		135	
	Leu Gly Thr Thr Leu Gly		Pro Ile Phe Gly Ser Leu		Leu Ile Phe Ser
		145		150	
	Thr Thr Lys Met Gly Asp		Asn Ala Ser Leu Ile Asp		Lys Leu Ala Asp
		165		170	
	Ala Lys Ser Val Gln Met		Pro Tyr Leu Gly Leu Ala		Val Phe Ser Leu
		180		185	
	Leu Leu Ala Leu Ile Met		Tyr Leu Leu Lys Leu Pro		Asp Val Glu Lys
		195		200	
	Glu Met Pro Lys Glu Thr		Thr Gln Lys Ser Leu Phe		Ser His Lys His
		210		215	
	Phe Val Phe Gly Ala Trp		Gly Ser Phe Phe Met Trp		Gly Glu Xaa Trp
		225		230	
	Arg Leu Ala His Ser Trp		Cys	235	240
		245			

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3084 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...3027
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GAATTAATGC ATTAAATAAC TCAAAATTTT TGATCAAAGG CTTGAAAT ATG TCA AAA	57
Met Ser Lys	
1	
AAA ATT CCC CTA AAA AAC CGC TTG AGA GCT GAT TTT ACA AAA ACC CCA	105
Lys Ile Pro Leu Lys Asn Arg Leu Arg Ala Asp Phe Thr Lys Thr Pro	
5 10 15	
ACA GAT TTA GAA GTC CCT AAT TTA TTA TTA TTA CAA CGA GAC AGC TAT	153
Thr Asp Leu Glu Val Pro Asn Leu Leu Leu Leu Gln Arg Asp Ser Tyr	
20 25 30 35	
GAT TCT TTC TTG TAT TCT AAA GAG GGT AAA GAG AGC GGG ATT GAA AAG	201

Asp	Ser	Phe	Leu	Tyr	Ser	Lys	Glu	Gly	Lys	Glu	Ser	Gly	Ile	Glu	Lys	
				40					45					50		
GTT	TTT	AAA	TCC	ATT	TTC	CCT	ATC	CAA	GAT	GAG	CAT	AAC	CGC	ATC	ACT	249
Val	Phe	Lys	Ser	Ile	Phe	Pro	Ile	Gln	Asp	Glu	His	Asn	Arg	Ile	Thr	
			55					60					65			
TTA	GAA	TAC	GCG	GGT	TGC	GAA	TTT	GGC	AAG	TCT	AAA	TAC	ACC	GTT	AGA	297
Leu	Glu	Tyr	Ala	Gly	Cys	Glu	Phe	Gly	Lys	Ser	Lys	Tyr	Thr	Val	Arg	
		70					75					80				
GAA	GCG	ATG	GAG	AGG	GGC	ATT	ACC	TAC	TCT	ATC	CCT	CTC	AAA	ATT	AAG	345
Glu	Ala	Met	Glu	Arg	Gly	Ile	Thr	Tyr	Ser	Ile	Pro	Leu	Lys	Ile	Lys	
	85					90					95					
GTG	CGC	TTG	ATC	TTG	TGG	GAA	AAA	GAT	ACC	AAG	AGT	GGC	GAA	AAG	AAC	393
Val	Arg	Leu	Ile	Leu	Trp	Glu	Lys	Asp	Thr	Lys	Ser	Gly	Glu	Lys	Asn	
100					105					110					115	
GGC	ATT	AAG	GAT	ATT	AAA	GAA	CAA	AGC	ATT	TTC	ATT	CGT	GAG	ATC	CCT	441
Gly	Ile	Lys	Asp	Ile	Lys	Glu	Gln	Ser	Ile	Phe	Ile	Arg	Glu	Ile	Pro	
				120					125					130		
TTG	ATG	ACA	GAA	CGC	ACT	TCA	TTT	ATT	ATT	AAT	GGG	GTG	GAG	CGC	GTG	489
Leu	Met	Thr	Glu	Arg	Thr	Ser	Phe	Ile	Ile	Asn	Gly	Val	Glu	Arg	Val	
			135					140					145			
GTG	GTC	AAT	CAA	CTC	CAC	AGA	AGC	CCC	GGT	GTG	ATT	TTC	AAA	GAA	GAA	537
Val	Val	Asn	Gln	Leu	His	Arg	Ser	Pro	Gly	Val	Ile	Phe	Lys	Glu	Glu	
		150					155					160				
GAG	TCT	AGC	ACT	TCT	TTA	AAC	AAG	CTC	ATT	TAC	ACA	GGG	CAA	ATC	ATT	585
Glu	Ser	Ser	Thr	Ser	Leu	Asn	Lys	Leu	Ile	Tyr	Thr	Gly	Gln	Ile	Ile	
	165					170					175					
CCT	GAT	AGG	GGT	TCG	TGG	TTG	TAT	TTT	GAA	TAC	GAT	TCT	AAA	GAT	GTT	633
Pro	Asp	Arg	Gly	Ser	Trp	Leu	Tyr	Phe	Glu	Tyr	Asp	Ser	Lys	Asp	Val	
180					185					190					195	
TTA	TAC	GCT	CGT	ATC	AAT	AAA	CGC	CGT	AAA	GTG	CCT	GTT	ACC	ATT	TTA	681
Leu	Tyr	Ala	Arg	Ile	Asn	Lys	Arg	Arg	Lys	Val	Pro	Val	Thr	Ile	Leu	
				200					205					210		
TTC	AGG	GCG	ATG	GAT	TAT	CAA	AAA	CAA	GAC	ATC	ATC	AAA	ATG	TTC	TAC	729
Phe	Arg	Ala	Met	Asp	Tyr	Gln	Lys	Gln	Asp	Ile	Ile	Lys	Met	Phe	Tyr	
			215					220					225			
CCG	CTT	GTT	AAA	GTG	CGT	TAT	GAA	AAC	GAT	AAA	TAT	TTG	ATC	CCG	TTT	777
Pro	Leu	Val	Lys	Val	Arg	Tyr	Glu	Asn	Asp	Lys	Tyr	Leu	Ile	Pro	Phe	
		230					235					240				
GCT	TCA	TTA	GAC	GCC	AAT	CAA	AGA	ATG	GAA	TTT	GAC	TTG	AAA	GAT	CCT	825
Ala	Ser	Leu	Asp	Ala	Asn	Gln	Arg	Met	Glu	Phe	Asp	Leu	Lys	Asp	Pro	
	245					250					255					
CAA	GCG	AAG	GTT	ATT	CTT	TTA	GCG	GGT	AAA	AAG	CTC	ACT	TCA	AGA	AAG	873
Gln	Gly	Lys	Val	Ile	Leu	Leu	Ala	Gly	Lys	Lys	Leu	Thr	Ser	Arg	Lys	
260					265					270					275	

ATT AAA GAG CTT AAA GAA AAC CAT TTA GAA TGG GTG GAA TAC CCT ATG	921
Ile Lys Glu Leu Lys Glu Asn His Leu Glu Trp Val Glu Tyr Pro Met	
280 285 290	
GAT ATT TTA CTC AAT CGC CAT TTA GCT GAG CCT GTT ATG GTA GGG AAA	969
Asp Ile Leu Leu Asn Arg His Leu Ala Glu Pro Val Met Val Gly Lys	
295 300 305	
GAA GTC TTA TTG GAC ATG CTC ACT CAG CTA GAT AAA AAC AAA TTA GAA	1017
Glu Val Leu Leu Asp Met Leu Thr Gln Leu Asp Lys Asn Lys Leu Glu	
310 315 320	
AAA ATC CAC GAT TTA GGC GTG CAA GAA TTT GTG ATC ATC AAC GAT CTG	1065
Lys Ile His Asp Leu Gly Val Gln Glu Phe Val Ile Ile Asn Asp Leu	
325 330 335	
GCG TTA GGG CAT GAC GCT TCC ATT ATC CAA TCT TTT TCA GCC GAT TCT	1113
Ala Leu Gly His Asp Ala Ser Ile Ile Gln Ser Phe Ser Ala Asp Ser	
340 345 350 355	
GAG TCT TTG AAA TTA CTC AAG CAA ACC GAA AAA ATT GAT GAT GAA AAC	1161
Glu Ser Leu Lys Leu Leu Lys Gln Thr Glu Lys Ile Asp Asp Glu Asn	
360 365 370	
GCT CTA GCG GCG ATT CGT ATC CAT AAG GTT ATG AAA CCA GGC GAT CCC	1209
Ala Leu Ala Ala Ile Arg Ile His Lys Val Met Lys Pro Gly Asp Pro	
375 380 385	
GTT ACG ACT GAA GTG GCT AAG CAG TTT GTC AAA AAA CTT TTC TTT GAT	1257
Val Thr Thr Glu Val Ala Lys Gln Phe Val Lys Lys Leu Phe Phe Asp	
390 395 400	
CCA GAA CGC TAT GAT TTG ACC ATG GTG GGC CGC ATG AAA ATG AAT CAC	1305
Pro Glu Arg Tyr Asp Leu Thr Met Val Gly Arg Met Lys Met Asn His	
405 410 415	
AAG TTA GGC TTG CAT GTG CCT GAT TAC ATT ACG ACT TTA ACG CAT GAA	1353
Lys Leu Gly Leu His Val Pro Asp Tyr Ile Thr Thr Leu Thr His Glu	
420 425 430 435	
GAT ATT ATC ACC ACC GTT AAA TAC CTC ATG AAG ATC AAA AAC AAT CAA	1401
Asp Ile Ile Thr Thr Val Lys Tyr Leu Met Lys Ile Lys Asn Asn Gln	
440 445 450	
GGC AAG ATT GAT GAC AGG GAC CAC TTG GGC AAT CGT AGG ATT AGG GCG	1449
Gly Lys Ile Asp Asp Arg Asp His Leu Gly Asn Arg Arg Ile Arg Ala	
455 460 465	
GTA GGG GAA TTG TTG GCC AAT GAA TTG CAT TCA GGT TTA GTG AAA ATG	1497
Val Gly Glu Leu Leu Ala Asn Glu Leu His Ser Gly Leu Val Lys Met	
470 475 480	
CAA AAG ACC ATT AAA GAC AAG CTC ACT ACC ATG AGC GGG GCT TTT GAT	1545
Gln Lys Thr Ile Lys Asp Lys Leu Thr Thr Met Ser Gly Ala Phe Asp	
485 490 495	
TCG CTC ATG CCC CAT GAC TTG GTC AAT TCT AAA ATG ATC ACA AGC ACC	1593
Ser Leu Met Pro His Asp Leu Val Asn Ser Lys Met Ile Thr Ser Thr	

500	505	510	515	
ATC ATG GAA TTT TTC ATG GGC GGT CAG CTC TCG CAA TTT ATG GAT CAA				1641
Ile Met Glu Phe Phe Met Gly Gly Gln Leu Ser Gln Phe Met Asp Gln	520	525	530	
ACG AAT CCC TTG AGT GAG GTT ACG CAC AAG CGC CGC CTT TCA GCG CTC				1689
Thr Asn Pro Leu Ser Glu Val Thr His Lys Arg Arg Leu Ser Ala Leu	535	540	545	
GGC GAA GGG GGG TTG GTG AAA GAC AGA GTG GGG TTT GAA GCC AGG GAT				1737
Gly Glu Gly Gly Leu Val Lys Asp Arg Val Gly Phe Glu Ala Arg Asp	550	555	560	
GTG CAC CCC ACG CAT TAT GGC CGA ATT TGT CCC ATT GAG ACC CCA GAA				1785
Val His Pro Thr His Tyr Gly Arg Ile Cys Pro Ile Glu Thr Pro Glu	565	570	575	
GGT CAA AAT ATC GGT CTG ATC AAC ACC CTT TCC ACT TTC ACA AGA GTG				1833
Gly Gln Asn Ile Gly Leu Ile Asn Thr Leu Ser Thr Phe Thr Arg Val	580	585	590	595
AAT GAT TTA GGC TTT ATT GAA GCC CCT TAT AAA AAG GTT GTG GAT GGC				1881
Asn Asp Leu Gly Phe Ile Glu Ala Pro Tyr Lys Lys Val Val Asp Gly	600	605	610	
AAG GTC GTG GGT GAG ACG ATT TAT TTG ACC GCT ATT CAA GAA GAC AGC				1929
Lys Val Val Gly Glu Thr Ile Tyr Leu Thr Ala Ile Gln Glu Asp Ser	615	620	625	
CAC ATC ATC GCT CCC GCA AGC ACC CCC ATT GAT GAA GAG GGG AAT ATT				1977
His Ile Ile Ala Pro Ala Ser Thr Pro Ile Asp Glu Glu Gly Asn Ile	630	635	640	
TTG GGC GAT TTG ATT GAA ACG CGC GTG GAA GGC GAG ATC GTT TTA AAC				2025
Leu Gly Asp Leu Ile Glu Thr Arg Val Glu Gly Glu Ile Val Leu Asn	645	650	655	
GAA AAA AGC AAA GTA ACC TTA ATG GAT TTA AGC TCT AGC ATG CTA GTG				2073
Glu Lys Ser Lys Val Thr Leu Met Asp Leu Ser Ser Ser Met Leu Val	660	665	670	675
GGG GTA GCC GCA TCG CTC ATT CCT TTC TTA GAG CAT GAT GAC GCC AAC				2121
Gly Val Ala Ala Ser Leu Ile Pro Phe Leu Glu His Asp Asp Ala Asn	680	685	690	
CGT GCC TTA ATG GGG ACT AAC ATG CAG CGC CAA GCG GTG CCC TTA TTA				2169
Arg Ala Leu Met Gly Thr Asn Met Gln Arg Gln Ala Val Pro Leu Leu	695	700	705	
AGA AGC GAC GCT CCC ATT GTA GGC ACG GGG ATT GAA AAA ATT ATT GCT				2217
Arg Ser Asp Ala Pro Ile Val Gly Thr Gly Ile Glu Lys Ile Ile Ala	710	715	720	
AGG GAT TCT TGG GGA GCG ATC AAA GCC AAT CGC GCA GGC GTT GTA GAA				2265
Arg Asp Ser Trp Gly Ala Ile Lys Ala Asn Arg Ala Gly Val Val Glu	725	730	735	

AAA	ATT	GAT	TCT	AAA	AAT	ATT	TAT	ATT	TTA	GGC	GAA	AGC	AAA	GAA	GAA	2313
Lys	Ile	Asp	Ser	Lys	Asn	Ile	Tyr	Ile	Leu	Gly	Glu	Ser	Lys	Glu	Glu	
740					745					750					755	
GCC	TAT	ATT	GAT	GCG	TAT	TCT	TTG	CAA	AAA	AAC	TTG	CGC	ACC	AAC	CAA	2361
Ala	Tyr	Ile	Asp	Ala	Tyr	Ser	Leu	Gln	Lys	Asn	Leu	Arg	Thr	Asn	Gln	
				760					765						770	
AAC	ACC	AGT	TTC	AAT	CAA	GTC	CCT	ATC	GTT	AAA	GTG	GGC	GAT	AAA	GTG	2409
Asn	Thr	Ser	Phe	Asn	Gln	Val	Pro	Ile	Val	Lys	Val	Gly	Asp	Lys	Val	
			775					780					785			
GGA	GCC	GGG	CAA	ATC	ATC	GCT	GAT	GGC	CCT	AGC	ATG	GAT	AGA	GGC	GAG	2457
Gly	Ala	Gly	Gln	Ile	Ile	Ala	Asp	Gly	Pro	Ser	Met	Asp	Arg	Gly	Glu	
		790					795					800				
TTG	GCG	TTA	GGG	AAA	AAT	GTG	CGC	GTG	GCG	TTC	ATG	CCT	TGG	AAT	GGC	2505
Leu	Ala	Leu	Gly	Lys	Asn	Val	Arg	Val	Ala	Phe	Met	Pro	Trp	Asn	Gly	
	805					810					815					
TAT	AAC	TTT	GAA	GAC	GCG	ATC	GTG	GTG	AGT	GAG	TGC	ATC	ACT	AAA	GAT	2553
Tyr	Asn	Phe	Glu	Asp	Ala	Ile	Val	Val	Ser	Glu	Cys	Ile	Thr	Lys	Asp	
820					825					830					835	
GAT	ATT	TTC	ACT	TCC	ACC	CAC	ATT	TAT	GAA	AAA	GAA	GTG	GAT	GCT	AGG	2601
Asp	Ile	Phe	Thr	Ser	Thr	His	Ile	Tyr	Glu	Lys	Glu	Val	Asp	Ala	Arg	
				840					845					850		
GAG	CTT	AAG	CAT	GGT	GTG	GAA	GAA	TTT	ACC	GCT	GAT	ATT	CCT	GAT	GTG	2649
Glu	Leu	Lys	His	Gly	Val	Glu	Glu	Phe	Thr	Ala	Asp	Ile	Pro	Asp	Val	
			855					860					865			
AAA	GAA	GAA	GCG	CTC	GCT	CAT	CTT	GAT	GAA	AGC	GGG	ATC	GTT	AAA	GTC	2697
Lys	Glu	Glu	Ala	Leu	Ala	His	Leu	Asp	Glu	Ser	Gly	Ile	Val	Lys	Val	
		870					875					880				
GGT	ACT	TAT	GTG	AGC	GCT	GGC	ATG	ATT	TTG	GTG	GGC	AAA	ACT	TCT	CCT	2745
Gly	Thr	Tyr	Val	Ser	Ala	Gly	Met	Ile	Leu	Val	Gly	Lys	Thr	Ser	Pro	
	885					890					895					
AAA	GGC	GAG	ATT	AAA	AGC	ACG	CCT	GAA	GAG	CGG	CTT	TTA	AGG	GCT	ATT	2793
Lys	Gly	Glu	Ile	Lys	Ser	Thr	Pro	Glu	Glu	Arg	Leu	Leu	Arg	Ala	Ile	
900					905					910					915	
TTT	GGG	GAT	AAA	GCC	GGG	CAT	GTG	GTC	AAT	AAG	AGT	TTG	TAT	TGC	CCT	2841
Phe	Gly	Asp	Lys	Ala	Gly	His	Val	Val	Asn	Lys	Ser	Leu	Tyr	Cys	Pro	
				920					925					930		
CCC	AGT	TTG	GAA	GGC	ACG	GTG	ATT	GAT	GTG	AAA	GTC	TTC	ACT	AAA	AAA	2889
Pro	Ser	Leu	Glu	Gly	Thr	Val	Ile	Asp	Val	Lys	Val	Phe	Thr	Lys	Lys	
			935					940					945			
GGC	TAT	GAG	AAA	GAC	GCG	CGA	GTT	TTG	AGC	GCG	TAT	GAA	GAA	GAA	AAA	2937
Gly	Tyr	Glu	Lys	Asp	Ala	Arg	Val	Leu	Ser	Ala	Tyr	Glu	Glu	Glu	Lys	
		950					955					960				
GCC	AAG	CTT	GAT	ATG	GAG	CAT	TTT	GAT	CGC	TTG	ACC	ATG	CTC	AAT	AGA	2985
Ala	Lys	Leu	Asp	Met	Glu	His	Phe	Asp	Arg	Leu	Thr	Met	Leu	Asn	Arg	

965

970

975

GAA GAA TTG TTG CGC GTT ACT CGC TCC TTT CTC AAG CGA TTT TAGAAGAGC 3036
 Glu Glu Leu Leu Arg Val Thr Arg Ser Phe Leu Lys Arg Phe
 980 985 990

CTTTCAGCCA TAACGGCAAG GATTATAAAG AAGGCGATCA AATCCCTA 3084

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 993 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Met Ser Lys Lys Ile Pro Leu Lys Asn Arg Leu Arg Ala Asp Phe Thr
 1 5 10 15
 Lys Thr Pro Thr Asp Leu Glu Val Pro Asn Leu Leu Leu Leu Gln Arg
 20 25 30
 Asp Ser Tyr Asp Ser Phe Leu Tyr Ser Lys Glu Gly Lys Glu Ser Gly
 35 40 45
 Ile Glu Lys Val Phe Lys Ser Ile Phe Pro Ile Gln Asp Glu His Asn
 50 55 60
 Arg Ile Thr Leu Glu Tyr Ala Gly Cys Glu Phe Gly Lys Ser Lys Tyr
 65 70 75 80
 Thr Val Arg Glu Ala Met Glu Arg Gly Ile Thr Tyr Ser Ile Pro Leu
 85 90 95
 Lys Ile Lys Val Arg Leu Ile Leu Trp Glu Lys Asp Thr Lys Ser Gly
 100 105 110
 Glu Lys Asn Gly Ile Lys Asp Ile Lys Glu Gln Ser Ile Phe Ile Arg
 115 120 125
 Glu Ile Pro Leu Met Thr Glu Arg Thr Ser Phe Ile Ile Asn Gly Val
 130 135 140
 Glu Arg Val Val Val Asn Gln Leu His Arg Ser Pro Gly Val Ile Phe
 145 150 155 160
 Lys Glu Glu Glu Ser Ser Thr Ser Leu Asn Lys Leu Ile Tyr Thr Gly
 165 170 175
 Gln Ile Ile Pro Asp Arg Gly Ser Trp Leu Tyr Phe Glu Tyr Asp Ser
 180 185 190
 Lys Asp Val Leu Tyr Ala Arg Ile Asn Lys Arg Arg Lys Val Pro Val
 195 200 205
 Thr Ile Leu Phe Arg Ala Met Asp Tyr Gln Lys Gln Asp Ile Ile Lys
 210 215 220
 Met Phe Tyr Pro Leu Val Lys Val Arg Tyr Glu Asn Asp Lys Tyr Leu
 225 230 235 240
 Ile Pro Phe Ala Ser Leu Asp Ala Asn Gln Arg Met Glu Phe Asp Leu
 245 250 255
 Lys Asp Pro Gln Gly Lys Val Ile Leu Leu Ala Gly Lys Lys Leu Thr
 260 265 270
 Ser Arg Lys Ile Lys Glu Leu Lys Glu Asn His Leu Glu Trp Val Glu
 275 280 285
 Tyr Pro Met Asp Ile Leu Leu Asn Arg His Leu Ala Glu Pro Val Met

290		295		300
Val Gly Lys Glu Val Leu Leu Asp Met Leu Thr Gln Leu Asp Lys Asn				
305		310		315
Lys Leu Glu Lys Ile His Asp Leu Gly Val Gln Glu Phe Val Ile Ile				320
		325		330
Asn Asp Leu Ala Leu Gly His Asp Ala Ser Ile Ile Gln Ser Phe Ser				335
		340		345
Ala Asp Ser Glu Ser Leu Lys Leu Leu Lys Gln Thr Glu Lys Ile Asp				350
		355		360
Asp Glu Asn Ala Leu Ala Ala Ile Arg Ile His Lys Val Met Lys Pro				365
		370		375
Gly Asp Pro Val Thr Thr Glu Val Ala Lys Gln Phe Val Lys Lys Leu				380
385		390		395
Phe Phe Asp Pro Glu Arg Tyr Asp Leu Thr Met Val Gly Arg Met Lys				400
		405		410
Met Asn His Lys Leu Gly Leu His Val Pro Asp Tyr Ile Thr Thr Leu				415
		420		425
Thr His Glu Asp Ile Ile Thr Thr Val Lys Tyr Leu Met Lys Ile Lys				430
		435		440
Asn Asn Gln Gly Lys Ile Asp Asp Arg Asp His Leu Gly Asn Arg Arg				445
		450		455
Ile Arg Ala Val Gly Glu Leu Leu Ala Asn Glu Leu His Ser Gly Leu				460
465		470		475
Val Lys Met Gln Lys Thr Ile Lys Asp Lys Leu Thr Thr Met Ser Gly				480
		485		490
Ala Phe Asp Ser Leu Met Pro His Asp Leu Val Asn Ser Lys Met Ile				495
		500		505
Thr Ser Thr Ile Met Glu Phe Phe Met Gly Gly Gln Leu Ser Gln Phe				510
		515		520
Met Asp Gln Thr Asn Pro Leu Ser Glu Val Thr His Lys Arg Arg Leu				525
		530		535
Ser Ala Leu Gly Glu Gly Gly Leu Val Lys Asp Arg Val Gly Phe Glu				540
545		550		555
Ala Arg Asp Val His Pro Thr His Tyr Gly Arg Ile Cys Pro Ile Glu				560
		565		570
Thr Pro Glu Gly Gln Asn Ile Gly Leu Ile Asn Thr Leu Ser Thr Phe				575
		580		585
Thr Arg Val Asn Asp Leu Gly Phe Ile Glu Ala Pro Tyr Lys Lys Val				590
		595		600
Val Asp Gly Lys Val Val Gly Glu Thr Ile Tyr Leu Thr Ala Ile Gln				605
		610		615
Glu Asp Ser His Ile Ile Ala Pro Ala Ser Thr Pro Ile Asp Glu Glu				620
625		630		635
Gly Asn Ile Leu Gly Asp Leu Ile Glu Thr Arg Val Glu Gly Glu Ile				640
		645		650
Val Leu Asn Glu Lys Ser Lys Val Thr Leu Met Asp Leu Ser Ser Ser				655
		660		665
Met Leu Val Gly Val Ala Ala Ser Leu Ile Pro Phe Leu Glu His Asp				670
		675		680
Asp Ala Asn Arg Ala Leu Met Gly Thr Asn Met Gln Arg Gln Ala Val				685
		690		695
Pro Leu Leu Arg Ser Asp Ala Pro Ile Val Gly Thr Gly Ile Glu Lys				700
705		710		715
Ile Ile Ala Arg Asp Ser Trp Gly Ala Ile Lys Ala Asn Arg Ala Gly				720
		725		730
Val Val Glu Lys Ile Asp Ser Lys Asn Ile Tyr Ile Leu Gly Glu Ser				735
		740		745
Lys Glu Glu Ala Tyr Ile Asp Ala Tyr Ser Leu Gln Lys Asn Leu Arg				750

755		760		765
Thr Asn Gln Asn Thr Ser Phe Asn Gln Val Pro Ile Val Lys Val Gly				
770		775		780
Asp Lys Val Gly Ala Gly Gln Ile Ile Ala Asp Gly Pro Ser Met Asp				
785		790		795
Arg Gly Glu Leu Ala Leu Gly Lys Asn Val Arg Val Ala Phe Met Pro				
		805		810
Trp Asn Gly Tyr Asn Phe Glu Asp Ala Ile Val Val Ser Glu Cys Ile				
		820		825
Thr Lys Asp Asp Ile Phe Thr Ser Thr His Ile Tyr Glu Lys Glu Val				
		835		840
Asp Ala Arg Glu Leu Lys His Gly Val Glu Glu Phe Thr Ala Asp Ile				
		850		855
Pro Asp Val Lys Glu Glu Ala Leu Ala His Leu Asp Glu Ser Gly Ile				
865		870		875
Val Lys Val Gly Thr Tyr Val Ser Ala Gly Met Ile Leu Val Gly Lys				
		885		890
Thr Ser Pro Lys Gly Glu Ile Lys Ser Thr Pro Glu Glu Arg Leu Leu				
		900		905
Arg Ala Ile Phe Gly Asp Lys Ala Gly His Val Val Asn Lys Ser Leu				
		915		920
Tyr Cys Pro Pro Ser Leu Glu Gly Thr Val Ile Asp Val Lys Val Phe				
		930		935
Thr Lys Lys Gly Tyr Glu Lys Asp Ala Arg Val Leu Ser Ala Tyr Glu				
945		950		955
Glu Glu Lys Ala Lys Leu Asp Met Glu His Phe Asp Arg Leu Thr Met				
		965		970
Leu Asn Arg Glu Glu Leu Leu Arg Val Thr Arg Ser Phe Leu Lys Arg				
		980		985
				990
Phe				

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...525
- (D) OTHER INFORMATION:

(xi). SEQUENCE DESCRIPTION: SEQ ID NO:81:

AGGTTAAAGT TTAAGACAAA CCAAAGAGTT TGTCTTGTTT GTTTTTGA ATG CAC TCT	57
Met His Ser	
1	
CCA AAT TTA GAA AAA GAA GAA ACC GAA ATC ATA GAA ACA CTC CTT ATG	105
Pro Asn Leu Glu Lys Glu Glu Thr Glu Ile Ile Glu Thr Leu Leu Met	
5 10 15	

CGT GAA AAA ATG CGT TTA TGC CCC TTG TAT TGG CGC ATC TTA GCG TTT	153
Arg Glu Lys Met Arg Leu Cys Pro Leu Tyr Trp Arg Ile Leu Ala Phe	
20 25 30 35	
TTA ACC GAT GGT TTG TTA GTG GCG TTT TTA TTG AGC GAT CTT TTA GAC	201
Leu Thr Asp Gly Leu Leu Val Ala Phe Leu Leu Ser Asp Leu Leu Asp	
40 45 50	
GCA TGC GAT TTC TTG CAT TCT TTA TAT TGG CTA GCT AAC CCT ATT TAT	249
Ala Cys Asp Phe Leu His Ser Leu Tyr Trp Leu Ala Asn Pro Ile Tyr	
55 60 65	
CAC AGC GCA TTT GTT GCG ATG GGT TTT ATC ATC TTG TAT GGC GTT TAT	297
His Ser Ala Phe Val Ala Met Gly Phe Ile Ile Leu Tyr Gly Val Tyr	
70 75 80	
GAA ATC TTT TTT GTG TGT TTG TGC AAG ATG AGC TTG GCT AAA CTG GTT	345
Glu Ile Phe Phe Val Cys Leu Cys Lys Met Ser Leu Ala Lys Leu Val	
85 90 95	
TTT AGG ATT AAG ATT ATT GAT ATT TAT TTG GCA GAT TGC CCC AGT AGG	393
Phe Arg Ile Lys Ile Ile Asp Ile Tyr Leu Ala Asp Cys Pro Ser Arg	
100 105 110 115	
GCT ATT TTA TTG AAG CGT TTA GGG TTA AAG ATC GTG GTT TTT CTA TGC	441
Ala Ile Leu Leu Lys Arg Leu Gly Leu Lys Ile Val Val Phe Leu Cys	
120 125 130	
CCC TTT TTA TGG TTT GTT GCG TTT AAA AAC CCC TAT CAT AGG GCG TGG	489
Pro Phe Leu Trp Phe Val Ala Phe Lys Asn Pro Tyr His Arg Ala Trp	
135 140 145	
CAT GAA GAA AAA AGC AAA AGT CTT TTG GTA TTG TTT TAATCATGAT TTATTG	541
His Glu Glu Lys Ser Lys Ser Leu Leu Val Leu Phe	
150 155	
GTTGTATTTG GCGGTCTTTT TTTTGTGAG CGCATTAGAC	581

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met His Ser Pro Asn Leu Glu Lys Glu Glu Thr Glu Ile Ile Glu Thr	
1 5 10 15	
Leu Leu Met Arg Glu Lys Met Arg Leu Cys Pro Leu Tyr Trp Arg Ile	
20 25 30	
Leu Ala Phe Leu Thr Asp Gly Leu Leu Val Ala Phe Leu Leu Ser Asp	
35 40 45	
Leu Leu Asp Ala Cys Asp Phe Leu His Ser Leu Tyr Trp Leu Ala Asn	

50	55	60
Pro Ile Tyr His Ser Ala Phe Val Ala Met Gly Phe Ile Ile Leu Tyr		
65	70	75
Gly Val Tyr Glu Ile Phe Phe Val Cys Leu Cys Lys Met Ser Leu Ala		80
	85	90
Lys Leu Val Phe Arg Ile Lys Ile Ile Asp Ile Tyr Leu Ala Asp Cys		95
	100	105
Pro Ser Arg Ala Ile Leu Leu Lys Arg Leu Gly Leu Lys Ile Val Val		110
	115	120
Phe Leu Cys Pro Phe Leu Trp Phe Val Ala Phe Lys Asn Pro Tyr His		125
	130	135
Arg Ala Trp His Glu Glu Lys Ser Lys Ser Leu Leu Val Leu Phe		140
145	150	155

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 901 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 67...852
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GAATTTAAGC GGCAGAGGGG ATAAGGATTT AAGCACCGTT TATAACGCTT TAAAAGGAGG	60
TTTAAA ATG AGG TAT CAA AAC ATG TTT GAA ACC TTA AAA AAA CAC GAA	108
Met Arg Tyr Gln Asn Met Phe Glu Thr Leu Lys Lys His Glu	
1 5 10	
AAA ATG GCG TTT ATC CCG TTT GTA ACC TTG GGC GAT CCT AAT TAT GAA	156
Lys Met Ala Phe Ile Pro Phe Val Thr Leu Gly Asp Pro Asn Tyr Glu	
15 20 25 30	
TTG AGT TTT GAA ATC ATT AAA ACC CTA ATT ATT AGC GGG GTG AGC GCT	204
Leu Ser Phe Glu Ile Ile Lys Thr Leu Ile Ile Ser Gly Val Ser Ala	
35 40 45	
TTA GAA TTG GGT CTT GCT TTT TCT GAT CCT GTG GCG GAT GGC ATT ACC	252
Leu Glu Leu Gly Leu Ala Phe Ser Asp Pro Val Ala Asp Gly Ile Thr	
50 55 60	
ATA CAA GCG AGC CAT TTA AGG GCG TTA AAA CAC GCT AGC ATG GCT AAA	300
Ile Gln Ala Ser His Leu Arg Ala Leu Lys His Ala Ser Met Ala Lys	
65 70 75	
AAT TTC CAG CTT TTA AAA AAG ATT AGA GAT TAC AAC CAC AAT ATT CCC	348
Asn Phe Gln Leu Leu Lys Lys Ile Arg Asp Tyr Asn His Asn Ile Pro	
80 85 90	

ATA GGG CTT TTA GCG TAT GCG AAT TTA ATT TTT TCT TAT GGC GTT GAT	396
Ile Gly Leu Leu Ala Tyr Ala Asn Leu Ile Phe Ser Tyr Gly Val Asp	
95 100 105 110	
GGC TTT TAC GCT CAA GCT AAA GAA TGC GGT ATA GAT AGC GTT TTA ATA	444
Gly Phe Tyr Ala Gln Ala Lys Glu Cys Gly Ile Asp Ser Val Leu Ile	
115 120 125	
GCG GAC ATG CCC CTA ATA GAA AAA GAA TTA GTC ATC AAA TCC GCT CAA	492
Ala Asp Met Pro Leu Ile Glu Lys Glu Leu Val Ile Lys Ser Ala Gln	
130 135 140	
AAA CAC CAA ATC AAG CAA ATC TTT ATC GCC AGC CCC AAT GCG AGC AGT	540
Lys His Gln Ile Lys Gln Ile Phe Ile Ala Ser Pro Asn Ala Ser Ser	
145 150 155	
AAA GAT TTA GAA CAA GTC GCT ACG CAT TCG CAA GGC TAT ATC TAC GCT	588
Lys Asp Leu Glu Gln Val Ala Thr His Ser Gln Gly Tyr Ile Tyr Ala	
160 165 170	
TTA GCC AGG AGT GGG GTT ACA GGG GCG AGC CGT ATT TTA GAG AAT GAT	636
Leu Ala Arg Ser Gly Val Thr Gly Ala Ser Arg Ile Leu Glu Asn Asp	
175 180 185 190	
TCG AGT GCT ATT ATT AAA ACC TTA AAA GCT TTT AGC CCT ACC CCA GCC	684
Ser Ser Ala Ile Ile Lys Thr Leu Lys Ala Phe Ser Pro Thr Pro Ala	
195 200 205	
TTA CTG GGC TTT GGC ATT TCC AAA AAA GAA CAC ATC ACA AAC GCT AAA	732
Leu Leu Gly Phe Gly Ile Ser Lys Lys Glu His Ile Thr Asn Ala Lys	
210 215 220	
GGC ATG GGT GCT GAT GGC GTG ATT TGC GGA TCA GCG TTA GTC AAA ATC	780
Gly Met Gly Ala Asp Gly Val Ile Cys Gly Ser Ala Leu Val Lys Ile	
225 230 235	
ATA GAA GAA AAT TTA AAC AAT GAA AAC GCC ATG CTG GAA AAA ATT AAA	828
Ile Glu Glu Asn Leu Asn Asn Glu Asn Ala Met Leu Glu Lys Ile Lys	
240 245 250	
GGG TTT ATA GGA GGA ATG ATT TTT TAAGGCTTTT AGGCTTTGTT GCGTTAAAAA	882
Gly Phe Ile Gly Gly Met Ile Phe	
255 260	
TTAAAGATCA CAGATTAAC	901

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Met	Arg	Tyr	Gln	Asn	Met	Phe	Glu	Thr	Leu	Lys	Lys	His	Glu	Lys	Met
1				5					10					15	
Ala	Phe	Ile	Pro	Phe	Val	Thr	Leu	Gly	Asp	Pro	Asn	Tyr	Glu	Leu	Ser
			20					25					30		
Phe	Glu	Ile	Ile	Lys	Thr	Leu	Ile	Ile	Ser	Gly	Val	Ser	Ala	Leu	Glu
		35					40					45			
Leu	Gly	Leu	Ala	Phe	Ser	Asp	Pro	Val	Ala	Asp	Gly	Ile	Thr	Ile	Gln
	50					55					60				
Ala	Ser	His	Leu	Arg	Ala	Leu	Lys	His	Ala	Ser	Met	Ala	Lys	Asn	Phe
65					70					75				80	
Gln	Leu	Leu	Lys	Lys	Ile	Arg	Asp	Tyr	Asn	His	Asn	Ile	Pro	Ile	Gly
				85					90					95	
Leu	Leu	Ala	Tyr	Ala	Asn	Leu	Ile	Phe	Ser	Tyr	Gly	Val	Asp	Gly	Phe
			100					105					110		
Tyr	Ala	Gln	Ala	Lys	Glu	Cys	Gly	Ile	Asp	Ser	Val	Leu	Ile	Ala	Asp
		115					120					125			
Met	Pro	Leu	Ile	Glu	Lys	Glu	Leu	Val	Ile	Lys	Ser	Ala	Gln	Lys	His
	130					135					140				
Gln	Ile	Lys	Gln	Ile	Phe	Ile	Ala	Ser	Pro	Asn	Ala	Ser	Ser	Lys	Asp
145					150					155				160	
Leu	Glu	Gln	Val	Ala	Thr	His	Ser	Gln	Gly	Tyr	Ile	Tyr	Ala	Leu	Ala
				165					170					175	
Arg	Ser	Gly	Val	Thr	Gly	Ala	Ser	Arg	Ile	Leu	Glu	Asn	Asp	Ser	Ser
			180					185					190		
Ala	Ile	Ile	Lys	Thr	Leu	Lys	Ala	Phe	Ser	Pro	Thr	Pro	Ala	Leu	Leu
		195					200					205			
Gly	Phe	Gly	Ile	Ser	Lys	Lys	Glu	His	Ile	Thr	Asn	Ala	Lys	Gly	Met
	210					215					220				
Gly	Ala	Asp	Gly	Val	Ile	Cys	Gly	Ser	Ala	Leu	Val	Lys	Ile	Ile	Glu
225					230					235				240	
Glu	Asn	Leu	Asn	Asn	Glu	Asn	Ala	Met	Leu	Glu	Lys	Ile	Lys	Gly	Phe
			245					250						255	
Ile	Gly	Gly	Met	Ile	Phe										
			260												

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1081 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...954
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

AAGTAATGCC CCTGTTGTAT CAGCTTGATT TAAGAGGAAT AAGTTATT ATG AAT AAA 57
Met Asn Lys
1

GCT ATT GCT AGT AAG ATA CTC ATC ACT TTG GGT TTT TTA TTT CTC TAC 105

Ala	Ile	Ala	Ser	Lys	Ile	Leu	Ile	Thr	Leu	Gly	Phe	Leu	Phe	Leu	Tyr	
5						10					15					
AGA	GTC	TTA	GCT	TAT	ATC	CCC	ATT	CCT	GGC	GTA	GAT	TTA	GCA	GCG	ATC	153
Arg	Val	Leu	Ala	Tyr	Ile	Pro	Ile	Pro	Gly	Val	Asp	Leu	Ala	Ala	Ile	
20					25				30						35	
AAG	GCT	TTT	TTT	GAC	AGC	AAT	TCC	AAC	AAC	GCT	TTG	GGG	TTG	TTT	AAT	201
Lys	Ala	Phe	Phe	Asp	Ser	Asn	Ser	Asn	Asn	Ala	Leu	Gly	Leu	Phe	Asn	
				40				45						50		
ATG	TTT	AGC	GGG	AAT	GCG	GTT	TCT	CGC	TTG	AGC	ATC	ATC	TCG	TTG	GGT	249
Met	Phe	Ser	Gly	Asn	Ala	Val	Ser	Arg	Leu	Ser	Ile	Ile	Ser	Leu	Gly	
			55					60					65			
ATC	ATG	CCC	TAT	ATC	ACT	TCT	TCA	ATT	ATC	ATG	GAG	CTT	TTG	AGC	GCG	297
Ile	Met	Pro	Tyr	Ile	Thr	Ser	Ser	Ile	Ile	Met	Glu	Leu	Leu	Ser	Ala	
		70					75					80				
ACT	TTC	CCT	AAC	CTG	GCT	AAA	ATG	AAA	AAA	GAG	CGG	GAT	GGC	ATG	CAA	345
Thr	Phe	Pro	Asn	Leu	Ala	Lys	Met	Lys	Lys	Glu	Arg	Asp	Gly	Met	Gln	
	85					90					95					
AAA	TAC	ATG	CAA	ATC	GTG	CGT	TAT	TTG	ACC	ATT	TTA	ATC	ACC	CTA	ATC	393
Lys	Tyr	Met	Gln	Ile	Val	Arg	Tyr	Leu	Thr	Ile	Leu	Ile	Thr	Leu	Ile	
100					105					110					115	
CAA	GCG	GTG	AGC	GTT	TCA	GTA	GGC	TTA	AGG	AGC	ATT	AGT	GGA	GGA	GCC	441
Gln	Ala	Val	Ser	Val	Ser	Val	Gly	Leu	Arg	Ser	Ile	Ser	Gly	Gly	Ala	
				120				125						130		
AAT	GGG	GCG	ATC	ATG	ATT	GAT	ATG	CAA	GTT	TTT	ATG	ATC	GTT	TCA	GCG	489
Asn	Gly	Ala	Ile	Met	Ile	Asp	Met	Gln	Val	Phe	Met	Ile	Val	Ser	Ala	
			135				140						145			
TTT	TCT	ATG	CTT	ACA	GGA	ACG	ATG	CTA	CTC	ATG	TGG	ATA	GGG	GAG	CAA	537
Phe	Ser	Met	Leu	Thr	Gly	Thr	Met	Leu	Leu	Met	Trp	Ile	Gly	Glu	Gln	
		150					155					160				
ATC	ACG	CAA	AGG	GGC	GTG	GGG	AAT	GGG	ATC	AGT	CTC	ATT	ATT	TTT	GCC	585
Ile	Thr	Gln	Arg	Gly	Val	Gly	Asn	Gly	Ile	Ser	Leu	Ile	Ile	Phe	Ala	
	165					170					175					
GGG	ATT	GTT	TCA	GGG	ATC	CCA	TCA	GCT	ATT	TCA	GGC	ACA	TTC	AAT	TTG	633
Gly	Ile	Val	Ser	Gly	Ile	Pro	Ser	Ala	Ile	Ser	Gly	Thr	Phe	Asn	Leu	
180					185					190					195	
GTC	AAT	ACG	GGC	GTT	ATT	AAT	ATC	TTA	ATG	CTC	ATT	GGT	ATT	GTG	CTG	681
Val	Asn	Thr	Gly	Val	Ile	Asn	Ile	Leu	Met	Leu	Ile	Gly	Ile	Val	Leu	
				200				205						210		
ATT	GTT	TTA	GCG	ACT	ATT	TTT	GCG	ATT	ATC	TAT	GTG	GAA	TTA	GCT	GAG	729
Ile	Val	Leu	Ala	Thr	Ile	Phe	Ala	Ile	Ile	Tyr	Val	Glu	Leu	Ala	Glu	
			215					220					225			
CGC	AGG	ATC	CCT	ATT	TCT	TAT	GCG	CGT	AAA	GTG	GTG	ATG	CAA	AAC	CAA	777
Arg	Arg	Ile	Pro	Ile	Ser	Tyr	Ala	Arg	Lys	Val	Val	Met	Gln	Asn	Gln	
		230					235					240				

AAC AAG CGC ATC ATG AAT TAC ATT CCT ATT AAG TTG AAT TTA AGT GGG	825
Asn Lys Arg Ile Met Asn Tyr Ile Pro Ile Lys Leu Asn Leu Ser Gly	
245 250 255	
GTG ATC CCC CCT ATT TTC GCT TCA GCT TTG CTC GTG TTC CCT TCT ACG	873
Val Ile Pro Pro Ile Phe Ala Ser Ala Leu Leu Val Phe Pro Ser Thr	
260 265 270 275	
ATT TTG CAG CAA GCC ACA AGC AAC AAA ACC TTG CAA GCG GTT GCG NAT	921
Ile Leu Gln Gln Ala Thr Ser Asn Lys Thr Leu Gln Ala Val Ala Xaa	
280 285 290	
TTT TTA AGC CCG CAA GGT ATG CGT ATA ATA TTT TGATGTTCTT GCTCATCATC	974
Phe Leu Ser Pro Gln Gly Met Arg Ile Ile Phe	
295 300	
TTTTTTGCTT ACTTTTATTC TTCTATTGTG TTCAATTCTA AGGATATTGC GGATAATTTG	1034
AGGCGTAATG GCGGGTATAT TCCAGGGCTT AGGCCTGGAG AGGGGAC	1081

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met Asn Lys Ala Ile Ala Ser Lys Ile Leu Ile Thr Leu Gly Phe Leu	
1 5 10 15	
Phe Leu Tyr Arg Val Leu Ala Tyr Ile Pro Ile Pro Gly Val Asp Leu	
20 25 30	
Ala Ala Ile Lys Ala Phe Phe Asp Ser Asn Ser Asn Asn Ala Leu Gly	
35 40 45	
Leu Phe Asn Met Phe Ser Gly Asn Ala Val Ser Arg Leu Ser Ile Ile	
50 55 60	
Ser Leu Gly Ile Met Pro Tyr Ile Thr Ser Ser Ile Ile Met Glu Leu	
65 70 75 80	
Leu Ser Ala Thr Phe Pro Asn Leu Ala Lys Met Lys Lys Glu Arg Asp	
85 90 95	
Gly Met Gln Lys Tyr Met Gln Ile Val Arg Tyr Leu Thr Ile Leu Ile	
100 105 110	
Thr Leu Ile Gln Ala Val Ser Val Ser Val Gly Leu Arg Ser Ile Ser	
115 120 125	
Gly Gly Ala Asn Gly Ala Ile Met Ile Asp Met Gln Val Phe Met Ile	
130 135 140	
Val Ser Ala Phe Ser Met Leu Thr Gly Thr Met Leu Leu Met Trp Ile	
145 150 155 160	
Gly Glu Gln Ile Thr Gln Arg Gly Val Gly Asn Gly Ile Ser Leu Ile	
165 170 175	
Ile Phe Ala Gly Ile Val Ser Gly Ile Pro Ser Ala Ile Ser Gly Thr	
180 185 190	
Phe Asn Leu Val Asn Thr Gly Val Ile Asn Ile Leu Met Leu Ile Gly	
195 200 205	

Ile Val Leu Ile Val Leu Ala Thr Ile Phe Ala Ile Ile Tyr Val Glu
 210 215 220
 Leu Ala Glu Arg Arg Ile Pro Ile Ser Tyr Ala Arg Lys Val Val Met
 225 230 235 240
 Gln Asn Gln Asn Lys Arg Ile Met Asn Tyr Ile Pro Ile Lys Leu Asn
 245 250 255
 Leu Ser Gly Val Ile Pro Pro Ile Phe Ala Ser Ala Leu Leu Val Phe
 260 265 270
 Pro Ser Thr Ile Leu Gln Gln Ala Thr Ser Asn Lys Thr Leu Gln Ala
 275 280 285
 Val Ala Xaa Phe Leu Ser Pro Gln Gly Met Arg Ile Ile Phe
 290 295 300

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 109...363
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

AATGGGGCAA TTCAAGGCGA TAGAAGCTTG AATGAGGGCT TCTTCTAAGG TTTTGGCTTT 60
 GATTTCATA AAATTTTGCA TCAATGTTCC TTTTGTGTTT GCGCATGC ATG CGT TTT 117
 Met Arg Phe
 1
 TTA TTC TCT AAG ACT TTA TTG ATG ATG AGT TGT TGC AAC ACC GAA AGG 165
 Leu Phe Ser Lys Thr Leu Leu Met Met Ser Cys Cys Asn Thr Glu Arg
 5 10 15
 ATG TTG TTC GTG GTC CAA TAC AAG ACT AAC CCT GCC GGG AAA GTG ATT 213
 Met Leu Phe Val Val Gln Tyr Lys Thr Asn Pro Ala Gly Lys Val Ile
 20 25 30 35
 AAA AAG ATT GTG AAT AAT AGG GGT AAG AGT TTA AAA ATC TTT GCT TGC 261
 Lys Lys Ile Val Asn Asn Arg Gly Lys Ser Leu Lys Ile Phe Ala Cys
 40 45 50
 ATG GGA TCG GTC ATG GTG TTT GGC GTA ACG CTT TGG TGC CAA TAC ATA 309
 Met Gly Ser Val Met Val Phe Gly Val Thr Leu Trp Cys Gln Tyr Ile
 55 60 65
 GAC GCT CCC ATA AGA AGC GGT AAA ATA AAA TAC GGA TCC ATG ATG GAT 357
 Asp Ala Pro Ile Arg Ser Gly Lys Ile Lys Tyr Gly Ser Met Met Asp
 70 75 80
 AAA TCA TGAATCCATA AGATCCACTC TGAGCTTTTC AATCCACAG CGTTATAAAG CA 415
 Lys Ser

85

CTCTATAA

423

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```

Met Arg Phe Leu Phe Ser Lys Thr Leu Leu Met Met Ser Cys Cys Asn
 1           5           10           15
Thr Glu Arg Met Leu Phe Val Val Gln Tyr Lys Thr Asn Pro Ala Gly
      20           25           30
Lys Val Ile Lys Lys Ile Val Asn Asn Arg Gly Lys Ser Leu Lys Ile
      35           40           45
Phe Ala Cys Met Gly Ser Val Met Val Phe Gly Val Thr Leu Trp Cys
      50           55           60
Gln Tyr Ile Asp Ala Pro Ile Arg Ser Gly Lys Ile Lys Tyr Gly Ser
65           70           75           80
Met Met Asp Lys Ser
              85

```

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 59...688
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```

TTTAAAATTA GAAACAGATG TATCTGTTTT AAATTTTGAA TAGGGAGTTT CTATCATT      58

ATG TTA TTG AAA ACA AAA TTA AAA ATT ATA AGC TCG GTG ATT TTG AGC      106
Met Leu Leu Lys Thr Lys Leu Lys Ile Ile Ser Ser Val Ile Leu Ser
 1           5           10           15

GCT TTA TTG TGG GTG GGT TGC TCA AGC GAA ATG GCA ACT TAT CAA AAC      154
Ala Leu Leu Trp Val Gly Cys Ser Ser Glu Met Ala Thr Tyr Gln Asn

```

20										25					30					
GTG	AAT	GAT	GCC	ACT	AAA	AAT	ACG	ACT	GCA	AGC	ATT	AAT	AGC	ACG	GAT	202				
Val	Asn	Asp	Ala	Thr	Lys	Asn	Thr	Thr	Ala	Ser	Ile	Asn	Ser	Thr	Asp					
		35					40					45								
TTA	TTG	CTA	ACC	GCT	AAC	GCG	ATG	TTA	GAT	TCC	ATG	TTT	AGC	GAC	CCT	250				
Leu	Leu	Leu	Thr	Ala	Asn	Ala	Met	Leu	Asp	Ser	Met	Phe	Ser	Asp	Pro					
	50					55					60									
AAT	TTT	GAG	CAA	CTC	AAG	GGC	AAG	CAT	TTG	ATT	GAA	GTT	TCA	GAT	GTG	298				
Asn	Phe	Glu	Gln	Leu	Lys	Gly	Lys	His	Leu	Ile	Glu	Val	Ser	Asp	Val					
65					70				75					80						
ATT	AAC	GAC	ACC	ACG	CAG	CCC	AAT	TTG	GAC	ATG	AAT	CTT	TTG	ACG	ACT	346				
Ile	Asn	Asp	Thr	Thr	Gln	Pro	Asn	Leu	Asp	Met	Asn	Leu	Leu	Thr	Thr					
				85				90						95						
GAA	ATC	GCG	CGG	CAG	TTG	CGG	TTG	CGA	TCT	AAT	GGG	AGG	TTC	AAT	ATC	394				
Glu	Ile	Ala	Arg	Gln	Leu	Arg	Leu	Arg	Ser	Asn	Gly	Arg	Phe	Asn	Ile					
			100				105						110							
ACA	AGG	GCG	AGC	GGA	GGG	AGT	GGC	ATT	GCA	GCC	GAT	AGC	AGA	ATG	GTG	442				
Thr	Arg	Ala	Ser	Gly	Gly	Ser	Gly	Ile	Ala	Ala	Asp	Ser	Arg	Met	Val					
		115					120					125								
AAA	CAG	CGC	GAA	AAA	GAA	CGA	GAG	AGC	GAA	GAG	TAT	AAT	CAA	GAC	ACC	490				
Lys	Gln	Arg	Glu	Lys	Glu	Arg	Glu	Ser	Glu	Glu	Tyr	Asn	Gln	Asp	Thr					
	130					135					140									
ACT	GTA	GAA	AAA	GGC	ACT	TTA	AAA	GCC	GCT	GAT	TTA	TCT	TTA	AGT	GGT	538				
Thr	Val	Glu	Lys	Gly	Thr	Leu	Lys	Ala	Ala	Asp	Leu	Ser	Leu	Ser	Gly					
145					150					155					160					
AAA	GTA	TCT	AGT	ATC	GCA	GCC	TCT	ATT	AGT	AGT	TCT	AGG	CAG	CGC	TTG	586				
Lys	Val	Ser	Ser	Ile	Ala	Ala	Ser	Ile	Ser	Ser	Ser	Arg	Gln	Arg	Leu					
				165					170					175						
GAC	TAT	GAC	TTC	ACC	CTA	AGC	CTT	ACC	AAC	AGG	AAA	ACG	GGT	GAA	GAG	634				
Asp	Tyr	Asp	Phe	Thr	Leu	Ser	Leu	Thr	Asn	Arg	Lys	Thr	Gly	Glu	Glu					
			180					185					190							
GTA	TGG	AGC	GAT	GTT	AAG	CCT	ATT	GTG	AAG	AAC	GCT	AGC	AAT	AAG	CGT	682				
Val	Trp	Ser	Asp	Val	Lys	Pro	Ile	Val	Lys	Asn	Ala	Ser	Asn	Lys	Arg					
		195				200						205								
ATG	TTT	TAAATTTATA	TTTGAAAGGA	TGAACAATGA	AAAATCAAGT	TAAAAAAATT	TT									740				
Met	Phe																			
	210																			

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 210 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```

Met Leu Leu Lys Thr Lys Leu Lys Ile Ile Ser Ser Val Ile Leu Ser
 1           5           10           15
Ala Leu Leu Trp Val Gly Cys Ser Ser Glu Met Ala Thr Tyr Gln Asn
 20           25           30
Val Asn Asp Ala Thr Lys Asn Thr Thr Ala Ser Ile Asn Ser Thr Asp
 35           40           45
Leu Leu Leu Thr Ala Asn Ala Met Leu Asp Ser Met Phe Ser Asp Pro
 50           55           60
Asn Phe Glu Gln Leu Lys Gly Lys His Leu Ile Glu Val Ser Asp Val
 65           70           75           80
Ile Asn Asp Thr Thr Gln Pro Asn Leu Asp Met Asn Leu Leu Thr Thr
 85           90           95
Glu Ile Ala Arg Gln Leu Arg Leu Arg Ser Asn Gly Arg Phe Asn Ile
100          105          110
Thr Arg Ala Ser Gly Gly Ser Gly Ile Ala Ala Asp Ser Arg Met Val
115          120          125
Lys Gln Arg Glu Lys Glu Arg Glu Ser Glu Glu Tyr Asn Gln Asp Thr
130          135          140
Thr Val Glu Lys Gly Thr Leu Lys Ala Ala Asp Leu Ser Leu Ser Gly
145          150          155          160
Lys Val Ser Ser Ile Ala Ala Ser Ile Ser Ser Ser Arg Gln Arg Leu
165          170          175
Asp Tyr Asp Phe Thr Leu Ser Leu Thr Asn Arg Lys Thr Gly Glu Glu
180          185          190
Val Trp Ser Asp Val Lys Pro Ile Val Lys Asn Ala Ser Asn Lys Arg
195          200          205
Met Phe
210

```

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1269 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 84...1214

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

```

TTATCATTGT GTTAAATAG TCGTTTAAAC AAACAAATT TTGTTAATAG ATTTTACCTA    60
ATCTGAGAGA GAATTATATT TTA ATG AAG ACA GAG AAA CAA AAA TTT TTA GAG    113
          Met Lys Thr Glu Lys Gln Lys Phe Leu Glu
                1                5                10

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ATG CGT AAA GAT GGG GCG AAC TCT GTG CTG ATT TTA AGA GGG GAT TGG	161
Met Arg Lys Asp Gly Ala Asn Ser Val Leu Ile Leu Arg Gly Asp Trp	
15 20 25	
GAT TTT AAA ACG AGC GTG TTT CGT TTA GAT GAG TTG AAA AAA AAT TTA	209
Asp Phe Lys Thr Ser Val Phe Arg Leu Asp Glu Leu Lys Lys Asn Leu	
30 35 40	
TTA GAT CAT CAA GGG CCT TTA AAA ATG GAT TTT TCA GGG TGC CAA AAA	257
Leu Asp His Gln Gly Pro Leu Lys Met Asp Phe Ser Gly Cys Gln Lys	
45 50 55	
GTG GAT TTT GTT TTT GGC ATG TTT TTA TTT GAT TTA GTT AAG GAG CGT	305
Val Asp Phe Val Phe Gly Met Phe Leu Phe Asp Leu Val Lys Glu Arg	
60 65 70	
TCT TTA AAC ATT GAA TTG TGT AAC GTG AGT GAG AAT AAC GCA TGC GCT	353
Ser Leu Asn Ile Glu Leu Cys Asn Val Ser Glu Asn Asn Ala Cys Ala	
75 80 85 90	
TTG AAA GTG GTT AAA GAC TGG CTT GAA AAA GAA GAG GAT TTA GAG TCT	401
Leu Lys Val Val Lys Asp Trp Leu Glu Lys Glu Glu Asp Leu Glu Ser	
95 100 105	
AAA AAA GCG GGC AAA CAC TAC GAA CTT TTG ATC ACT AAA TTG GGT AAG	449
Lys Lys Ala Gly Lys His Tyr Glu Leu Leu Ile Thr Lys Leu Gly Lys	
110 115 120	
AGT ATC GTA GAG ACT TAT AAT ACC TTT TTA AAC GCA TTC AAT TTT TGC	497
Ser Ile Val Glu Thr Tyr Asn Thr Phe Leu Asn Ala Phe Asn Phe Cys	
125 130 135	
GGC ATG ATT TTA TTC TAC TTC ATT AAA AGC GTT TTC AAC CCC AAA CGC	545
Gly Met Ile Leu Phe Tyr Phe Ile Lys Ser Val Phe Asn Pro Lys Arg	
140 145 150	
TTT TGT ATC ACT CCT TTG CTC TAT CAT ATC AAT GAA TCC GGG TTT AAG	593
Phe Cys Ile Thr Pro Leu Leu Tyr His Ile Asn Glu Ser Gly Phe Lys	
155 160 165 170	
GTT TTG CCA GTG AGT ATT TTA ACG GTG TTT ATC GTG GGG TTT GCC GTT	641
Val Leu Pro Val Ser Ile Leu Thr Val Phe Ile Val Gly Phe Ala Val	
175 180 185	
GCT TTA CAA GGG GCT TTA CAA TTA CAA GAC ATG GGC GCG CCT TTA ATG	689
Ala Leu Gln Gly Ala Leu Gln Leu Gln Asp Met Gly Ala Pro Leu Met	
190 195 200	
TCG GTG GAA ATG ACG GCT AAA CTC GCT TTA AGA GAA ATC GGC CCT TTT	737
Ser Val Glu Met Thr Ala Lys Leu Ala Leu Arg Glu Ile Gly Pro Phe	
205 210 215	
ATT TTA ACC CTT GTG GTG GCC GGG AGG AGC GCG AGC AGT TTT ACC GCG	785
Ile Leu Thr Leu Val Val Ala Gly Arg Ser Ala Ser Ser Phe Thr Ala	
220 225 230	
CAA ATT GGG GTG ATG AAG ATC ACT GAG GAA TTA GAC GCG ATG AAA ACC	833
Gln Ile Gly Val Met Lys Ile Thr Glu Glu Leu Asp Ala Met Lys Thr	

235	240	245	250	
ATG GGC TTT AAC CCT TTT GAA TTT TTA GTG TTG CCT AGG GTG TTA GCC				881
Met Gly Phe Asn Pro Phe Glu Phe Leu Val Leu Pro Arg Val Leu Ala	255	260	265	
TTA GTG ATT GTT TTG CCT TTA TTG GTG TTT ATT GCC GAT GCG TTC GCC				929
Leu Val Ile Val Leu Pro Leu Leu Val Phe Ile Ala Asp Ala Phe Ala	270	275	280	
ATT CTT GGG GGC ATG TTT GCG ATT AAA TAC CAA TTG GAT TTA GGC TTC				977
Ile Leu Gly Gly Met Phe Ala Ile Lys Tyr Gln Leu Asp Leu Gly Phe	285	290	295	
CCG AGC TAT ATT GAC AGA TTC CAT GAC ACA GTG GGT TGG AAC CAT TTT				1025
Pro Ser Tyr Ile Asp Arg Phe His Asp Thr Val Gly Trp Asn His Phe	300	305	310	
TTG GTA GGG ATT GTC AAA GCC CCT TTT TGG GGG TTT GCG ATT GCG ATG				1073
Leu Val Gly Ile Val Lys Ala Pro Phe Trp Gly Phe Ala Ile Ala Met	315	320	325	330
GTA GGG TGC ATG CGC GGG TTT GAA GTC AAG GGG GAT ACT GAG AGC ATT				1121
Val Gly Cys Met Arg Gly Phe Glu Val Lys Gly Asp Thr Glu Ser Ile	335	340	345	
GGG CGC TTG ACC ACT ATT AGC GTC GTG AAC GCT TTG TTT TGG ATC ATT				1169
Gly Arg Leu Thr Thr Ile Ser Val Val Asn Ala Leu Phe Trp Ile Ile	350	355	360	
TTC TTA GAC GCT ATT TTT TCT ATC ATC TTT TCT AAG TTG AAC ATA TAATG				1219
Phe Leu Asp Ala Ile Phe Ser Ile Ile Phe Ser Lys Leu Asn Ile	365	370	375	
AACGCTACTA ACAATCAAGT CTTAATTGAA GTGAAGGATC TCCATAGCGC				1269

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Met	Lys	Thr	Glu	Lys	Gln	Lys	Phe	Leu	Glu	Met	Arg	Lys	Asp	Gly	Ala
1				5					10					15	
Asn	Ser	Val	Leu	Ile	Leu	Arg	Gly	Asp	Trp	Asp	Phe	Lys	Thr	Ser	Val
			20					25					30		
Phe	Arg	Leu	Asp	Glu	Leu	Lys	Lys	Asn	Leu	Leu	Asp	His	Gln	Gly	Pro
			35				40					45			
Leu	Lys	Met	Asp	Phe	Ser	Gly	Cys	Gln	Lys	Val	Asp	Phe	Val	Phe	Gly
			50			55					60				
Met	Phe	Leu	Phe	Asp	Leu	Val	Lys	Glu	Arg	Ser	Leu	Asn	Ile	Glu	Leu

65					70					75					80
Cys	Asn	Val	Ser	Glu	Asn	Asn	Ala	Cys	Ala	Leu	Lys	Val	Val	Lys	Asp
				85					90					95	
Trp	Leu	Glu	Lys	Glu	Glu	Asp	Leu	Glu	Ser	Lys	Lys	Ala	Gly	Lys	His
			100					105					110		
Tyr	Glu	Leu	Leu	Ile	Thr	Lys	Leu	Gly	Lys	Ser	Ile	Val	Glu	Thr	Tyr
		115					120					125			
Asn	Thr	Phe	Leu	Asn	Ala	Phe	Asn	Phe	Cys	Gly	Met	Ile	Leu	Phe	Tyr
	130					135					140				
Phe	Ile	Lys	Ser	Val	Phe	Asn	Pro	Lys	Arg	Phe	Cys	Ile	Thr	Pro	Leu
145					150					155					160
Leu	Tyr	His	Ile	Asn	Glu	Ser	Gly	Phe	Lys	Val	Leu	Pro	Val	Ser	Ile
				165					170					175	
Leu	Thr	Val	Phe	Ile	Val	Gly	Phe	Ala	Val	Ala	Leu	Gln	Gly	Ala	Leu
			180					185					190		
Gln	Leu	Gln	Asp	Met	Gly	Ala	Pro	Leu	Met	Ser	Val	Glu	Met	Thr	Ala
		195					200					205			
Lys	Leu	Ala	Leu	Arg	Glu	Ile	Gly	Pro	Phe	Ile	Leu	Thr	Leu	Val	Val
	210					215					220				
Ala	Gly	Arg	Ser	Ala	Ser	Ser	Phe	Thr	Ala	Gln	Ile	Gly	Val	Met	Lys
225					230					235					240
Ile	Thr	Glu	Glu	Leu	Asp	Ala	Met	Lys	Thr	Met	Gly	Phe	Asn	Pro	Phe
				245					250					255	
Glu	Phe	Leu	Val	Leu	Pro	Arg	Val	Leu	Ala	Leu	Val	Ile	Val	Leu	Pro
			260					265					270		
Leu	Leu	Val	Phe	Ile	Ala	Asp	Ala	Phe	Ala	Ile	Leu	Gly	Gly	Met	Phe
		275					280					285			
Ala	Ile	Lys	Tyr	Gln	Leu	Asp	Leu	Gly	Phe	Pro	Ser	Tyr	Ile	Asp	Arg
	290					295					300				
Phe	His	Asp	Thr	Val	Gly	Trp	Asn	His	Phe	Leu	Val	Gly	Ile	Val	Lys
305					310					315					320
Ala	Pro	Phe	Trp	Gly	Phe	Ala	Ile	Ala	Met	Val	Gly	Cys	Met	Arg	Gly
				325					330					335	
Phe	Glu	Val	Lys	Gly	Asp	Thr	Glu	Ser	Ile	Gly	Arg	Leu	Thr	Thr	Ile
			340					345					350		
Ser	Val	Val	Asn	Ala	Leu	Phe	Trp	Ile	Ile	Phe	Leu	Asp	Ala	Ile	Phe
		355					360					365			
Ser	Ile	Ile	Phe	Ser	Lys	Leu	Asn	Ile							
370						375									

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 60...503
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CACAAGAGAA AATTTGCAAG CGTTTTTACA ACAAATAAG ATAAATTAGG GAGAGTGGT 59

 ATG GGA TTT TTG AAT GGG TAT TTT TTA TGG GTT AAG GCT TTC CAT GTG 107
 Met Gly Phe Leu Asn Gly Tyr Phe Leu Trp Val Lys Ala Phe His Val
 1 5 10 15

 ATA GCG GTC ATT TCG TGG ATG GCA GCG TTG TTT TAT TTG CCG CGC CTT 155
 Ile Ala Val Ile Ser Trp Met Ala Ala Leu Phe Tyr Leu Pro Arg Leu
 20 25 30

 TTT GTC TAT CAT GCA GAA AAC GCG CAT AAA AAA GAG TTT GTA GGA GTG 203
 Phe Val Tyr His Ala Glu Asn Ala His Lys Lys Glu Phe Val Gly Val
 35 40 45

 GTT CAA ATC CAA GAA AAA AAG CTT TAT TCC TTT ATC GCT TCA CCG GCT 251
 Val Gln Ile Gln Glu Lys Lys Leu Tyr Ser Phe Ile Ala Ser Pro Ala
 50 55 60

 ATG GGT TTT ACG CTT ATT ACA GGG ATT TTA ATG CTG TTG ATA GAG CCT 299
 Met Gly Phe Thr Leu Ile Thr Gly Ile Leu Met Leu Leu Ile Glu Pro
 65 70 75 80

 ACG CTC TTT AAA AGT GGG GGT TGG TTG CAT GCT AAA TTG GCT TTA GTG 347
 Thr Leu Phe Lys Ser Gly Gly Trp Leu His Ala Lys Leu Ala Leu Val
 85 90 95

 GTT TTA CTT TTA GCC TAT CAT TTT TAT TGC AAA AAA TGC ATG CGC GAG 395
 Val Leu Leu Leu Ala Tyr His Phe Tyr Cys Lys Lys Cys Met Arg Glu
 100 105 110

 CTG GAA AAA GAC CCC ACA AGG AGA AAC GCA AGG TTT TAT CGC GTG TTT 443
 Leu Glu Lys Asp Pro Thr Arg Arg Asn Ala Arg Phe Tyr Arg Val Phe
 115 120 125

 AAT GAG GCG CCA ACG ATT TTA ATG ATC CTC ATT GTG ATT TTA GTG GTT 491
 Asn Glu Ala Pro Thr Ile Leu Met Ile Leu Ile Val Ile Leu Val Val
 130 135 140

 GTC AAG CCT TTT TAAAGACAAG CCATGAAAAA AGAAAAGTCA TGAAAAAAGA AAAGCA 549
 Val Lys Pro Phe
 145

 TCTCAAGC 557

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

```

Met Gly Phe Leu Asn Gly Tyr Phe Leu Trp Val Lys Ala Phe His Val
 1           5           10           15
Ile Ala Val Ile Ser Trp Met Ala Ala Leu Phe Tyr Leu Pro Arg Leu
      20           25           30
Phe Val Tyr His Ala Glu Asn Ala His Lys Lys Glu Phe Val Gly Val
 35           40           45
Val Gln Ile Gln Glu Lys Lys Leu Tyr Ser Phe Ile Ala Ser Pro Ala
 50           55           60
Met Gly Phe Thr Leu Ile Thr Gly Ile Leu Met Leu Leu Ile Glu Pro
65           70           75           80
Thr Leu Phe Lys Ser Gly Gly Trp Leu His Ala Lys Leu Ala Leu Val
      85           90           95
Val Leu Leu Leu Ala Tyr His Phe Tyr Cys Lys Lys Cys Met Arg Glu
      100           105           110
Leu Glu Lys Asp Pro Thr Arg Arg Asn Ala Arg Phe Tyr Arg Val Phe
      115           120           125
Asn Glu Ala Pro Thr Ile Leu Met Ile Leu Ile Val Ile Leu Val Val
      130           135           140
Val Lys Pro Phe
145

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(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 50...1624
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```

CAAAATTATC TGGTGCTAAG ACTTTGAAAC AACGCCAAAT AACAACTGA ATG AAA CTT      58
                                     Met Lys Leu
                                     1

TTT AAC GCT CGT TTA ATC GTT TTT ATT GGC GCG CTT CTT TTA GGG GTA      106
Phe Asn Ala Arg Leu Ile Val Phe Ile Gly Ala Leu Leu Leu Gly Val
 5           10           15

GGG TTT TCT GTG CCT TCT TTA CTA GAA ACT AAA GGC CCT AAA ATC ACT      154
Gly Phe Ser Val Pro Ser Leu Leu Glu Thr Lys Gly Pro Lys Ile Thr
20           25           30           35

TTA GGT TTG GAT TTA AGG GGG GGG TTG AAC ATG CTT TTA GGG GTA CAA      202
Leu Gly Leu Asp Leu Arg Gly Gly Leu Asn Met Leu Leu Gly Val Gln
      40           45           50

ACC GAT GAG GCT TTA AAA AAC AAG TAT TTA AGC TTG GCG TCC GCT TTA      250
Thr Asp Glu Ala Leu Lys Asn Lys Tyr Leu Ser Leu Ala Ser Ala Leu

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55										60					65					
GAA	TAC	AAC	GCT	AAA	AAG	CAA	AAT	ATC	TTG	CTT	AAA	GAT	ATT	AAA	TCC	298				
Glu	Tyr	Asn	Ala	Lys	Lys	Gln	Asn	Ile	Leu	Leu	Lys	Asp	Ile	Lys	Ser					
		70						75					80							
AAT	TTA	GAA	GGG	ATC	AGT	TTT	GAG	CTT	TTA	GAT	GAA	GAT	GAA	GCG	AAA	346				
Asn	Leu	Glu	Gly	Ile	Ser	Phe	Glu	Leu	Leu	Asp	Glu	Asp	Glu	Ala	Lys					
	85					90					95									
AAA	TTA	GAC	GCG	CTT	TTA	TTG	GAA	TTG	CAA	GGC	CAT	AGC	CAG	TTT	GAA	394				
Lys	Leu	Asp	Ala	Leu	Leu	Leu	Glu	Leu	Gln	Gly	His	Ser	Gln	Phe	Glu					
100					105					110					115					
ATC	AAA	AAG	GAA	GCG	GGG	TTT	TAT	AGC	GTG	AAT	CTC	ACC	CCT	TTA	GAG	442				
Ile	Lys	Lys	Glu	Ala	Gly	Phe	Tyr	Ser	Val	Asn	Leu	Thr	Pro	Leu	Glu					
				120					125					130						
CAA	GAA	GAA	TTG	CGT	AAA	AAC	ACG	ATT	TTG	CAA	GTG	ATA	GGG	ATC	ATT	490				
Gln	Glu	Glu	Leu	Arg	Lys	Asn	Thr	Ile	Leu	Gln	Val	Ile	Gly	Ile	Ile					
			135					140					145							
CGT	AAC	CGC	TTG	GAT	CAA	TTT	GGT	TTG	GCA	GAG	CCT	GTA	GTC	ATT	CAG	538				
Arg	Asn	Arg	Leu	Asp	Gln	Phe	Gly	Leu	Ala	Glu	Pro	Val	Val	Ile	Gln					
		150					155					160								
CAA	GGT	AAA	GAA	GAA	ATT	TCG	GTG	CAA	TTG	CCT	GGC	ATT	AAG	ACT	TTA	586				
Gln	Gly	Lys	Glu	Glu	Ile	Ser	Val	Gln	Leu	Pro	Gly	Ile	Lys	Thr	Leu					
	165					170					175									
GAA	GAA	GAA	CGG	CGC	GCT	AAA	GAC	TTG	ATT	TCA	AGA	TCC	GCT	CAT	TTG	634				
Glu	Glu	Glu	Arg	Arg	Ala	Lys	Asp	Leu	Ile	Ser	Arg	Ser	Ala	His	Leu					
180					185					190					195					
CAG	ATG	ATG	GCG	GTG	GAT	GAA	GAA	CAC	AAT	AAA	GAT	GCG	ATG	AAA	ATG	682				
Gln	Met	Met	Ala	Val	Asp	Glu	Glu	His	Asn	Lys	Asp	Ala	Met	Lys	Met					
			200						205					210						
ACG	GAT	TTA	GAG	GCT	CAA	AAA	TTA	GGC	AGC	GTG	TTG	TTG	TCT	GAT	GTG	730				
Thr	Asp	Leu	Glu	Ala	Gln	Lys	Leu	Gly	Ser	Val	Leu	Leu	Ser	Asp	Val					
			215					220					225							
GAA	ATG	GGG	GGT	AAA	ATC	TTG	CTC	AAA	GCG	ATC	CCC	ATT	TTA	GAT	GGC	778				
Glu	Met	Gly	Gly	Lys	Ile	Leu	Leu	Lys	Ala	Ile	Pro	Ile	Leu	Asp	Gly					
		230						235				240								
GAA	ATG	CTT	ACA	GAT	GCG	AAA	GTG	GTG	TAT	GAC	CAA	AAC	AAC	CAG	CCG	826				
Glu	Met	Leu	Thr	Asp	Ala	Lys	Val	Val	Tyr	Asp	Gln	Asn	Asn	Gln	Pro					
	245					250					255									
GTG	GTG	AGC	TTC	ACG	CTG	GAT	GCG	CAA	GGG	GCT	AAG	ATT	TTT	GGG	GAT	874				
Val	Val	Ser	Phe	Thr	Leu	Asp	Ala	Gln	Gly	Ala	Lys	Ile	Phe	Gly	Asp					
260					265				270					275						
TTC	TCA	GGT	GCG	AAT	GTG	GGC	AAA	CGC	ATG	GCG	ATT	GTT	TTA	GAC	AAT	922				
Phe	Ser	Gly	Ala	Asn	Val	Gly	Lys	Arg	Met	Ala	Ile	Val	Leu	Asp	Asn					
				280					285					290						

AAG GTC TAT TCA GCC CCG GTG ATT AGG GAG CGT ATC GGT GGG GGG AGC	970
Lys Val Tyr Ser Ala Pro Val Ile Arg Glu Arg Ile Gly Gly Gly Ser	
295 300 305	
GGG CAG ATT AGC GGG AAT TTT AGC GTG GCT CAA GCG AGC GAT TTA GCG	1018
Gly Gln Ile Ser Gly Asn Phe Ser Val Ala Gln Ala Ser Asp Leu Ala	
310 315 320	
ATC GCT TTA AGG AGT GGG GCG ATG AGC GCT CCC ATT CAG GTT TTA GAA	1066
Ile Ala Leu Arg Ser Gly Ala Met Ser Ala Pro Ile Gln Val Leu Glu	
325 330 335	
AAA AGA ATT ATA GGC CCA AGT TTA GGG AAA GAC AGC GTT AAA ACT TCC	1114
Lys Arg Ile Ile Gly Pro Ser Leu Gly Lys Asp Ser Val Lys Thr Ser	
340 345 350 355	
ATT ATC GCT CTA GTT GGG GGC TTT ATT TTA GTG ATG GGC TTT ATG GTG	1162
Ile Ile Ala Leu Val Gly Gly Phe Ile Leu Val Met Gly Phe Met Val	
360 365 370	
CTT TAT TAC TCT ATG GCG GGG GTG ATC GCT TGT TTG GCG TTA GTG GTC	1210
Leu Tyr Tyr Ser Met Ala Gly Val Ile Ala Cys Leu Ala Leu Val Val	
375 380 385	
AAT CTT TTT TTG ATT GTG GCG GTC ATG GCG ATT TTT GGA GCG ACG CTG	1258
Asn Leu Phe Leu Ile Val Ala Val Met Ala Ile Phe Gly Ala Thr Leu	
390 395 400	
ACT TTA CCG GGA ATG GCG GGG ATT GTT TTA ACC GTG GGG ATT GCC GTG	1306
Thr Leu Pro Gly Met Ala Gly Ile Val Leu Thr Val Gly Ile Ala Val	
405 410 415	
GAT GCT AAT ATC ATC ATC AAC GAG CGC ATT AGA GAA GTC TTA AGA GAG	1354
Asp Ala Asn Ile Ile Ile Asn Glu Arg Ile Arg Glu Val Leu Arg Glu	
420 425 430 435	
AAT GAG GGC ATC GCT AAA GCG ATC CAT TTA GGC TAT ATC AAT GCG AGC	1402
Asn Glu Gly Ile Ala Lys Ala Ile His Leu Gly Tyr Ile Asn Ala Ser	
440 445 450	
CGG GCG ATT TTT GAT TCT AAT ATC ACT TCT TTG ATC GCT TCA GTG TTA	1450
Arg Ala Ile Phe Asp Ser Asn Ile Thr Ser Leu Ile Ala Ser Val Leu	
455 460 465	
TTA TAC GCT TAT GGC ACA GGA GCG ATT AAA GGC TTT GCC CTA ACT ACA	1498
Leu Tyr Ala Tyr Gly Thr Gly Ala Ile Lys Gly Phe Ala Leu Thr Thr	
470 475 480	
GGC ATT GGG ATT TTA GCC TCT ATT ATC ACC GCT ATT GTT GGC ACG CAA	1546
Gly Ile Gly Ile Leu Ala Ser Ile Ile Thr Ala Ile Val Gly Thr Gln	
485 490 495	
GGG ATT TAT CAA GCC CTT TTA CCT AAA CTC ACT CAA ACA AAA AGC CTT	1594
Gly Ile Tyr Gln Ala Leu Leu Pro Lys Leu Thr Gln Thr Lys Ser Leu	
500 505 510 515	
TAC TTT TGG TTT GGC GTG AAT AAA AGA GCT TAGGAGGTTT TATGGAATTA TTC	1647
Tyr Phe Trp Phe Gly Val Asn Lys Arg Ala	

520

525

AAACGAACTA GAATCTTAAG CTTC

1671

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Met	Lys	Leu	Phe	Asn	Ala	Arg	Leu	Ile	Val	Phe	Ile	Gly	Ala	Leu	Leu	1	5	10	15
Leu	Gly	Val	Gly	Phe	Ser	Val	Pro	Ser	Leu	Leu	Glu	Thr	Lys	Gly	Pro	20	25	30	
Lys	Ile	Thr	Leu	Gly	Leu	Asp	Leu	Arg	Gly	Gly	Leu	Asn	Met	Leu	Leu	35	40	45	
Gly	Val	Gln	Thr	Asp	Glu	Ala	Leu	Lys	Asn	Lys	Tyr	Leu	Ser	Leu	Ala	50	55	60	
Ser	Ala	Leu	Glu	Tyr	Asn	Ala	Lys	Lys	Gln	Asn	Ile	Leu	Leu	Lys	Asp	65	70	75	80
Ile	Lys	Ser	Asn	Leu	Glu	Gly	Ile	Ser	Phe	Glu	Leu	Leu	Asp	Glu	Asp	85	90	95	
Glu	Ala	Lys	Lys	Leu	Asp	Ala	Leu	Leu	Leu	Glu	Leu	Gln	Gly	His	Ser	100	105	110	
Gln	Phe	Glu	Ile	Lys	Lys	Glu	Ala	Gly	Phe	Tyr	Ser	Val	Asn	Leu	Thr	115	120	125	
Pro	Leu	Glu	Gln	Glu	Glu	Leu	Arg	Lys	Asn	Thr	Ile	Leu	Gln	Val	Ile	130	135	140	
Gly	Ile	Ile	Arg	Asn	Arg	Leu	Asp	Gln	Phe	Gly	Leu	Ala	Glu	Pro	Val	145	150	155	160
Val	Ile	Gln	Gln	Gly	Lys	Glu	Glu	Ile	Ser	Val	Gln	Leu	Pro	Gly	Ile	165	170	175	
Lys	Thr	Leu	Glu	Glu	Glu	Arg	Arg	Ala	Lys	Asp	Leu	Ile	Ser	Arg	Ser	180	185	190	
Ala	His	Leu	Gln	Met	Met	Ala	Val	Asp	Glu	Glu	His	Asn	Lys	Asp	Ala	195	200	205	
Met	Lys	Met	Thr	Asp	Leu	Glu	Ala	Gln	Lys	Leu	Gly	Ser	Val	Leu	Leu	210	215	220	
Ser	Asp	Val	Glu	Met	Gly	Gly	Lys	Ile	Leu	Leu	Lys	Ala	Ile	Pro	Ile	225	230	235	240
Leu	Asp	Gly	Glu	Met	Leu	Thr	Asp	Ala	Lys	Val	Val	Tyr	Asp	Gln	Asn	245	250	255	
Asn	Gln	Pro	Val	Val	Ser	Phe	Thr	Leu	Asp	Ala	Gln	Gly	Ala	Lys	Ile	260	265	270	
Phe	Gly	Asp	Phe	Ser	Gly	Ala	Asn	Val	Gly	Lys	Arg	Met	Ala	Ile	Val	275	280	285	
Leu	Asp	Asn	Lys	Val	Tyr	Ser	Ala	Pro	Val	Ile	Arg	Glu	Arg	Ile	Gly	290	295	300	
Gly	Gly	Ser	Gly	Gln	Ile	Ser	Gly	Asn	Phe	Ser	Val	Ala	Gln	Ala	Ser	305	310	315	320
Asp	Leu	Ala	Ile	Ala	Leu	Arg	Ser	Gly	Ala	Met	Ser	Ala	Pro	Ile	Gln				

Val	Leu	Glu	Lys	Arg	Ile	Ile	Gly	Pro	Ser	Leu	Gly	Lys	Asp	Ser	Val
			340					345					350		
Lys	Thr	Ser	Ile	Ile	Ala	Leu	Val	Gly	Gly	Phe	Ile	Leu	Val	Met	Gly
			355					360					365		
Phe	Met	Val	Leu	Tyr	Tyr	Ser	Met	Ala	Gly	Val	Ile	Ala	Cys	Leu	Ala
			370					375				380			
Leu	Val	Val	Asn	Leu	Phe	Leu	Ile	Val	Ala	Val	Met	Ala	Ile	Phe	Gly
385															400
Ala	Thr	Leu	Thr	Leu	Pro	Gly	Met	Ala	Gly	Ile	Val	Leu	Thr	Val	Gly
				405					410						
Ile	Ala	Val	Asp	Ala	Asn	Ile	Ile	Ile	Asn	Glu	Arg	Ile	Arg	Glu	Val
			420					425					430		
Leu	Arg	Glu	Asn	Glu	Gly	Ile	Ala	Lys	Ala	Ile	His	Leu	Gly	Tyr	Ile
			435					440					445		
Asn	Ala	Ser	Arg	Ala	Ile	Phe	Asp	Ser	Asn	Ile	Thr	Ser	Leu	Ile	Ala
							455					460			
Ser	Val	Leu	Leu	Tyr	Ala	Tyr	Gly	Thr	Gly	Ala	Ile	Lys	Gly	Phe	Ala
465											475				480
Leu	Thr	Thr	Gly	Ile	Gly	Ile	Leu	Ala	Ser	Ile	Ile	Thr	Ala	Ile	Val
				485						490					
Gly	Thr	Gln	Gly	Ile	Tyr	Gln	Ala	Leu	Leu	Pro	Lys	Leu	Thr	Gln	Thr
			500					505					510		
Lys	Ser	Leu	Tyr	Phe	Trp	Phe	Gly	Val	Asn	Lys	Arg	Ala			
			515				520					525			

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 64...654
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CAGGGGGGCAA	GGGGGCTGTT	AGGGAAGCGA	TTGATTATCT	TTTAACATTA	GAAGGCTTGC	60										
AAG	ATG	AAG	CGC	TCA	AGC	TTT	ACC	TCT	AAT	AGC	GTT	TTA	AAC	TTT	TTT	108
	Met	Lys	Arg	Ser	Ser	Phe	Thr	Ser	Asn	Ser	Val	Leu	Asn	Phe	Phe	
	1				5					10					15	
GTA	GTT	TTG	TCT	TTC	ATT	ACG	ATA	GGA	TTA	GTG	TTT	TTC	TTT	TTG	CGT	156
Val	Val	Leu	Ser	Phe	Ile	Thr	Ile	Gly	Leu	Val	Phe	Phe	Phe	Leu	Arg	
				20					25					30		
TCC	CAA	CCC	ACT	AGC	GTA	GTT	TCT	AAA	GAA	AAT	ATC	CCT	AAA	ATT	GAA	204
Ser	Gln	Pro	Thr	Ser	Val	Val	Ser	Lys	Glu	Asn	Ile	Pro	Lys	Ile	Glu	
			35					40					45			

TTA GAA AAT TTT AAA GCG TTT CAA ATC AAC GAT AAA ATC CTT GAT CTG	252
Leu Glu Asn Phe Lys Ala Phe Gln Ile Asn Asp Lys Ile Leu Asp Leu	
50 55 60	
TCC ATA GAG GGC AAA AAA GCC CTA CAA TAC GAT GAT CAT GAA ATC TTT	300
Ser Ile Glu Gly Lys Lys Ala Leu Gln Tyr Asp Asp His Glu Ile Phe	
65 70 75	
TTT GAT TCC AAA ATC AAG CGC TAT GAT GAA GAC ACC ATT GAA AGC GTT	348
Phe Asp Ser Lys Ile Lys Arg Tyr Asp Glu Asp Thr Ile Glu Ser Val	
80 85 90 95	
GAG TCT CCT AAG GCC AAA CGG CAG CAG GAT TTG TAT TTC TTC CCT AAT	396
Glu Ser Pro Lys Ala Lys Arg Gln Gln Asp Leu Tyr Phe Phe Pro Asn	
100 105 110	
GGG GTT ACT TAT AAA AGA AGC GAT GAT TCC AGT TTT TGG AGT GAA ACA	444
Gly Val Thr Tyr Lys Arg Ser Asp Asp Ser Ser Phe Trp Ser Glu Thr	
115 120 125	
GGG ATT TAT AAC CAT AAG GAG CAA AAT TTT AAA GGC AAG GGC CGT TTC	492
Gly Ile Tyr Asn His Lys Glu Gln Asn Phe Lys Gly Lys Gly Arg Phe	
130 135 140	
ATT CTC ACT TCA AAG GAC AGC AAG ATT GAA GGG CTT GAC ATT TCT TAT	540
Ile Leu Thr Ser Lys Asp Ser Lys Ile Glu Gly Leu Asp Ile Ser Tyr	
145 150 155	
TCG CAT GCA TTA GCT ATT ATT GAA GCT CAA AGC ATT CAA GCG CAT TTA	588
Ser His Ala Leu Ala Ile Ile Glu Ala Gln Ser Ile Gln Ala His Leu	
160 165 170 175	
TTC TTA GAT GAA ATC AAA CAA AGC CAA AAA GAA AAG AAA AAA TTC CCC	636
Phe Leu Asp Glu Ile Lys Gln Ser Gln Lys Glu Lys Lys Lys Phe Pro	
180 185 190	
ACT TTC AAA GGA GGT TTT TAATGCGTTG GTGGTGT TTTT TTGGTGTGTT GTTTTGGT	692
Thr Phe Lys Gly Gly Phe	
195	
ATTTTAAGCG TGAT	706

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Met Lys Arg Ser Ser Phe Thr Ser Asn Ser Val Leu Asn Phe Phe Val
1 5 10 15
Val Leu Ser Phe Ile Thr Ile Gly Leu Val Phe Phe Phe Leu Arg Ser

[illegible]

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 130...957
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

AAGCGAGCAA	GAATGAATTA	AAAATTTTTG	GTTGGCACTA	CATCATAGAA	ACAGGCAGGA	60
TTTATAATTA	TAATTTTGAA	AGCCATTTTT	TTGAGCCGAT	TGGAGAAACC	ATTAAACAAA	120
GGAAAAGTC	ATG AAA ACT	TCT AAA ACA	AAA ACC CCT	AAA TCC GTT	TTA ATC	171
	Met Lys Thr	Ser Lys Thr	Lys Thr Pro	Lys Ser Val	Leu Ile	
	1	5		10		
GCT GGG CCA	TGC GTC ATT	GAG AGC TTA	GAA AAT CTA	AGA AGT ATC	GCC	219
Ala Gly Pro	Cys Val Ile	Glu Ser Leu	Glu Asn Leu	Arg Ser Ile	Ala	
15		20		25	30	
ACT AAA TTG	CAA CCC CTA	GCC AAC AAC	GAG CGG TTG	GAT TTT TAT	TTT	267
Thr Lys Leu	Gln Pro Leu	Ala Asn Asn	Glu Arg Leu	Asp Phe Tyr	Phe	
		35		40	45	
AAA GCG AGT	TTT GAT AAG	GCG AAC CGC	ACG AGT TTA	GAG AGT TAC	AGA	315

Lys	Ala	Ser	Phe	Asp	Lys	Ala	Asn	Arg	Thr	Ser	Leu	Glu	Ser	Tyr	Arg	
			50					55					60			
GGG	CCT	GGT	TTA	GAA	AAA	GGC	CTA	GAA	ATG	TTA	CAA	ACG	ATC	AAA	GAG	363
Gly	Pro	Gly	Leu	Glu	Lys	Gly	Leu	Glu	Met	Leu	Gln	Thr	Ile	Lys	Glu	
		65					70					75				
GAA	TTT	GGT	TAT	AAA	ATC	TTA	ACC	GAT	GTG	CAT	GAG	AGT	TAT	CAA	GCA	411
Glu	Phe	Gly	Tyr	Lys	Ile	Leu	Thr	Asp	Val	His	Glu	Ser	Tyr	Gln	Ala	
	80					85					90					
AGC	GTG	GCA	GCC	AAA	GTG	GCG	GAT	ATT	TTA	CAA	ATC	CCG	GCG	TTT	TTG	459
Ser	Val	Ala	Ala	Lys	Val	Ala	Asp	Ile	Leu	Gln	Ile	Pro	Ala	Phe	Leu	
95					100					105					110	
TGC	CGC	CAA	ACG	GAT	CTG	ATT	GTA	GAA	GTG	AGC	CAG	ACT	AAC	GCT	ATT	507
Cys	Arg	Gln	Thr	Asp	Leu	Ile	Val	Glu	Val	Ser	Gln	Thr	Asn	Ala	Ile	
				115					120						125	
GTC	AAT	ATC	AAA	AAA	GGG	CAA	TTC	ATG	AAC	CCA	AAA	GAC	ATG	CAA	TAT	555
Val	Asn	Ile	Lys	Lys	Gly	Gln	Phe	Met	Asn	Pro	Lys	Asp	Met	Gln	Tyr	
			130					135					140			
TCT	GTT	CTA	AAG	GCC	CTT	AAA	ACG	AGA	GAT	AAA	AGC	ATT	CAA	AGC	CCC	603
Ser	Val	Leu	Lys	Ala	Leu	Lys	Thr	Arg	Asp	Lys	Ser	Ile	Gln	Ser	Pro	
		145					150					155				
ACT	TAT	GAA	ACA	GCG	TTA	AAA	AAT	GGC	GTG	TGG	CTG	TGT	GAA	AGG	GGG	651
Thr	Tyr	Glu	Thr	Ala	Leu	Lys	Asn	Gly	Val	Trp	Leu	Cys	Glu	Arg	Gly	
	160					165					170					
AGC	AGC	TTT	GGG	TAT	GGG	AAT	TTA	GTG	GTG	GAT	ATG	CGC	TCT	TTA	AAA	699
Ser	Ser	Phe	Gly	Tyr	Gly	Asn	Leu	Val	Val	Asp	Met	Arg	Ser	Leu	Lys	
175					180					185					190	
ATC	ATG	CGA	GAA	TTT	GCC	CCT	GTG	ATT	TTT	GAC	GCT	ACC	CAT	AGC	GTG	747
Ile	Met	Arg	Glu	Phe	Ala	Pro	Val	Ile	Phe	Asp	Ala	Thr	His	Ser	Val	
				195					200					205		
CAA	ATG	CCA	GGG	GGA	GCG	AAC	GGG	AAA	AGT	TCA	GGA	GAC	AGC	TCT	TTT	795
Gln	Met	Pro	Gly	Gly	Ala	Asn	Gly	Lys	Ser	Ser	Gly	Asp	Ser	Ser	Phe	
			210					215					220			
GCC	CCT	ATT	TTA	GCG	AGA	GCT	GCG	GCG	GCG	GTG	GGG	ATT	GAT	GGG	TTG	843
Ala	Pro	Ile	Leu	Ala	Arg	Ala	Ala	Ala	Ala	Val	Gly	Ile	Asp	Gly	Leu	
		225					230					235				
TTT	GCT	GAA	ACG	CAT	GTT	GAT	CCT	AAA	AAC	GCC	CTA	AGC	GAT	GGA	GCA	891
Phe	Ala	Glu	Thr	His	Val	Asp	Pro	Lys	Asn	Ala	Leu	Ser	Asp	Gly	Ala	
	240					245					250					
AAC	ATG	CTA	AAA	CCT	GAC	GAG	CTA	GAA	CAA	TTA	GTA	ACC	GAC	ATG	TTA	939
Asn	Met	Leu	Lys	Pro	Asp	Glu	Leu	Glu	Gln	Leu	Val	Thr	Asp	Met	Leu	
255					260					265					270	
AAA	ATC	CAA	AAT	TTA	TTT	TAAAGGAATT	TCATGCAAAT	CATAGAAGGG	AAATTGCA							995
Lys	Ile	Gln	Asn	Leu	Phe											
				275												

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 59...196

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

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AACAAATCTT TTTTAAGCAA AAACAAAACA AAATTAAGGC ATAATCACTC TTTTAA   58

ATG AAA GGT CGC GTA GCT CAG TTG GTA GAG CAC TAC CTT GAC ATG GTA   106
Met Lys Gly Arg Val Ala Gln Leu Val Glu His Tyr Leu Asp Met Val
 1           5           10           15

GTG GCC GCT GGT TCA AGT CCA GTC GTG GCC ACC ATT ATC ACT CCA ATT   154
Val Ala Ala Gly Ser Ser Pro Val Val Ala Thr Ile Ile Thr Pro Ile
      20           25           30

TTA ATT CTC ATT TTT TTG CGA GTT TTT GAT CTT TAT AAA TTC TAAAGGGGTA   206
Leu Ile Leu Ile Phe Leu Arg Val Phe Asp Leu Tyr Lys Phe
 35           40           45

TTAAACGCAC TTCTAATAAC GATTTTATAG CGCT                               240

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(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

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Met Lys Gly Arg Val Ala Gln Leu Val Glu His Tyr Leu Asp Met Val
 1           5           10           15
Val Ala Ala Gly Ser Ser Pro Val Val Ala Thr Ile Ile Thr Pro Ile
      20           25           30
Leu Ile Leu Ile Phe Leu Arg Val Phe Asp Leu Tyr Lys Phe
 35           40           45

```

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1382 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 91...1329

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ACCACCCCTT AATCTCAAAA AACCCCAATC ATAAAAAGCT TTATGCTACA ATGAAAGCTC	60
TTTAACACGA TAAAAGGGCG GTTTAATAGC ATG GCA CAA GAA AAA GCA GTT CCA	114
Met Ala Gln Glu Lys Ala Val Pro	
1 5	
AGA GAT CCT AAA AAA CTC AAT GCG TTT GAT TTG CGT TGG ATG GTG TCC	162
Arg Asp Pro Lys Lys Leu Asn Ala Phe Asp Leu Arg Trp Met Val Ser	
10 15 20	
TTA TTT GGC ACG GCG GTG GGG GCT GGG ATT TTA TTT TTG CCT ATT AGA	210
Leu Phe Gly Thr Ala Val Gly Ala Gly Ile Leu Phe Leu Pro Ile Arg	
25 30 35 40	
GCC GGT GGG CAT GGG GTA TGG GCT ATT GTG GTA ATG AGC GCG ATC ATT	258
Ala Gly Gly His Gly Val Trp Ala Ile Val Val Met Ser Ala Ile Ile	
45 50 55	
TTC CCT TTA ACT TAT CTA GGG CAT AGA GCT TTA GCT TAT TTC ATA GGA	306
Phe Pro Leu Thr Tyr Leu Gly His Arg Ala Leu Ala Tyr Phe Ile Gly	
60 65 70	
TCT AAA GAC AAA GAA GAC ATT ACC ATG GTC GTT CGC TCT CAT TTT GGC	354
Ser Lys Asp Lys Glu Asp Ile Thr Met Val Val Arg Ser His Phe Gly	
75 80 85	
GCT CAA TGG GGT TTT CTT ATC ACT TTG CTT TAT TTC TTA GCG ATT TAT	402
Ala Gln Trp Gly Phe Leu Ile Thr Leu Leu Tyr Phe Leu Ala Ile Tyr	
90 95 100	
CCT ATT TGC TTG GTT TAT GGG GTG GGT ATC ACT AAC GTG TTT GAT CAT	450
Pro Ile Cys Leu Val Tyr Gly Val Gly Ile Thr Asn Val Phe Asp His	
105 110 115 120	
TTT TTC ACT AAC CAG TTG CAT TTA GCG CCT TTT CAT CGG GGA TTA TTG	498
Phe Phe Thr Asn Gln Leu His Leu Ala Pro Phe His Arg Gly Leu Leu	
125 130 135	
GCT GTA GCG TTA GTT TCT TTA ATG ATG TTG GTG ATG GTT TTT AAC GCT	546
Ala Val Ala Leu Val Ser Leu Met Met Leu Val Met Val Phe Asn Ala	
140 145 150	
ACG ATT GTT ACG CGC ATT TGT AAC GCT TTA GTG TAT CCT TTA TGC TTG	594
Thr Ile Val Thr Arg Ile Cys Asn Ala Leu Val Tyr Pro Leu Cys Leu	
155 160 165	
ATT TTA TTG CTT TTT TCT TTG TAT CTT ATC CCT TAT TGG CAA GGC GCT	642
Ile Leu Leu Leu Phe Ser Leu Tyr Leu Ile Pro Tyr Trp Gln Gly Ala	
170 175 180	

AAT CTT TTT GTG GTG CCG AGT TTT AAA GAA TTT GTG TTA GCG ATT TGG	690
Asn Leu Phe Val Val Pro Ser Phe Lys Glu Phe Val Leu Ala Ile Trp	
185 190 195 200	
CTA ACC TTA CCG GTG CTT GTG TTT GCA TTC GAC CAT AGC CCC ATC ATT	738
Leu Thr Leu Pro Val Leu Val Phe Ala Phe Asp His Ser Pro Ile Ile	
205 210 215	
TCA ACC TTC ACT CAA AAT GTG GGA AAA GAA TAC GGC GTT TTC AAA GAA	786
Ser Thr Phe Thr Gln Asn Val Gly Lys Glu Tyr Gly Val Phe Lys Glu	
220 225 230	
TAC AAA CTC AAT CAA ATT GAA TTA GGG ACA TCG CTG ATG CTT TTA GGG	834
Tyr Lys Leu Asn Gln Ile Glu Leu Gly Thr Ser Leu Met Leu Leu Gly	
235 240 245	
TTT GTG ATG TTT TTT GTG TTT TCG TGC GTC ATG TGC TTG AAT GCT GAT	882
Phe Val Met Phe Phe Val Phe Ser Cys Val Met Cys Leu Asn Ala Asp	
250 255 260	
GAT TTT GTG AAA GCA AGG GAA CAA AAT ATC CCC ATT TTA AGC TAT TTG	930
Asp Phe Val Lys Ala Arg Glu Gln Asn Ile Pro Ile Leu Ser Tyr Leu	
265 270 275 280	
GCT AAC ACT TTA AAC AAC CCT TTA ATC AAT TAT GCG GGG CCT GTG GTG	978
Ala Asn Thr Leu Asn Asn Pro Leu Ile Asn Tyr Ala Gly Pro Val Val	
285 290 295	
GCT TTT TTA GCG ATT TTT TCA TCT TTT TTT GGG CAT TAT TAT GGG GCT	1026
Ala Phe Leu Ala Ile Phe Ser Ser Phe Phe Gly His Tyr Tyr Gly Ala	
300 305 310	
AAG GAG GGT TTA GAA GGC ATT ATT ATT CAA AGC TTA AAA TTG AAA AAA	1074
Lys Glu Gly Leu Glu Gly Ile Ile Ile Gln Ser Leu Lys Leu Lys Lys	
315 320 325	
GCT TCT AAA CCC TTG AGC GTT AGC GTA ACG ATT TTT TTA TGG CTG ACT	1122
Ala Ser Lys Pro Leu Ser Val Ser Val Thr Ile Phe Leu Trp Leu Thr	
330 335 340	
ATC ACG CTT GTG GCT TAT ATT AAC CCC AAT ATC TTG GAT TTT ATT GAA	1170
Ile Thr Leu Val Ala Tyr Ile Asn Pro Asn Ile Leu Asp Phe Ile Glu	
345 350 355 360	
AAT TTA GGC GGC CCC ATT ATC GCG CTC ATT CTG TTT GTG ATG CCC ATG	1218
Asn Leu Gly Gly Pro Ile Ile Ala Leu Ile Leu Phe Val Met Pro Met	
365 370 375	
ATA GCT TTT TAT AGT GTT TCT AGT TTG AAG CGT TTT AGA AAT TTC AAA	1266
Ile Ala Phe Tyr Ser Val Ser Ser Leu Lys Arg Phe Arg Asn Phe Lys	
380 385 390	
GTG GAT ATT TTT GTG TTT GTC TTT GGG AGC TTG ACG GCT TTG AGC GTG	1314
Val Asp Ile Phe Val Phe Val Phe Gly Ser Leu Thr Ala Leu Ser Val	
395 400 405	
TTT TTA GGA CTA TTT TAATGGCTAG TTTTCTATT TTATCTATTT TTAAATCGG C	1370
Phe Leu Gly Leu Phe	

410

GTGGGGCCTA GC

1382

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met	Ala	Gln	Glu	Lys	Ala	Val	Pro	Arg	Asp	Pro	Lys	Lys	Leu	Asn	Ala	1	5	10	15
Phe	Asp	Leu	Arg	Trp	Met	Val	Ser	Leu	Phe	Gly	Thr	Ala	Val	Gly	Ala	20	25	30	
Gly	Ile	Leu	Phe	Leu	Pro	Ile	Arg	Ala	Gly	Gly	His	Gly	Val	Trp	Ala	35	40	45	
Ile	Val	Val	Met	Ser	Ala	Ile	Ile	Phe	Pro	Leu	Thr	Tyr	Leu	Gly	His	50	55	60	
Arg	Ala	Leu	Ala	Tyr	Phe	Ile	Gly	Ser	Lys	Asp	Lys	Glu	Asp	Ile	Thr	65	70	75	80
Met	Val	Val	Arg	Ser	His	Phe	Gly	Ala	Gln	Trp	Gly	Phe	Leu	Ile	Thr	85	90	95	
Leu	Leu	Tyr	Phe	Leu	Ala	Ile	Tyr	Pro	Ile	Cys	Leu	Val	Tyr	Gly	Val	100	105	110	
Gly	Ile	Thr	Asn	Val	Phe	Asp	His	Phe	Phe	Thr	Asn	Gln	Leu	His	Leu	115	120	125	
Ala	Pro	Phe	His	Arg	Gly	Leu	Leu	Ala	Val	Ala	Leu	Val	Ser	Leu	Met	130	135	140	
Met	Leu	Val	Met	Val	Phe	Asn	Ala	Thr	Ile	Val	Thr	Arg	Ile	Cys	Asn	145	150	155	160
Ala	Leu	Val	Tyr	Pro	Leu	Cys	Leu	Ile	Leu	Leu	Leu	Phe	Ser	Leu	Tyr	165	170	175	
Leu	Ile	Pro	Tyr	Trp	Gln	Gly	Ala	Asn	Leu	Phe	Val	Val	Pro	Ser	Phe	180	185	190	
Lys	Glu	Phe	Val	Leu	Ala	Ile	Trp	Leu	Thr	Leu	Pro	Val	Leu	Val	Phe	195	200	205	
Ala	Phe	Asp	His	Ser	Pro	Ile	Ile	Ser	Thr	Phe	Thr	Gln	Asn	Val	Gly	210	215	220	
Lys	Glu	Tyr	Gly	Val	Phe	Lys	Glu	Tyr	Lys	Leu	Asn	Gln	Ile	Glu	Leu	225	230	235	240
Gly	Thr	Ser	Leu	Met	Leu	Leu	Gly	Phe	Val	Met	Phe	Phe	Val	Phe	Ser	245	250	255	
Cys	Val	Met	Cys	Leu	Asn	Ala	Asp	Asp	Phe	Val	Lys	Ala	Arg	Glu	Gln	260	265	270	
Asn	Ile	Pro	Ile	Leu	Ser	Tyr	Leu	Ala	Asn	Thr	Leu	Asn	Asn	Pro	Leu	275	280	285	
Ile	Asn	Tyr	Ala	Gly	Pro	Val	Val	Ala	Phe	Leu	Ala	Ile	Phe	Ser	Ser	290	295	300	
Phe	Phe	Gly	His	Tyr	Tyr	Gly	Ala	Lys	Glu	Gly	Leu	Glu	Gly	Ile	Ile	305	310	315	320
Ile	Gln	Ser	Leu	Lys	Leu	Lys	Lys	Ala	Ser	Lys	Pro	Leu	Ser	Val	Ser				

Val	Thr	Ile	Phe	Leu	Trp	Leu	Thr	Ile	Thr	Leu	Val	Ala	Tyr	Ile	Asn
			340					345					350		
Pro	Asn	Ile	Leu	Asp	Phe	Ile	Glu	Asn	Leu	Gly	Gly	Pro	Ile	Ile	Ala
		355					360					365			
Leu	Ile	Leu	Phe	Val	Met	Pro	Met	Ile	Ala	Phe	Tyr	Ser	Val	Ser	Ser
	370					375					380				
Leu	Lys	Arg	Phe	Arg	Asn	Phe	Lys	Val	Asp	Ile	Phe	Val	Phe	Val	Phe
385					390					395					400
Gly	Ser	Leu	Thr	Ala	Leu	Ser	Val	Phe	Leu	Gly	Leu	Phe			
				405					410						

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 875 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 63...827
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TTTGCCACCT	TATTGCAAAC	CCTAATGCTA	ACGCACTACT	TTTTTATCTT	TAAAGAGAAA	60
GA ATG CTA	GAT TTT ATT	CAA GAG CTT	AGC ACC CCC	CAT GTT AGG	GAT	107
Met Leu Asp	Phe Ile Gln	Glu Leu Ser	Thr Pro His	Val Arg Asp		
1	5	10	15			
TTT TTC TTG TTG TTT TTA AGG GTT AGC GGC GTG CTG TCT TTC TTC CCT	155					
Phe Phe Leu Leu Phe Leu Arg Val Ser Gly Val Leu Ser Phe Phe Pro						
20	25	30				
TTT TTT GAA AAC CAT TTA GTG CCT TTG TCG GTG CGT GGG GCT TTG AGT	203					
Phe Phe Glu Asn His Leu Val Pro Leu Ser Val Arg Gly Ala Leu Ser						
35	40	45				
TTG TAT GTG AGC GCG ATT TTT TAC CCC ACT TTA GAA TTT TCA AAC GCC	251					
Leu Tyr Val Ser Ala Ile Phe Tyr Pro Thr Leu Glu Phe Ser Asn Ala						
50	55	60				
GCT TAC ACG CCA GAG GGT TTT ATC ATT GCT TGC TTG TGC GAA TTG TTT	299					
Ala Tyr Thr Pro Glu Gly Phe Ile Ile Ala Cys Leu Cys Glu Leu Phe						
65	70	75				
TTA GGG GTG TGC GCG TCT GTC TTT TTA CAA ATC GTC TTT GCA AGC TTA	347					
Leu Gly Val Cys Ala Ser Val Phe Leu Gln Ile Val Phe Ala Ser Leu						
80	85	90	95			
GTG TTT GCA ACC GAT AGC ATC AGC TTT TCT ATG GGG CTT ACG ATG GCG	395					
Val Phe Ala Thr Asp Ser Ile Ser Phe Ser Met Gly Leu Thr Met Ala						

100										105					110					
AGC	GCG	TAT	GAT	CCT	ATT	TCA	GGA	TCG	CAA	AAA	CCC	ATT	GTG	GGG	CAA	443				
Ser	Ala	Tyr	Asp	Pro	Ile	Ser	Gly	Ser	Gln	Lys	Pro	Ile	Val	Gly	Gln					
			115					120					125							
GCC	CTT	TTA	TTG	TTA	GCG	ATT	TTA	ATT	TTA	TTG	GAT	TTA	TCG	TTC	CAC	491				
Ala	Leu	Leu	Leu	Leu	Ala	Ile	Leu	Ile	Leu	Leu	Asp	Leu	Ser	Phe	His					
		130					135					140								
CAT	CAA	ATC	ATT	TTG	TTT	GTG	GAT	CAC	AGC	TTA	AAA	GCC	GTC	CCT	TTA	539				
His	Gln	Ile	Ile	Leu	Phe	Val	Asp	His	Ser	Leu	Lys	Ala	Val	Pro	Leu					
	145					150					155									
GGG	CAA	TTT	GTC	TTT	GAG	CCA	GCG	TTG	GCT	AAA	AAC	ATC	GTT	AAA	GCC	587				
Gly	Gln	Phe	Val	Phe	Glu	Pro	Ala	Leu	Ala	Lys	Asn	Ile	Val	Lys	Ala					
160					165				170					175						
TTT	TCG	CAC	CTC	TTT	GTC	ATA	GGG	TTT	TCT	ATG	GCG	TTC	CCT	ATT	TTA	635				
Phe	Ser	His	Leu	Phe	Val	Ile	Gly	Phe	Ser	Met	Ala	Phe	Pro	Ile	Leu					
			180					185						190						
TGC	TTG	GTG	TTA	TTG	AGC	GAT	ATT	ATT	TTT	GGC	ATG	ATC	ATG	AAA	ACC	683				
Cys	Leu	Val	Leu	Leu	Ser	Asp	Ile	Ile	Phe	Gly	Met	Ile	Met	Lys	Thr					
		195					200					205								
CAC	CCT	CAG	TTC	AAC	CTG	CTC	GCT	ATT	GGG	TTT	CCG	GTT	AAA	ATT	GCG	731				
His	Pro	Gln	Phe	Asn	Leu	Leu	Ala	Ile	Gly	Phe	Pro	Val	Lys	Ile	Ala					
		210					215					220								
ATC	GGG	TTT	GTG	GGC	ATT	ATC	TTA	ATC	GCT	TCG	GCT	ATC	ATG	GGG	CGT	779				
Ile	Gly	Phe	Val	Gly	Ile	Ile	Leu	Ile	Ala	Ser	Ala	Ile	Met	Gly	Arg					
	225					230				235										
TTT	AAA	GAA	GAA	ATC	AGC	CTG	GCC	TTT	AGC	GCC	ATT	AGC	AAA	ATC	TTT	T				
Phe	Lys	Glu	Glu	Ile	Ser	Leu	Ala	Phe	Ser	Ala	Ile	Ser	Lys	Ile	Phe					
240					245				250					255						
AAAGGATAAA CATGATTAGT TTTAAAGAAG CTCTAAAAAT CCATTCT																875				

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Met	Leu	Asp	Phe	Ile	Gln	Glu	Leu	Ser	Thr	Pro	His	Val	Arg	Asp	Phe
1				5					10					15	
Phe	Leu	Leu	Phe	Leu	Arg	Val	Ser	Gly	Val	Leu	Ser	Phe	Phe	Pro	Phe
			20					25					30		

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Phe Glu Asn His Leu Val Pro Leu Ser Val Arg Gly Ala Leu Ser Leu
      35              40              45
Tyr Val Ser Ala Ile Phe Tyr Pro Thr Leu Glu Phe Ser Asn Ala Ala
      50              55              60
Tyr Thr Pro Glu Gly Phe Ile Ile Ala Cys Leu Cys Glu Leu Phe Leu
      65              70              75              80
Gly Val Cys Ala Ser Val Phe Leu Gln Ile Val Phe Ala Ser Leu Val
              85              90              95
Phe Ala Thr Asp Ser Ile Ser Phe Ser Met Gly Leu Thr Met Ala Ser
              100              105              110
Ala Tyr Asp Pro Ile Ser Gly Ser Gln Lys Pro Ile Val Gly Gln Ala
              115              120              125
Leu Leu Leu Leu Ala Ile Leu Ile Leu Leu Asp Leu Ser Phe His His
      130              135              140
Gln Ile Ile Leu Phe Val Asp His Ser Leu Lys Ala Val Pro Leu Gly
      145              150              155              160
Gln Phe Val Phe Glu Pro Ala Leu Ala Lys Asn Ile Val Lys Ala Phe
              165              170              175
Ser His Leu Phe Val Ile Gly Phe Ser Met Ala Phe Pro Ile Leu Cys
              180              185              190
Leu Val Leu Leu Ser Asp Ile Ile Phe Gly Met Ile Met Lys Thr His
      195              200              205
Pro Gln Phe Asn Leu Leu Ala Ile Gly Phe Pro Val Lys Ile Ala Ile
      210              215              220
Gly Phe Val Gly Ile Ile Leu Ile Ala Ser Ala Ile Met Gly Arg Phe
      225              230              235              240
Lys Glu Glu Ile Ser Leu Ala Phe Ser Ala Ile Ser Lys Ile Phe
              245              250              255

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(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 373...1110
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

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GAGATATTAA AAAGAGATAT TAAATGGCT TTTAAGCTTC TATGAAGCCC CCCCCCTCC      60
TCCTTTTGCC CTTTATTTTCG TGGGCAAATC GCCCACAGGA CAAGCGGCCA CACCCACGCT      120
TGGGCGGGTG ATTTTCTCTA CATTTCCTTG AGCTTTTTTG GGGTCATTCA CCAAGTTTT      180
ATAGAACTCA AAAGGGCATT CCGCCACACC CTTATCCCCA TCGCCACTAG CAAAAACCCC      240
ACTATAACCT CTGTGCAAGA GTTTGAAGAG TTGGTTTTGG CTTTGGTCGT ATTTTCTCGC      300
ATCACGGATT TGTTCACAG AAAGTTGAGC GTATTGAAGA CCATTTTCTT CTTCCCCGCA      360
TTCGCCCAAA GT ATG CCC GTC AAA ACC AAT AAT GCT AGA ATG CCC AAA ATA      411
          Met Pro Val Lys Thr Asn Asn Ala Arg Met Pro Lys Ile
              1              5              10

GGA ATA CAC CCC ATC AAA ACC GGT CGC ATT CGC TAC CGC TAC ATA ACA      459

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Gly	Ile	His	Pro	Ile	Lys	Thr	Gly	Arg	Ile	Arg	Tyr	Arg	Tyr	Ile	Thr	
15						20					25					
TTG	ATT	GGC	CCA	CGC	CAT	AGC	TTT	TAC	TAT	TGC	AAT	TTG	TTG	CTC	CTT	507
Leu	Ile	Gly	Pro	Arg	His	Ser	Phe	Tyr	Tyr	Cys	Asn	Leu	Leu	Leu	Leu	
30					35					40					45	
AGC	CGG	ATA	CAT	GTA	ACC	TTG	ACA	GCG	CAC	AAT	GAG	TTC	TGC	CCC	ACG	555
Ser	Arg	Ile	His	Val	Thr	Leu	Thr	Ala	His	Asn	Glu	Phe	Cys	Pro	Thr	
				50					55					60		
CAT	CGC	GCA	ATC	GCG	CCA	AAT	TTC	AGG	GTA	GTT	TCC	ATC	ATC	GCA	AAT	603
His	Arg	Ala	Ile	Ala	Pro	Asn	Phe	Arg	Val	Val	Ser	Ile	Ile	Ala	Asn	
			65					70					75			
AAT	CAA	AGA	AAC	TTT	CAA	GCC	CTT	AGG	CCC	ATC	AAC	CAC	ATA	AGT	TTT	651
Asn	Gln	Arg	Asn	Phe	Gln	Ala	Leu	Arg	Pro	Ile	Asn	His	Ile	Ser	Phe	
	80						85					90				
ATC	CCC	AGG	ATA	CCA	ACA	TTC	AAT	AGG	GCA	CCA	AGG	CAA	GAT	TTT	GCG	699
Ile	Pro	Arg	Ile	Pro	Thr	Phe	Asn	Arg	Ala	Pro	Arg	Gln	Asp	Phe	Ala	
	95					100					105					
GTA	TTT	TTG	CAC	GAT	CTC	ACC	CTT	ATC	ATT	GAC	AAG	AAT	CAA	AGT	GTT	747
Val	Phe	Leu	His	Asp	Leu	Thr	Leu	Ile	Ile	Asp	Lys	Asn	Gln	Ser	Val	
110					115					120					125	
ATA	GGG	ATT	CTT	TTT	GGC	TTG	CTC	GTG	TTT	TTC	CCC	TGT	CAA	AGA	GAA	795
Ile	Gly	Ile	Leu	Phe	Gly	Leu	Leu	Val	Phe	Phe	Pro	Cys	Gln	Arg	Glu	
				130					135					140		
CAC	TCC	CCA	AAC	CTT	GTT	TTT	CTT	ACA	AGC	TTC	AGC	AAA	GAT	CGC	GGT	843
His	Ser	Pro	Asn	Leu	Val	Phe	Leu	Thr	Ser	Phe	Ser	Lys	Asp	Arg	Gly	
			145					150					155			
TTC	TTC	TCC	AGG	AAC	GCT	TGC	GGC	TGT	ATC	AAA	CAT	TTC	TTG	TCT	GTC	891
Phe	Phe	Ser	Arg	Asn	Ala	Cys	Gly	Cys	Ile	Lys	His	Phe	Leu	Ser	Val	
		160					165					170				
ATA	CAT	AAT	CCC	ATG	CGT	GCT	GTA	TTC	AGG	GAA	AAT	AAT	CAG	ATC	CAA	939
Ile	His	Asn	Pro	Met	Arg	Ala	Val	Phe	Arg	Glu	Asn	Asn	Gln	Ile	Gln	
	175					180					185					
CCC	AGG	CAA	ACC	CTG	TTT	GAC	CCC	ACC	AAT	CAC	CTT	AGC	GAT	ATT	GCG	987
Pro	Arg	Gln	Thr	Leu	Phe	Asp	Pro	Thr	Asn	His	Leu	Ser	Asp	Ile	Ala	
190					195					200					205	
ACA	ATT	TTC	CAA	CAC	CTC	ATT	CTT	AGT	GTG	GAG	TCT	AGG	CAT	CTT	ATA	1035
Thr	Ile	Phe	Gln	His	Leu	Ile	Leu	Ser	Val	Glu	Ser	Arg	His	Leu	Ile	
				210					215					220		
ATT	AAC	TAC	CGC	TAC	ACC	CAC	AGT	ATC	TGG	GCT	GCT	ACT	AAT	ATC	TCC	1083
Ile	Asn	Tyr	Arg	Tyr	Thr	His	Ser	Ile	Trp	Ala	Ala	Thr	Asn	Ile	Ser	
			225					230					235			
ATG	TCT	CAT	ATT	ATG	TTC	CTT	GTT	TTT	TGATGAGAGT	TCCTACAAAC	CCTCTAC					1137
Met	Ser	His	Ile	Met	Phe	Leu	Val	Phe								
		240					245									

TTGAATTTAT AAAATAATTG TGT

1160

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Met	Pro	Val	Lys	Thr	Asn	Asn	Ala	Arg	Met	Pro	Lys	Ile	Gly	Ile	His	1	5	10	15
Pro	Ile	Lys	Thr	Gly	Arg	Ile	Arg	Tyr	Arg	Tyr	Ile	Thr	Leu	Ile	Gly	20	25	30	
Pro	Arg	His	Ser	Phe	Tyr	Tyr	Cys	Asn	Leu	Leu	Leu	Leu	Ser	Arg	Ile	35	40	45	
His	Val	Thr	Leu	Thr	Ala	His	Asn	Glu	Phe	Cys	Pro	Thr	His	Arg	Ala	50	55	60	
Ile	Ala	Pro	Asn	Phe	Arg	Val	Val	Ser	Ile	Ile	Ala	Asn	Asn	Gln	Arg	65	70	75	80
Asn	Phe	Gln	Ala	Leu	Arg	Pro	Ile	Asn	His	Ile	Ser	Phe	Ile	Pro	Arg	85	90	95	
Ile	Pro	Thr	Phe	Asn	Arg	Ala	Pro	Arg	Gln	Asp	Phe	Ala	Val	Phe	Leu	100	105	110	
His	Asp	Leu	Thr	Leu	Ile	Ile	Asp	Lys	Asn	Gln	Ser	Val	Ile	Gly	Ile	115	120	125	
Leu	Phe	Gly	Leu	Leu	Val	Phe	Phe	Pro	Cys	Gln	Arg	Glu	His	Ser	Pro	130	135	140	
Asn	Leu	Val	Phe	Leu	Thr	Ser	Phe	Ser	Lys	Asp	Arg	Gly	Phe	Phe	Ser	145	150	155	160
Arg	Asn	Ala	Cys	Gly	Cys	Ile	Lys	His	Phe	Leu	Ser	Val	Ile	His	Asn	165	170	175	
Pro	Met	Arg	Ala	Val	Phe	Arg	Glu	Asn	Asn	Gln	Ile	Gln	Pro	Arg	Gln	180	185	190	
Thr	Leu	Phe	Asp	Pro	Thr	Asn	His	Leu	Ser	Asp	Ile	Ala	Thr	Ile	Phe	195	200	205	
Gln	His	Leu	Ile	Leu	Ser	Val	Glu	Ser	Arg	His	Leu	Ile	Ile	Asn	Tyr	210	215	220	
Arg	Tyr	Thr	His	Ser	Ile	Trp	Ala	Ala	Thr	Asn	Ile	Ser	Met	Ser	His	225	230	235	240
Ile	Met	Phe	Leu	Val	Phe											245			

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1661 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 79...1611
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

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GGCTTTATAA AAAATGTTAG AAACCCTTAC AAAACAAGCT AATATATTCT ATTCAATTTG      60
CCTCAAGGAC AAACAAAC ATG AAA AAA CTT CTT TAT ACC ATA CTC GCG CTT      111
           Met Lys Lys Leu Leu Tyr Thr Ile Leu Ala Leu
                1                5                10

CTT TTA ATC GGC CTT TTA ACA ATC TAT CTC ATC CTT TTT ACA GAA TGG      159
Leu Leu Ile Gly Leu Leu Thr Ile Tyr Leu Ile Leu Phe Thr Glu Trp
                15                20                25

GGG AAT AAG ATC ATC GCT TCG TAT ATA GAG AAA AAA ATC AAC CCG AAC      207
Gly Asn Lys Ile Ile Ala Ser Tyr Ile Glu Lys Lys Ile Asn Pro Asn
                30                35                40

GAG CAC TAC TTG AGC GTT AAA ACC TTT AAA TTG AGA TTC AAC TCT TTG      255
Glu His Tyr Leu Ser Val Lys Thr Phe Lys Leu Arg Phe Asn Ser Leu
                45                50                55

GAT TTT AAA GCT CAA GCC AAC GAT GAT TCC ACG CTC ATT CTT AAG GGG      303
Asp Phe Lys Ala Gln Ala Asn Asp Asp Ser Thr Leu Ile Leu Lys Gly
        60                65                70                75

GAT TTT TCA CTT TTA AAG CAA AGC GTA AAT TTG AAT TAC CAT ATA GAT      351
Asp Phe Ser Leu Leu Lys Gln Ser Val Asn Leu Asn Tyr His Ile Asp
                80                85                90

ATT AAA GAT TTA CGC TCT TTC AAA GAA TGG ATA CCC TAC CCT TTA AGG      399
Ile Lys Asp Leu Arg Ser Phe Lys Glu Trp Ile Pro Tyr Pro Leu Arg
                95                100                105

GGG GCT GTT ATC ACT TCT GGG AAT ATT AAA GGG CAT AGA AAA GCC CTT      447
Gly Ala Val Ile Thr Ser Gly Asn Ile Lys Gly His Arg Lys Ala Leu
                110                115                120

ATG ATT CAA GGC GTC TCT AAT GTG GCT CAA TCC CAC ACT GCC TAC AAT      495
Met Ile Gln Gly Val Ser Asn Val Ala Gln Ser His Thr Ala Tyr Asn
                125                130                135

GCC CTT TTA GAT GAT TTC AAG CTT TCT CGC TTA AAT TTG AAC GCA CAA      543
Ala Leu Leu Asp Asp Phe Lys Leu Ser Arg Leu Asn Leu Asn Ala Gln
        140                145                150                155

GAC GCC AAT TTA GAA GAT TTG CTT TAT TTA ATC AAT CGC CCC GCT TAT      591
Asp Ala Asn Leu Glu Asp Leu Leu Tyr Leu Ile Asn Arg Pro Ala Tyr
                160                165                170

GCG AAC GCA AAA GTG TCC TTA CAG GCG GAT TTT AAC TCT CTA AAG CCT      639
Ala Asn Ala Lys Val Ser Leu Gln Ala Asp Phe Asn Ser Leu Lys Pro
                175                180                185

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TTA	GAG	GGG	CAT	TTG	ATC	CTA	ACA	GCT	AAT	AAC	GCT	TTA	ATC	AAT	AAC	687
Leu	Glu	Gly	His	Leu	Ile	Leu	Thr	Ala	Asn	Asn	Ala	Leu	Ile	Asn	Asn	
		190					195					200				
GCC	CTA	ATC	AAT	CAA	ATT	TTT	CAT	TTA	AAC	CTT	AAA	GAC	ACG	CTT	GTT	735
Ala	Leu	Ile	Asn	Gln	Ile	Phe	His	Leu	Asn	Leu	Lys	Asp	Thr	Leu	Val	
	205					210					215					
TTC	AGC	CTC	TCG	CAT	TCA	AGC	GAC	TTT	AAA	GGA	AAC	AAA	GCC	ATC	AGC	783
Phe	Ser	Leu	Ser	His	Ser	Ser	Asp	Phe	Lys	Gly	Asn	Lys	Ala	Ile	Ser	
220					225					230					235	
GAT	ACC	ACC	CTG	ACT	AGC	CCT	TTA	GCC	AAT	TTC	AAA	GCC	CTA	AAA	AGC	831
Asp	Thr	Thr	Leu	Thr	Ser	Pro	Leu	Ala	Asn	Phe	Lys	Ala	Leu	Lys	Ser	
				240				245						250		
GAA	TAC	CTT	TTC	TCT	ATT	TTA	AAA	CTC	AAC	GCC	CCC	TAC	ACT	TTA	GAA	879
Glu	Tyr	Leu	Phe	Ser	Ile	Leu	Lys	Leu	Asn	Ala	Pro	Tyr	Thr	Leu	Glu	
			255					260					265			
ATC	CCC	AAT	CTA	GCC	AAA	CTC	TAT	AAC	ATT	ACC	AAC	CAC	CCC	TTA	AAA	927
Ile	Pro	Asn	Leu	Ala	Lys	Leu	Tyr	Asn	Ile	Thr	Asn	His	Pro	Leu	Lys	
		270					275					280				
GGG	AGC	TTG	ACT	TTA	AAA	GGC	GCT	ATA	GAA	CAA	AGC	CCC	AAA	CTT	TTA	975
Gly	Ser	Leu	Thr	Leu	Lys	Gly	Ala	Ile	Glu	Gln	Ser	Pro	Lys	Leu	Leu	
	285					290					295					
AAA	GTC	AGC	GGC	CAT	TCA	AAT	TTA	CTA	GAC	GGC	GCG	CTG	GAT	TTC	ACG	1023
Lys	Val	Ser	Gly	His	Ser	Asn	Leu	Leu	Asp	Gly	Ala	Leu	Asp	Phe	Thr	
300					305					310					315	
CTT	TTA	AAT	AAA	GAT	TTG	AAA	GGG	CGT	TTT	TCC	AAT	ATT	TCC	ACT	TTA	1071
Leu	Leu	Asn	Lys	Asp	Leu	Lys	Gly	Arg	Phe	Ser	Asn	Ile	Ser	Thr	Leu	
				320				325						330		
AAA	GCT	TTA	GAT	TTA	TTC	CAT	TAC	CCT	AAG	TTT	TTC	CAA	TCC	GTT	GCA	1119
Lys	Ala	Leu	Asp	Leu	Phe	His	Tyr	Pro	Lys	Phe	Phe	Gln	Ser	Val	Ala	
			335					340					345			
GAC	GCT	AAT	TTG	GAT	TAT	GAT	CTT	ATC	GCT	AAG	CAA	GGC	GTA	TTG	AAA	1167
Asp	Ala	Asn	Leu	Asp	Tyr	Asp	Leu	Ile	Ala	Lys	Gln	Gly	Val	Leu	Lys	
		350					355					360				
GCC	CGC	CTA	AAA	AAC	GCA	AGA	TTC	CTC	AAA	AAT	GCA	TTC	AGC	GAT	TTT	1215
Ala	Arg	Leu	Lys	Asn	Ala	Arg	Phe	Leu	Lys	Asn	Ala	Phe	Ser	Asp	Phe	
	365					370					375					
CTC	TAC	TCC	ATT	TCT	AAA	TTT	GAT	ATT	ACA	AAA	GAA	ATT	TAT	AAC	GAT	1263
Leu	Tyr	Ser	Ile	Ser	Lys	Phe	Asp	Ile	Thr	Lys	Glu	Ile	Tyr	Asn	Asp	
380					385					390					395	
GCC	AAT	CTG	GTA	AGC	CAA	ATC	AAC	CAG	CAA	CGC	CTG	CTC	TCT	GAT	CTG	1311
Ala	Asn	Leu	Val	Ser	Gln	Ile	Asn	Gln	Gln	Arg	Leu	Leu	Ser	Asp	Leu	
				400				405						410		
AGT	TTA	AAA	AGC	CCC	AAA	ACC	CAA	TTG	AAA	ATC	CAT	AAC	GGT	TTG	TTG	1359
Ser	Leu	Lys	Ser	Pro	Lys	Thr	Gln	Leu	Lys	Ile	His	Asn	Gly	Leu	Leu	

415	420	425	
GAT TTA AAC ACC AAA CAA ATG AAC ATG CTC ATG GAT GCG GAA ATT TTA			1407
Asp Leu Asn Thr Lys Gln Met Asn Met Leu Met Asp Ala Glu Ile Leu			
430	435	440	
AAA TTC ATT TTT AAA ATG AAA CTT CAA GGC AAC ATG CAC CAG CCA AAA			1455
Lys Phe Ile Phe Lys Met Lys Leu Gln Gly Asn Met His Gln Pro Lys			
445	450	455	
TTT TCT CTC ATT TTA AAC GAA AAA GCC ATT CAG CAA AAC TTG CAA CAA			1503
Phe Ser Leu Ile Leu Asn Glu Lys Ala Ile Gln Gln Asn Leu Gln Gln			
460	465	470	475
GGC TTG AAA GAA ATC TTA AAA AAC GAC ACC CTT AAA AAA GGT TTA GAT			1551
Gly Leu Lys Glu Ile Leu Lys Asn Asp Thr Leu Lys Lys Gly Leu Asp			
480	485	490	
CAT TTG CTT AAA GAT GAT AAG CTC AAA GAA AAG CTT GAA AAA GGG CTT			1599
His Leu Leu Lys Asp Asp Lys Leu Lys Glu Lys Leu Glu Lys Gly Leu			
495	500	505	
AAG GGG CTT TTT TAAAAATTTTA AAGGATAGAA ATGGCGCACA TTTTAGTTAG CGGGG			1656
Lys Gly Leu Phe			
510			
CGACT			1661

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met	Lys	Lys	Leu	Leu	Tyr	Thr	Ile	Leu	Ala	Leu	Leu	Leu	Ile	Gly	Leu
1			5						10					15	
Leu	Thr	Ile	Tyr	Leu	Ile	Leu	Phe	Thr	Glu	Trp	Gly	Asn	Lys	Ile	Ile
		20					25					30			
Ala	Ser	Tyr	Ile	Glu	Lys	Lys	Ile	Asn	Pro	Asn	Glu	His	Tyr	Leu	Ser
	35					40					45				
Val	Lys	Thr	Phe	Lys	Leu	Arg	Phe	Asn	Ser	Leu	Asp	Phe	Lys	Ala	Gln
	50				55					60					
Ala	Asn	Asp	Asp	Ser	Thr	Leu	Ile	Leu	Lys	Gly	Asp	Phe	Ser	Leu	Leu
65				70					75					80	
Lys	Gln	Ser	Val	Asn	Leu	Asn	Tyr	His	Ile	Asp	Ile	Lys	Asp	Leu	Arg
		85					90						95		
Ser	Phe	Lys	Glu	Trp	Ile	Pro	Tyr	Pro	Leu	Arg	Gly	Ala	Val	Ile	Thr
	100					105						110			
Ser	Gly	Asn	Ile	Lys	Gly	His	Arg	Lys	Ala	Leu	Met	Ile	Gln	Gly	Val
	115					120					125				
Ser	Asn	Val	Ala	Gln	Ser	His	Thr	Ala	Tyr	Asn	Ala	Leu	Leu	Asp	Asp

130		135		140
Phe Lys Leu Ser Arg	Leu Asn Leu Asn Ala Gln Asp Ala Asn Leu Glu			
145		150		155
Asp Leu Leu Tyr Leu	Ile Asn Arg Pro Ala Tyr Ala Asn Ala Lys Val			160
		165		170
Ser Leu Gln Ala Asp	Phe Asn Ser Leu Lys Pro Leu Glu Gly His Leu			175
		180		185
Ile Leu Thr Ala Asn	Asn Ala Leu Ile Asn Asn Ala Leu Ile Asn Gln			190
		195		200
Ile Phe His Leu Asn	Leu Lys Asp Thr Leu Val Phe Ser Leu Ser His			205
		210		215
Ser Ser Asp Phe Lys	Gly Asn Lys Ala Ile Ser Asp Thr Thr Leu Thr			220
225		230		235
Ser Pro Leu Ala Asn	Phe Lys Ala Leu Lys Ser Glu Tyr Leu Phe Ser			240
		245		250
Ile Leu Lys Leu Asn	Ala Pro Tyr Thr Leu Glu Ile Pro Asn Leu Ala			255
		260		265
Lys Leu Tyr Asn Ile	Thr Asn His Pro Leu Lys Gly Ser Leu Thr Leu			270
		275		280
Lys Gly Ala Ile Glu	Gln Ser Pro Lys Leu Leu Lys Val Ser Gly His			285
		290		295
Ser Asn Leu Leu Asp	Gly Ala Leu Asp Phe Thr Leu Leu Asn Lys Asp			300
305		310		315
Leu Lys Gly Arg Phe	Ser Asn Ile Ser Thr Leu Lys Ala Leu Asp Leu			320
		325		330
Phe His Tyr Pro Lys	Phe Phe Gln Ser Val Ala Asp Ala Asn Leu Asp			335
		340		345
Tyr Asp Leu Ile Ala	Lys Gln Gly Val Leu Lys Ala Arg Leu Lys Asn			350
		355		360
Ala Arg Phe Leu Lys	Asn Ala Phe Ser Asp Phe Leu Tyr Ser Ile Ser			365
		370		375
Lys Phe Asp Ile Thr	Lys Glu Ile Tyr Asn Asp Ala Asn Leu Val Ser			380
385		390		395
Gln Ile Asn Gln Gln	Arg Leu Leu Ser Asp Leu Ser Leu Lys Ser Pro			400
		405		410
Lys Thr Gln Leu Lys	Ile His Asn Gly Leu Leu Asp Leu Asn Thr Lys			415
		420		425
Gln Met Asn Met Leu	Met Asp Ala Glu Ile Leu Lys Phe Ile Phe Lys			430
		435		440
Met Lys Leu Gln Gly	Asn Met His Gln Pro Lys Phe Ser Leu Ile Leu			445
		450		455
Asn Glu Lys Ala Ile	Gln Gln Asn Leu Gln Gln Gly Leu Lys Glu Ile			460
465		470		475
Leu Lys Asn Asp Thr	Leu Lys Lys Gly Leu Asp His Leu Leu Lys Asp			480
		485		490
Asp Lys Leu Lys Glu	Lys Leu Glu Lys Gly Leu Lys Gly Leu Phe			495
		500		505
				510

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 53...352
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CTAATTCTGT CTATTACACC AACAATCAAT CTCAAAACAA AGGACATGAAAG ATG AAA	58
Met Lys	
1	
ACA AAA CAT AAA GGA ATA AGA ATG TTT AAG CAA ATT CGT AGA ATG ATG	106
Thr Lys His Lys Gly Ile Arg Met Phe Lys Gln Ile Arg Arg Met Met	
5 10 15	
AGT TTG GCA ATA TTA ATG CCT AGT TTT TTA TTG GCG GCA CCA GAT TAC	154
Ser Leu Ala Ile Leu Met Pro Ser Phe Leu Leu Ala Ala Pro Asp Tyr	
20 25 30	
AAA CAA AAA TTC ACT CAA ATA TTG GAT TTC ATA AGC AAT GAC TTT ATC	202
Lys Gln Lys Phe Thr Gln Ile Leu Asp Phe Ile Ser Asn Asp Phe Ile	
35 40 45 50	
AAG GCT ATT GGT GGT CTA ATC ATT GTT GGG ACT TGC ATT TAC GCC TAT	250
Lys Ala Ile Gly Gly Leu Ile Ile Val Gly Thr Cys Ile Tyr Ala Tyr	
55 60 65	
AAA AAT TGG GAC AGG CTT GGA GAA ATT GGT TGG AAA TGC GTT GGG ATT	298
Lys Asn Trp Asp Arg Leu Gly Glu Ile Gly Trp Lys Cys Val Gly Ile	
70 75 80	
ATC ATT ATA ACC GCT GCT ATT TCT AAT GCT AAA ACT TTA AGT CAA TGG	346
Ile Ile Ile Thr Ala Ala Ile Ser Asn Ala Lys Thr Leu Ser Gln Trp	
85 90 95	
TTA TTT TAGATGGCAT TGCATATTGT TTGTGTTGAA AGTATCAACA TTAGA	397
Leu Phe	
100	

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Lys Thr Lys His Lys Gly Ile Arg Met Phe Lys Gln Ile Arg Arg	
1 5 10 15	
Met Met Ser Leu Ala Ile Leu Met Pro Ser Phe Leu Leu Ala Ala Pro	
20 25 30	

```

Asp Tyr Lys Gln Lys Phe Thr Gln Ile Leu Asp Phe Ile Ser Asn Asp
      35              40              45
Phe Ile Lys Ala Ile Gly Gly Leu Ile Ile Val Gly Thr Cys Ile Tyr
      50              55              60
Ala Tyr Lys Asn Trp Asp Arg Leu Gly Glu Ile Gly Trp Lys Cys Val
      65              70              75              80
Gly Ile Ile Ile Ile Thr Ala Ala Ile Ser Asn Ala Lys Thr Leu Ser
              85              90              95
Gln Trp Leu Phe
              100

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(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...318
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

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CTTGCCAATC CCTTCAATAT CCACCGAATT GATGCCATGC TCAATTAAAA A ATG ATC      57
                                   Met Ile
                                   1
CAA AGC GAC GCT GTC TTT AAG ATA AAT TTC TGT CTT GCC CTT CTT GTA      105
Gln Ser Asp Ala Val Phe Lys Ile Asn Phe Cys Leu Ala Leu Leu Val
      5              10              15
TTT GTA AAG AGG GGC TTG AGC GAT ATA AAC ATG CCC TTG TTC AAT CAG      153
Phe Val Lys Arg Gly Leu Ser Asp Ile Asn Met Pro Leu Phe Asn Gln
      20              25              30
CGG GCG CAA ATA ACG ATA GAA AAA AGT CAT CAG CAA GGT TTG GAT ATG      201
Arg Ala Gln Ile Thr Ile Glu Lys Ser His Gln Gln Gly Leu Asp Met
      35              40              45              50
GCT CCC ATC CAC ATC AGC ATC GGT CAT GAT AAT GAT TTT ATG ATA GCG      249
Ala Pro Ile His Ile Ser Ile Gly His Asp Asn Asp Phe Met Ile Ala
              55              60              65
CAA TCT TTC TAT ATC AAA ACT CTC TTG AAT GCC GCA CCC AAA AGC CGT      297
Gln Ser Phe Tyr Ile Lys Thr Leu Leu Asn Ala Ala Pro Lys Ser Arg
              70              75              80
GAT CAT GTT TTT AAT TTC TTC TGATTTTAGG ATTTTGTATA AATGGCTTTT TTCC      352
Asp His Val Phe Asn Phe Phe
      85

```

ACATTTAAAA TCTTA

367

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

```

Met Ile Gln Ser Asp Ala Val Phe Lys Ile Asn Phe Cys Leu Ala Leu
 1             5             10             15
Leu Val Phe Val Lys Arg Gly Leu Ser Asp Ile Asn Met Pro Leu Phe
          20             25             30
Asn Gln Arg Ala Gln Ile Thr Ile Glu Lys Ser His Gln Gln Gly Leu
          35             40             45
Asp Met Ala Pro Ile His Ile Ser Ile Gly His Asp Asn Asp Phe Met
          50             55             60
Ile Ala Gln Ser Phe Tyr Ile Lys Thr Leu Leu Asn Ala Ala Pro Lys
65             70             75             80
Ser Arg Asp His Val Phe Asn Phe Phe
          85

```

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 54...344
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

```

TAAAAAGCAC TTTAGAGAGA TTTACGAAAG TGTTTTGAAG CGAAGAATGT CTG ATG      56
                                     Met
                                     1

ATT ATC TTT GGA AAA GAT TAC CTA TCT ACA GAC TTG CAA AAT AGC GCT      104
Ile Ile Phe Gly Lys Asp Tyr Leu Ser Thr Asp Leu Gln Asn Ser Ala
          5             10             15

AAA GAT ATT CTT CTC ATC GCT TCG CAA ATT CTC AAA GAA AGA CTT TTT      152
Lys Asp Ile Leu Leu Ile Ala Ser Gln Ile Leu Lys Glu Arg Leu Phe
          20             25             30

```

GCC CAC AAA AAT GAG ATT TTC TTT TGC CCT AGA AAT AGC TAC ATT CAA 200
 Ala His Lys Asn Glu Ile Phe Phe Cys Pro Arg Asn Ser Tyr Ile Gln
 35 40 45

GCG TTT AGA ATC TAT CAA GAA AGA AAG ATT ACC ATA AGT TTT CAC GGT 248
 Ala Phe Arg Ile Tyr Gln Glu Arg Lys Ile Thr Ile Ser Phe His Gly
 50 55 60 65

GGA ATA AAT AAT AAT ATC TGC CTT CTC GCC TTG AAA GGC ATC CAC AGT 296
 Gly Ile Asn Asn Asn Ile Cys Leu Leu Ala Leu Lys Gly Ile His Ser
 70 75 80

GTC TAT TTT GAG CTC ATC AAA ATT CTT GAA GCC GTA TTT TTC CAC TTC T 345
 Val Tyr Phe Glu Leu Ile Lys Ile Leu Glu Ala Val Phe Phe His Phe
 85 90 95

GATCGCAAGC ATCTTTTGTG GGCATTATAA GGTGTGATAA T 386

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Met Ile Ile Phe Gly Lys Asp Tyr Leu Ser Thr Asp Leu Gln Asn Ser
 1 5 10 15
 Ala Lys Asp Ile Leu Leu Ile Ala Ser Gln Ile Leu Lys Glu Arg Leu
 20 25 30
 Phe Ala His Lys Asn Glu Ile Phe Cys Pro Arg Asn Ser Tyr Ile
 35 40 45
 Gln Ala Phe Arg Ile Tyr Gln Glu Arg Lys Ile Thr Ile Ser Phe His
 50 55 60
 Gly Gly Ile Asn Asn Asn Ile Cys Leu Leu Ala Leu Lys Gly Ile His
 65 70 75 80
 Ser Val Tyr Phe Glu Leu Ile Lys Ile Leu Glu Ala Val Phe Phe His
 85 90 95
 Phe

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

(B) LOCATION: 55...516
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GCGGTTTGGGA TCTTCATTAA AAATTCGTTG CTCACCCCTG GGTTATAAGC TTGA GCT	57
Ala	
1	
TCA GAA GTG GCC CCC TCA GAG GTT TTG TTG GAT TCT TCT TGC TTG TCT	105
Ser Glu Val Ala Pro Ser Glu Val Leu Leu Asp Ser Ser Cys Leu Ser	
5 10 15	
TTT TCT TTG ACT ATA TCC TTA GTT GTT ACT TGT TTA GGA GCG CTT TTT	153
Phe Ser Leu Thr Ile Ser Leu Val Val Thr Cys Leu Gly Ala Leu Phe	
20 25 30	
TCT TTA GCT TCC TCT TTA GCT TCT TCT TTT TTG GGC TCT TCT TTA GGC	201
Ser Leu Ala Ser Ser Leu Ala Ser Ser Phe Leu Gly Ser Ser Leu Gly	
35 40 45	
TCT TCT TTT TTA ACC TCT TCA ACT TTA GGC TCA GGC TTA GGC TCG GGT	249
Ser Ser Phe Leu Thr Ser Ser Thr Leu Gly Ser Gly Leu Gly Ser Gly	
50 55 60 65	
TTT GGT TCA GGT TTG GGT TCA GGC TTA GGT TTT GGT TTT GGC TTT GGC	297
Phe Gly Ser Gly Leu Gly Ser Gly Leu Gly Phe Gly Phe Gly Phe Gly	
70 75 80	
TTG GGT TTA GGC TTA GGT TTA GGC TTT GTA ACC TCC TTT TTG GGT TCT	345
Leu Gly Leu Gly Leu Gly Leu Gly Phe Val Thr Ser Phe Leu Gly Ser	
85 90 95	
TCT TTT TTT GGC TCT TCT TTC TTG GGT TTT TCT TTA GGC TCT TCT TTG	393
Ser Phe Phe Gly Ser Ser Phe Leu Gly Phe Ser Leu Gly Ser Ser Leu	
100 105 110	
GGT TTA GCC GAC TCA GCA TTA GTC TTT GTA TTG GAA TTA GTG TTG ATG	441
Gly Leu Ala Asp Ser Ala Leu Val Phe Val Leu Glu Leu Val Leu Met	
115 120 125	
CTG GCT AAA CTC ATG GTA ACC TTA GTG GTC CCG GCT TGC GCT AAA GGC	489
Leu Ala Lys Leu Met Val Thr Leu Val Val Pro Ala Cys Ala Lys Gly	
130 135 140 145	
TCT GGG GCG TCT TCG CGC AGT AAA AAA TAGCCAAACC CTATAGCGTA TAGGGCA	543
Ser Gly Ala Ser Ser Arg Ser Lys Lys	
150	
AAAGAGATTA AAAAGCTAAC ACTCGT	569

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Ala	Ser	Glu	Val	Ala	Pro	Ser	Glu	Val	Leu	Leu	Asp	Ser	Ser	Cys	Leu
1				5					10					15	
Ser	Phe	Ser	Leu	Thr	Ile	Ser	Leu	Val	Val	Thr	Cys	Leu	Gly	Ala	Leu
			20					25					30		
Phe	Ser	Leu	Ala	Ser	Ser	Leu	Ala	Ser	Ser	Phe	Leu	Gly	Ser	Ser	Leu
		35				40						45			
Gly	Ser	Ser	Phe	Leu	Thr	Ser	Ser	Thr	Leu	Gly	Ser	Gly	Leu	Gly	Ser
	50					55					60				
Gly	Phe	Gly	Ser	Gly	Leu	Gly	Ser	Gly	Leu	Gly	Phe	Gly	Phe	Gly	Phe
65					70				75						80
Gly	Leu	Gly	Leu	Gly	Leu	Gly	Leu	Gly	Phe	Val	Thr	Ser	Phe	Leu	Gly
				85					90					95	
Ser	Ser	Phe	Phe	Gly	Ser	Ser	Phe	Leu	Gly	Phe	Ser	Leu	Gly	Ser	Ser
			100					105					110		
Leu	Gly	Leu	Ala	Asp	Ser	Ala	Leu	Val	Phe	Val	Leu	Glu	Leu	Val	Leu
		115					120					125			
Met	Leu	Ala	Lys	Leu	Met	Val	Thr	Leu	Val	Val	Pro	Ala	Cys	Ala	Lys
	130					135					140				
Gly	Ser	Gly	Ala	Ser	Ser	Arg	Ser	Lys	Lys						
145					150										

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 77...310
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CCCCACAAAT	CCTAGCGATA	GTGAAATGCC	CTAATTCATG	GACAAAGATT	AAAAACGCCA	60							
GCATCAAAAC	CGCTAC	AAT GAA	CAT CAT	ACC CCT	GCA GGC	TCT TTG	GTG TTA	112					
		Asn	Glu	His	His	Thr	Pro	Ala	Gly	Ser	Leu	Val	Leu
		1				5					10		
GGA TCT	TTT ATC	ATC GGC	TCT TTT	AAA GGC	GTG GGT	GCT ATA	GGG GGC	160					
Gly Ser	Phe Ile	Ile Gly	Ser Phe	Lys Gly	Val Gly	Ala Ile	Gly Gly						
	15			20			25						
GTG GGT	GCT GTG	GTT TTT	GGG ATT	TCT TTA	TTT TCT	TTT GGG	GGT TTT	208					

Val Gly Ala Val Val Phe Gly Ile Ser Leu Phe Ser Phe Gly Gly Phe
 30 35 40

TGC CAC AAC TCT GTC AAA GCC GCC GCT TTT TTA GGA TCC ATT TTG GCT 256
 Cys His Asn Ser Val Lys Ala Ala Ala Phe Leu Gly Ser Ile Leu Ala
 45 50 55 60

AAA ATT TTA CCG AGT TCT TGG GGT TTT AGC GCC ATT AAA ATT TCT AAT 304
 Lys Ile Leu Pro Ser Ser Trp Gly Phe Ser Ala Ile Lys Ile Ser Asn
 65 70 75

GCG TTT TGAGTGGGTA AATTTTCTAA AATCAGAGCC GATTTAGAAT CTTTCATTT 359
 Ala Phe

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Asn Glu His His Thr Pro Ala Gly Ser Leu Val Leu Gly Ser Phe Ile
 1 5 10 15
 Ile Gly Ser Phe Lys Gly Val Gly Ala Ile Gly Gly Val Gly Ala Val
 20 25 30
 Val Phe Gly Ile Ser Leu Phe Ser Phe Gly Gly Phe Cys His Asn Ser
 35 40 45
 Val Lys Ala Ala Ala Phe Leu Gly Ser Ile Leu Ala Lys Ile Leu Pro
 50 55 60
 Ser Ser Trp Gly Phe Ser Ala Ile Lys Ile Ser Asn Ala Phe
 65 70 75

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1051 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...998
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GGGTTTGTG AATGACGACT AAAAGAGTGA ATACTGCCAC AAACAAGATA ATG ACA	56
Met Thr	
1	
TTA AAT ACT TTC TTG GAT ACA TGT TTT CTT TTA TTC ATC AGT ATT CTT	104
Leu Asn Thr Phe Leu Asp Thr Cys Phe Leu Leu Phe Ile Ser Ile Leu	
5 10 15	
TTT TAT TTA AGT ATA CCA ATT TAT CCT AAC AAA GTG GTG GTT GTC CCG	152
Phe Tyr Leu Ser Ile Pro Ile Tyr Pro Asn Lys Val Val Val Val Pro	
20 25 30	
CAA GGT TCG CTC AAA AAA GTG TTT TTT TCT TTA AAA GAG CAA GGC GTG	200
Gln Gly Ser Leu Lys Lys Val Phe Phe Ser Leu Lys Glu Gln Gly Val	
35 40 45 50	
GAT ATG AAC GCT TTG GAT TTG CTT TTT TTA CGC CTG ATG GGC ATG CCT	248
Asp Met Asn Ala Leu Asp Leu Leu Phe Leu Arg Leu Met Gly Met Pro	
55 60 65	
AAA AAA GGT TAT ATT GAT ATG GGC GAT GGG GCT TTA AGG AAG GGG GAT	296
Lys Lys Gly Tyr Ile Asp Met Gly Asp Gly Ala Leu Arg Lys Gly Asp	
70 75 80	
TTT TTA GTC CGT TTG ATT AAG GCA AAA GCG GCA CAA AAA AGT GCG ACT	344
Phe Leu Val Arg Leu Ile Lys Ala Lys Ala Ala Gln Lys Ser Ala Thr	
85 90 95	
CTA ATC CCT GGG GAA AGC CGC TAT TTT TTC ACG CAA ATT TTG AGC GAG	392
Leu Ile Pro Gly Glu Ser Arg Tyr Phe Phe Thr Gln Ile Leu Ser Glu	
100 105 110	
ACT TAC CAA CTA GAA ACA AGC GAT CTC AAT CAG GCT TAT GAA AGC ATC	440
Thr Tyr Gln Leu Glu Thr Ser Asp Leu Asn Gln Ala Tyr Glu Ser Ile	
115 120 125 130	
GCT CCA CGA TTG AAT GGC GAA GTG ATA GAA GAT GGG GTG ATA TGG CCA	488
Ala Pro Arg Leu Asn Gly Glu Val Ile Glu Asp Gly Val Ile Trp Pro	
135 140 145	
GAC ACT TAT CAT TTG CCT TTA GGG GAG GAC GCT TTT AAA ATC ATG CAA	536
Asp Thr Tyr His Leu Pro Leu Gly Glu Asp Ala Phe Lys Ile Met Gln	
150 155 160	
ACT TTG ATT GGT CAA TCC ATG AAA AAA CAC GAA GCC TTA AGC AAA CAA	584
Thr Leu Ile Gly Gln Ser Met Lys Lys His Glu Ala Leu Ser Lys Gln	
165 170 175	
TGG CTT GGA TAC TAC CAT AAA GAA GAG TGG TTT GAA AAA ATC ATT CTC	632
Trp Leu Gly Tyr Tyr His Lys Glu Glu Trp Phe Glu Lys Ile Ile Leu	
180 185 190	
GCT TCT ATT GTG CAA AAA GAA GCC GCT AAT GTT GAA GAA ATG CCC TTG	680
Ala Ser Ile Val Gln Lys Glu Ala Ala Asn Val Glu Glu Met Pro Leu	
195 200 205 210	
ATT GCG AGC GTG ATT TTT AAC CGC TTG AAA AAA GGC ATG CCT TTA CAA	728
Ile Ala Ser Val Ile Phe Asn Arg Leu Lys Lys Gly Met Pro Leu Gln	

1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

130	135	140
Trp Pro Asp Thr Tyr His	Leu Pro Leu Gly Glu	Asp Ala Phe Lys Ile
145	150	155
Met Gln Thr Leu Ile Gly	Gln Ser Met Lys Lys	His Glu Ala Leu Ser
165	170	175
Lys Gln Trp Leu Gly Tyr	Tyr His Lys Glu Glu	Trp Phe Glu Lys Ile
180	185	190
Ile Leu Ala Ser Ile Val	Gln Lys Glu Ala Ala	Asn Val Glu Glu Met
195	200	205
Pro Leu Ile Ala Ser Val	Ile Phe Asn Arg Leu	Lys Lys Gly Met Pro
210	215	220
Leu Gln Met Asp Gly Ala	Leu Asn Tyr Gln Glu	Phe Ser His Ala Lys
225	230	235
Val Thr Lys Glu Arg Ile	Lys Thr Asp Asn Thr	Pro Tyr Asn Thr Tyr
245	250	255
Lys Phe Lys Gly Leu Pro	Lys Asn Pro Val Gly	Ser Val Ser Leu Glu
260	265	270
Ala Ile Arg Ala Val Ile	Phe Pro Lys Lys Thr	Asp Phe Leu Tyr Phe
275	280	285
Val Lys Met Pro Asp Lys	Lys His Ala Phe Ser	Ala Thr Tyr Lys Glu
290	295	300
His Leu Lys Asn Ile Asn	Leu Ser Asn Asn His	Phe
305	310	315

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...584
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GAAAGTTCGG GGGCGGATTC TATGATTAAT GGCTATGGTT ATACCAAAGA ATG AGT	56
Met Ser	
1	
CAA AAA ATC CTA ATT CTA GGT ATT GGC AAT ATC CTT TTT GGC GAT GAA	104
Gln Lys Ile Leu Ile Leu Gly Ile Gly Asn Ile Leu Phe Gly Asp Glu	
5 10 15	
GGG ATT GGG GTG CAT TTA GCC CAC TAC CTC AAA AAA AAT TTT TCT TTT	152
Gly Ile Gly Val His Leu Ala His Tyr Leu Lys Lys Asn Phe Ser Phe	
20 25 30	
TTC CCT AGC GTG GAT ATT ATA GAT GGG GGG ACA ATG GCC CAG CAG CTC	200
Phe Pro Ser Val Asp Ile Ile Asp Gly Gly Thr Met Ala Gln Gln Leu	
35 40 45 50	

ATT CCT TTA ATC ACT TCG TAT GAA AAG GTT TTG ATT TTG GAT TGC GTG	248
Ile Pro Leu Ile Thr Ser Tyr Glu Lys Val Leu Ile Leu Asp Cys Val	
55 60 65	
AGC GCT GAA GGC GTT GAG ATA GGA TCA GTC TAT GCT TTT GAT TTT AAG	296
Ser Ala Glu Gly Val Glu Ile Gly Ser Val Tyr Ala Phe Asp Phe Lys	
70 75 80	
GAC GCT CCT AAA GAA ATC ACA TGG GCT GGG AGC GCT CAT GAA GTG GAA	344
Asp Ala Pro Lys Glu Ile Thr Trp Ala Gly Ser Ala His Glu Val Glu	
85 90 95	
ATG CTA CAC ACT TTA AGG CTC ACG GAG TTT TTA GGG GAT TTG CCT AAA	392
Met Leu His Thr Leu Arg Leu Thr Glu Phe Leu Gly Asp Leu Pro Lys	
100 105 110	
ACT TTT ATC GTG GGG CTT GTG CCT TTT GTG ATA GGG AGC GAG ACC ACT	440
Thr Phe Ile Val Gly Leu Val Pro Phe Val Ile Gly Ser Glu Thr Thr	
115 120 125 130	
TTC AAG CTT TCA AGC AAA ATT TTA AAC GCT TTA GAA ACC GCC TTA AAA	488
Phe Lys Leu Ser Ser Lys Ile Leu Asn Ala Leu Glu Thr Ala Leu Lys	
135 140 145	
GCC ATA GAA ACC CAA CTC AAC GCA TGG GGG GTT AAA ATG CAA CGC ACC	536
Ala Ile Glu Thr Gln Leu Asn Ala Trp Gly Val Lys Met Gln Arg Thr	
150 155 160	
GAT CAT ATC GCT TTA GAA TGT ATC GCT GAA CTT TCT TAT AAG GGT TTT T	585
Asp His Ile Ala Leu Glu Cys Ile Ala Glu Leu Ser Tyr Lys Gly Phe	
165 170 175	
GAATTGGTTT TTGTTTTTCT TTTTAAATGC GTTAATGAAG AAACAAGCCT GA	637

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Met Ser Gln Lys Ile Leu Ile Leu Gly Ile Gly Asn Ile Leu Phe Gly	
1 5 10 15	
Asp Glu Gly Ile Gly Val His Leu Ala His Tyr Leu Lys Lys Asn Phe	
20 25 30	
Ser Phe Phe Pro Ser Val Asp Ile Ile Asp Gly Gly Thr Met Ala Gln	
35 40 45	
Gln Leu Ile Pro Leu Ile Thr Ser Tyr Glu Lys Val Leu Ile Leu Asp	
50 55 60	
Cys Val Ser Ala Glu Gly Val Glu Ile Gly Ser Val Tyr Ala Phe Asp	
65 70 75 80	
Phe Lys Asp Ala Pro Lys Glu Ile Thr Trp Ala Gly Ser Ala His Glu	

[illegible]

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...161
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

[illegible]

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Met	Met	Trp	Arg	Ser	Leu	Xaa	Val	Ala	Phe	Thr	Ile	Thr	Asp	Ile	Ser
1				5					10					15	
Lys	Thr	Phe	Gln	Ser	Gln	Pro	Lys	His	His	Gln	Ile	Gly	Thr	Leu	Glu
			20					25					30		
Leu	Asn	Phe	Ala	Phe											
			35												

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1523
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

CTGTATTTCGC TTCTGTGGAT TACTACCCTC AAAGAAAAGA AAGCCACAGA ATG AAC	56
Met Asn	
1	
ACC ACC ATC TTA GAA GCT TAT GCG GCT GAG CCA AGC AGG CAA ACC CTC	104
Thr Thr Ile Leu Glu Ala Tyr Ala Ala Glu Pro Ser Arg Gln Thr Leu	
5 10 15	
TCT AAA GTC AGC AAC CGA TTC AAA GAG CAT GGC GCT AAA TTT GAT CTT	152
Ser Lys Val Ser Asn Arg Phe Lys Glu His Gly Ala Lys Phe Asp Leu	
20 25 30	
CGT GTG ATG GCA ACG CAT GGA GGC ACC ATT AGT TGG AAA GCT AAA GAA	200
Arg Val Met Ala Thr His Gly Gly Thr Ile Ser Trp Lys Ala Lys Glu	
35 40 45 50	
CTC GCT AGG ACT ATT GTG AGC GGC CCT ATT GGA GGC GTG ATT GGA TCT	248
Leu Ala Arg Thr Ile Val Ser Gly Pro Ile Gly Gly Val Ile Gly Ser	
55 60 65	
AAA TTG CTA GGC GAA ACG CTT GGT TAT GAC AAT ATT GCA TGC AGT GAT	296
Lys Leu Leu Gly Glu Thr Leu Gly Tyr Asp Asn Ile Ala Cys Ser Asp	
70 75 80	
ATT GGK GGC ACG AGC TTT GAT ATG GCG CTT ATC GTT AAG AGC AAT TTT	344
Ile Xaa Gly Thr Ser Phe Asp Met Ala Leu Ile Val Lys Ser Asn Phe	
85 90 95	

AAC ATC GCT TCT GAC CCT GAT ATG GCA CGC CTT GTT TTA TCT CTA CCG	392
Asn Ile Ala Ser Asp Pro Asp Met Ala Arg Leu Val Leu Ser Leu Pro	
100 105 110	
CTT GTG GCT ATG GAT TCT GTT GGC GCA GGT GCT GGG AGT TTT GTG CGC	440
Leu Val Ala Met Asp Ser Val Gly Ala Gly Ala Gly Ser Phe Val Arg	
115 120 125 130	
ATT GAT CCA CAC AGC CGA TCT GTC AAA CTA GGG CCT GAC AGC GCG GGG	488
Ile Asp Pro His Ser Arg Ser Val Lys Leu Gly Pro Asp Ser Ala Gly	
135 140 145	
TAT AGA GTT GGC ACT TGT TGG AAA GAC AGC GGG TTA GAC ACG GTT TCA	536
Tyr Arg Val Gly Thr Cys Trp Lys Asp Ser Gly Leu Asp Thr Val Ser	
150 155 160	
GTA ACC GAT TGC CAT ATT GTT TTA GGC TAT TTG AAC CCG GAT AAT TTC	584
Val Thr Asp Cys His Ile Val Leu Gly Tyr Leu Asn Pro Asp Asn Phe	
165 170 175	
TTA GGC GGT TTG ATC AAA TTA GAT GTG GAT AGG GCT AAA AAA CAC ATT	632
Leu Gly Gly Leu Ile Lys Leu Asp Val Asp Arg Ala Lys Lys His Ile	
180 185 190	
AAA GAA CAA ATC GCT GAT CCG CTA GGC ATT AGC GTA GAA GAT GCG GCT	680
Lys Glu Gln Ile Ala Asp Pro Leu Gly Ile Ser Val Glu Asp Ala Ala	
195 200 205 210	
GCT GGT GTG ATT GAA TTG CTT GAT TTG GAG CTT AAA GAA TAC TTG CGA	728
Ala Gly Val Ile Glu Leu Leu Asp Leu Glu Leu Lys Glu Tyr Leu Arg	
215 220 225	
TCC AAC ATT AGC GCT AAA GGG TAT AGC CCA TCT GAT TTT GTG TGC TTT	776
Ser Asn Ile Ser Ala Lys Gly Tyr Ser Pro Ser Asp Phe Val Cys Phe	
230 235 240	
TCA TAT GGT GGC GCA GGA CCT GTG CAT ACC TAT GGC TAT ACA GAA GGA	824
Ser Tyr Gly Gly Ala Gly Pro Val His Thr Tyr Gly Tyr Thr Glu Gly	
245 250 255	
TTA GGG TTT AAG GAT GTG GTA GTG CCT GCG TGG GCG GCT GGA TTT AGC	872
Leu Gly Phe Lys Asp Val Val Val Pro Ala Trp Ala Ala Gly Phe Ser	
260 265 270	
GCT TTT GGT TGT GCT TGC GCT GAT TTT GAA TAC AGA TAC GAC AAG AGC	920
Ala Phe Gly Cys Ala Cys Ala Asp Phe Glu Tyr Arg Tyr Asp Lys Ser	
275 280 285 290	
GTG GAT ATT GCC ATT CCG CAG TAT TCT TCA GAC AAG TCA AAA ATA GAC	968
Val Asp Ile Ala Ile Pro Gln Tyr Ser Ser Asp Lys Ser Lys Ile Asp	
295 300 305	
GCA TGC AAA ATC ATT CAA GAC GCA TGG GAT GAA TTG ACT TTG AAA GTG	1016
Ala Cys Lys Ile Ile Gln Asp Ala Trp Asp Glu Leu Thr Leu Lys Val	
310 315 320	
ATT GAA GAG TTC AAG ATC AAT GGA TTT TCT CAA AAA GAT GTG ATC TTA	1064
Ile Glu Glu Phe Lys Ile Asn Gly Phe Ser Gln Lys Asp Val Ile Leu	

325	330	335	
AGA CCT GGA TAC AGG ATG CAG TAT ATG GGG CAA TTG AAT GAT TTA GAG			1112
Arg Pro Gly Tyr Arg Met Gln Tyr Met Gly Gln Leu Asn Asp Leu Glu			
340	345	350	
ATC ACT TCT CCT GTG TCA AAA GCT GCA AGC GTG GCT GAT TGG GAA GAG			1160
Ile Thr Ser Pro Val Ser Lys Ala Ala Ser Val Ala Asp Trp Glu Glu			
355	360	365	370
ATT GTC AAA GAA TAT GAA AAA ACC TAC GCT CGC GTT TAT TCT GAA TCA			1208
Ile Val Lys Glu Tyr Glu Lys Thr Tyr Ala Arg Val Tyr Ser Glu Ser			
	375	380	385
GCG TGT TCT CCA GAG CTT GGT TTT AGC GTG ACT GGC GTG ATC ATG CGT			1256
Ala Cys Ser Pro Glu Leu Gly Phe Ser Val Thr Gly Val Ile Met Arg			
	390	395	400
GGT GTT GTG GCT ACG CAA AAA CCT GTG ATT CCG GTT GAA AAA GAG CAT			1304
Gly Val Val Ala Thr Gln Lys Pro Val Ile Pro Val Glu Lys Glu His			
	405	410	415
GGT GCT ACG CCC CCA AAA GAA GCC AAA ATA GGC GTT AGA AAA TTC TAT			1352
Gly Ala Thr Pro Pro Lys Glu Ala Lys Ile Gly Val Arg Lys Phe Tyr			
	420	425	430
CGG CAT AAA AAA TGG GTG GAT GCA GAT GTG TGG CAA ATG GAA AAA TTA			1400
Arg His Lys Lys Trp Val Asp Ala Asp Val Trp Gln Met Glu Lys Leu			
	435	440	445
CTG CCT GGA AAT GAA GTC ATA GGA CCT GCG ATC GTG GAA TCA GAT GCG			1448
Leu Pro Gly Asn Glu Val Ile Gly Pro Ala Ile Val Glu Ser Asp Ala			
	455	460	465
ACC ACT TTC GTG ATA CCC AAA GGC TTT GCG ACA AGA CTA GAC AAA CAC			1496
Thr Thr Phe Val Ile Pro Lys Gly Phe Ala Thr Arg Leu Asp Lys His			
	470	475	480
CGA TTG TTC CAC TTG AAA GAA ATT AAA TAAAGGAGTT CAAAATGGCA AATTTAT			1550
Arg Leu Phe His Leu Lys Glu Ile Lys			
	485	490	
TGAAAAACGG CAAAACCTTTA AAACAA			1576

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Met Asn Thr Thr Ile Leu Glu Ala Tyr Ala Ala Glu Pro Ser Arg Gln

1	5	10	15
Thr Leu Ser Lys Val Ser Asn Arg Phe Lys Glu His Gly Ala Lys Phe			
20	25	30	
Asp Leu Arg Val Met Ala Thr His Gly Gly Thr Ile Ser Trp Lys Ala			
35	40	45	
Lys Glu Leu Ala Arg Thr Ile Val Ser Gly Pro Ile Gly Gly Val Ile			
50	55	60	
Gly Ser Lys Leu Leu Gly Glu Thr Leu Gly Tyr Asp Asn Ile Ala Cys			
65	70	75	80
Ser Asp Ile Xaa Gly Thr Ser Phe Asp Met Ala Leu Ile Val Lys Ser			
85	90	95	
Asn Phe Asn Ile Ala Ser Asp Pro Asp Met Ala Arg Leu Val Leu Ser			
100	105	110	
Leu Pro Leu Val Ala Met Asp Ser Val Gly Ala Gly Ala Gly Ser Phe			
115	120	125	
Val Arg Ile Asp Pro His Ser Arg Ser Val Lys Leu Gly Pro Asp Ser			
130	135	140	
Ala Gly Tyr Arg Val Gly Thr Cys Trp Lys Asp Ser Gly Leu Asp Thr			
145	150	155	160
Val Ser Val Thr Asp Cys His Ile Val Leu Gly Tyr Leu Asn Pro Asp			
165	170	175	
Asn Phe Leu Gly Gly Leu Ile Lys Leu Asp Val Asp Arg Ala Lys Lys			
180	185	190	
His Ile Lys Glu Gln Ile Ala Asp Pro Leu Gly Ile Ser Val Glu Asp			
195	200	205	
Ala Ala Ala Gly Val Ile Glu Leu Leu Asp Leu Glu Leu Lys Glu Tyr			
210	215	220	
Leu Arg Ser Asn Ile Ser Ala Lys Gly Tyr Ser Pro Ser Asp Phe Val			
225	230	235	240
Cys Phe Ser Tyr Gly Gly Ala Gly Pro Val His Thr Tyr Gly Tyr Thr			
245	250	255	
Glu Gly Leu Gly Phe Lys Asp Val Val Val Pro Ala Trp Ala Ala Gly			
260	265	270	
Phe Ser Ala Phe Gly Cys Ala Cys Ala Asp Phe Glu Tyr Arg Tyr Asp			
275	280	285	
Lys Ser Val Asp Ile Ala Ile Pro Gln Tyr Ser Ser Asp Lys Ser Lys			
290	295	300	
Ile Asp Ala Cys Lys Ile Ile Gln Asp Ala Trp Asp Glu Leu Thr Leu			
305	310	315	320
Lys Val Ile Glu Glu Phe Lys Ile Asn Gly Phe Ser Gln Lys Asp Val			
325	330	335	
Ile Leu Arg Pro Gly Tyr Arg Met Gln Tyr Met Gly Gln Leu Asn Asp			
340	345	350	
Leu Glu Ile Thr Ser Pro Val Ser Lys Ala Ala Ser Val Ala Asp Trp			
355	360	365	
Glu Glu Ile Val Lys Glu Tyr Glu Lys Thr Tyr Ala Arg Val Tyr Ser			
370	375	380	
Glu Ser Ala Cys Ser Pro Glu Leu Gly Phe Ser Val Thr Gly Val Ile			
385	390	395	400
Met Arg Gly Val Val Ala Thr Gln Lys Pro Val Ile Pro Val Glu Lys			
405	410	415	
Glu His Gly Ala Thr Pro Pro Lys Glu Ala Lys Ile Gly Val Arg Lys			
420	425	430	
Phe Tyr Arg His Lys Lys Trp Val Asp Ala Asp Val Trp Gln Met Glu			
435	440	445	
Lys Leu Leu Pro Gly Asn Glu Val Ile Gly Pro Ala Ile Val Glu Ser			
450	455	460	
Asp Ala Thr Thr Phe Val Ile Pro Lys Gly Phe Ala Thr Arg Leu Asp			

465 470 475 480
Lys His Arg Leu Phe His Leu Lys Glu Ile Lys
 485 490

(2) INFORMATION FOR SEO ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 52...261
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GTAAGCTAGA	GTTTATGCAA	AGGGAGATGA	GTAGCCTAGA	AGCTAAGCAT	T ATG ATT		57
					Met Ile		
					1		
<hr/>							
CAG TTA AAA TCA AAT TTG GAT TGG TAC GCA GAT TAT TTG AAT TTT TTA							105
Gln Leu Lys Ser Asn Leu Asp Trp Tyr Ala Asp Tyr Leu Asn Phe Leu							
	5					10	15
<hr/>							
GAT CGC TTT GGG GAA AAA ATG GAA GAA TCC AAA GAG CGA AAA CAA CTC							153
Asp Arg Phe Gly Glu Lys Met Glu Glu Ser Lys Glu Arg Lys Gln Leu							
	20				25		30
<hr/>							
CTG ATC GCT TCC CTT GCA CCT CTT GCG GGC TTT GCT GCA AGA ATA TCG							201
Leu Ile Ala Ser Leu Ala Pro Leu Ala Gly Phe Ala Ala Arg Ile Ser							
	35			40		45	50
<hr/>							
CCG GGA TTA TTG AGC TTA TTG GGT TTG ATG CTG GCA ATG GGG TGT GCA							249
Pro Gly Leu Leu Ser Leu Leu Gly Leu Met Leu Ala Met Gly Cys Ala							
			55			60	65
<hr/>							
AAT TTT TGG ATT TAGAAACCAA TCTGTGCAAG ATTTATGAAT CGCGCCCGTT AA							303
Asn Phe Trp Ile							
			70				

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(v) FRAGMENT TYPE: internal
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Met	Ile	Gln	Leu	Lys	Ser	Asn	Leu	Asp	Trp	Tyr	Ala	Asp	Tyr	Leu	Asn
1				5					10					15	
Phe	Leu	Asp	Arg	Phe	Gly	Glu	Lys	Met	Glu	Glu	Ser	Lys	Glu	Arg	Lys
			20					25					30		
Gln	Leu	Leu	Ile	Ala	Ser	Leu	Ala	Pro	Leu	Ala	Gly	Phe	Ala	Ala	Arg
		35					40					45			
Ile	Ser	Pro	Gly	Leu	Leu	Ser	Leu	Leu	Gly	Leu	Met	Leu	Ala	Met	Gly
	50					55					60				
Cys	Ala	Asn	Phe	Trp	Ile										
65					70										

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...773
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

TGGCTTAATT GTTAAGCCGG CTAGAAAAAG AGCGTTATTT GCGCCATATC	ATG CTA	56
	Met Leu	
	1	
GAA GAT GTG GGC GAA GAG GGT CAA TTG AAG CTT TTA AAA TCT AGC GTT		104
Glu Asp Val Gly Glu Glu Gly Gln Leu Lys Leu Leu Lys Ser Ser Val		
5	10	15
TTA GTC ATT GGG GCT GGG GGT CTT GGA TCG GCG GTT TTG ATG TAT TTG		152
Leu Val Ile Gly Ala Gly Gly Leu Gly Ser Ala Val Leu Met Tyr Leu		
20	25	30
TGT GCC GCT GGG ATA GGA AAA ATC GGT ATT GTA GAT TTT GAT GTA GTA		200
Cys Ala Ala Gly Ile Gly Lys Ile Gly Ile Val Asp Phe Asp Val Val		
35	40	45
GAT ATG AGT AAT TTG CAA CGC CAA ATC ATC CAT TCA CAG GAT TTT TTA		248
Asp Met Ser Asn Leu Gln Arg Gln Ile Ile His Ser Gln Asp Phe Leu		
55	60	65
AAC CAA TCT AAA GCC TCT AGC GCG AAA GCG CGC TTA AAA CAA CTC AAT		296
Asn Gln Ser Lys Ala Ser Ser Ala Lys Ala Arg Leu Lys Gln Leu Asn		
70	75	80
GCG GGT ATT GAA ATA GAG GCT TTT GAA GAA CGC TTT AAG GCT CAT AAC		344
Ala Gly Ile Glu Ile Glu Ala Phe Glu Glu Arg Phe Lys Ala His Asn		
85	90	95

GCT CTT TCT CTC ATA GAG CCT TAT GAT TTT ATC ATA GAC GCC ACG GAC	392
Ala Leu Ser Leu Ile Glu Pro Tyr Asp Phe Ile Ile Asp Ala Thr Asp	
100 105 110	
AAT TTT AAC GCT AAA TTT TTG ATC AAT GAC GCT TGC GTG TTA GCC CAA	440
Asn Phe Asn Ala Lys Phe Leu Ile Asn Asp Ala Cys Val Leu Ala Gln	
115 120 125 130	
AAA CCC TAT TCG CAT GCC GGG GTT TTA GAA TAC AGG GGG CAA AGC ATG	488
Lys Pro Tyr Ser His Ala Gly Val Leu Glu Tyr Arg Gly Gln Ser Met	
135 140 145	
AGC GTT TTA CCC CAT AGC GCA TGC TTA GCG TGC GTT TTT GAT AAG CCC	536
Ser Val Leu Pro His Ser Ala Cys Leu Ala Cys Val Phe Asp Lys Pro	
150 155 160	
CCT AAA AAG GGA TTA AAT CCC ATT TCA GGG CTT TTT GGG GTC TTA CCC	584
Pro Lys Lys Gly Leu Asn Pro Ile Ser Gly Leu Phe Gly Val Leu Pro	
165 170 175	
GGA GTT TTA GGG TGT ATC CAA GCG AGC GAA TGC CTT AAA TAT TTT TTA	632
Gly Val Leu Gly Cys Ile Gln Ala Ser Glu Cys Leu Lys Tyr Phe Leu	
180 185 190	
GGG TTT GAA ACT TTA CTT ATA AAT ACT TTA CTT ATA GCC GAT ATT AAA	680
Gly Phe Glu Thr Leu Leu Ile Asn Thr Leu Leu Ile Ala Asp Ile Lys	
195 200 205 210	
ACG ATG GAT TTT AAA AAA ATT CAA GCA CCC AAA AAC CCT GAA TGT AGG	728
Thr Met Asp Phe Lys Lys Ile Gln Ala Pro Lys Asn Pro Glu Cys Arg	
215 220 225	
GTT TGT GGC ACG CAT AAA ATC ACG CAT TTA CAG GAT TAT GAA ATT TAGAT	778
Val Cys Gly Thr His Lys Ile Thr His Leu Gln Asp Tyr Glu Ile	
230 235 240	
TAAGGGGTAA GTTTTGGATT TATCAACCAT ATTAGGCTTG GTATTGGC	826

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Met Leu Glu Asp Val Gly Glu Glu Gly Gln Leu Lys Leu Leu Lys Ser	
1 5 10 15	
Ser Val Leu Val Ile Gly Ala Gly Gly Leu Gly Ser Ala Val Leu Met	
20 25 30	
Tyr Leu Cys Ala Ala Gly Ile Gly Lys Ile Gly Ile Val Asp Phe Asp	
35 40 45	
Val Val Asp Met Ser Asn Leu Gln Arg Gln Ile Ile His Ser Gln Asp	

50		55		60											
Phe	Leu	Asn	Gln	Ser	Lys	Ala	Ser	Ser	Ala	Lys	Ala	Arg	Leu	Lys	Gln
65		70		75		80									
Leu	Asn	Ala	Gly	Ile	Glu	Ile	Glu	Ala	Phe	Glu	Glu	Arg	Phe	Lys	Ala
		85		90		95									
His	Asn	Ala	Leu	Ser	Leu	Ile	Glu	Pro	Tyr	Asp	Phe	Ile	Ile	Asp	Ala
		100		105		110									
Thr	Asp	Asn	Phe	Asn	Ala	Lys	Phe	Leu	Ile	Asn	Asp	Ala	Cys	Val	Leu
		115		120		125									
Ala	Gln	Lys	Pro	Tyr	Ser	His	Ala	Gly	Val	Leu	Glu	Tyr	Arg	Gly	Gln
		130		135		140									
Ser	Met	Ser	Val	Leu	Pro	His	Ser	Ala	Cys	Leu	Ala	Cys	Val	Phe	Asp
145				150		155									
Lys	Pro	Pro	Lys	Lys	Gly	Leu	Asn	Pro	Ile	Ser	Gly	Leu	Phe	Gly	Val
				165		170									
Leu	Pro	Gly	Val	Leu	Gly	Cys	Ile	Gln	Ala	Ser	Glu	Cys	Leu	Lys	Tyr
				180		185									
Phe	Leu	Gly	Phe	Glu	Thr	Leu	Leu	Ile	Asn	Thr	Leu	Leu	Ile	Ala	Asp
		195		200		205									
Ile	Lys	Thr	Met	Asp	Phe	Lys	Lys	Ile	Gln	Ala	Pro	Lys	Asn	Pro	Glu
		210		215		220									
Cys	Arg	Val	Cys	Gly	Thr	His	Lys	Ile	Thr	His	Leu	Gln	Asp	Tyr	Glu
225				230		235									
Ile															

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...494
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

AAAATTCATT CTATTTTAGA TAATGAGTTC AATCCCCACA AACAGCAAGA ATG AAT	56
Met Asn	
1	
CGC ATG AAT AAA AAT TAT CTT TTA ATC TTT TTG TTG TTA GCG AGT CTT	104
Arg Met Asn Lys Asn Tyr Leu Leu Ile Phe Leu Leu Leu Ala Ser Leu	
5 10 15	
GTT GCT AGA GAG AAG GAC GCT TCT TCA AAC CTT TTT GAT TTG ATT GAT	152
Val Ala Arg Glu Lys Asp Ala Ser Ser Asn Leu Phe Asp Leu Ile Asp	
20 25 30	
AAG GGG ATC AAC AGA GAA CAA GAA TTA AAA GAG CAG GAG CAA AAA ACG	200

Lys	Gly	Ile	Asn	Arg	Glu	Gln	Glu	Leu	Lys	Glu	Gln	Glu	Gln	Lys	Thr		
35					40					45					50		
CGC	TTA	AAA	CTG	GCT	CAA	AGC	CCT	TTA	GTA	GCG	TTA	GAG	ATT	GTC	CCC	248	
Arg	Leu	Lys	Leu	Ala	Gln	Ser	Pro	Leu	Val	Ala	Leu	Glu	Ile	Val	Pro		
			55						60					65			
CAA	GAA	ACG	CCC	TAT	TTA	GAA	TGG	CAA	GGG	GCT	AGG	GAG	TCG	TAT	TAT	296	
Gln	Glu	Thr	Pro	Tyr	Leu	Glu	Trp	Gln	Gly	Ala	Arg	Glu	Ser	Tyr	Tyr		
			70					75					80				
TTA	AAG	GTG	AGC	GCT	GTA	GTG	GAG	AGC	GTG	GTT	ATC	TTA	AAA	ATT	GAC	344	
Leu	Lys	Val	Ser	Ala	Val	Val	Glu	Ser	Val	Val	Ile	Leu	Lys	Ile	Asp		
		85					90					95					
ATC	AAT	CAA	GGG	CGT	TCT	TGC	TCG	CTC	TAC	CCC	ACG	CCT	AAA	AGC	GTT	392	
Ile	Asn	Gln	Gly	Arg	Ser	Cys	Ser	Leu	Tyr	Pro	Thr	Pro	Lys	Ser	Val		
	100					105						110					
TCT	TTA	GTG	AGG	AAT	CAA	AGC	GTA	GCC	TAT	GAA	ATT	TTA	TGC	GAA	AAC	440	
Ser	Leu	Val	Arg	Asn	Gln	Ser	Val	Ala	Tyr	Glu	Ile	Leu	Cys	Glu	Asn		
115					120					125					130		
CAA	CCC	CTA	TGG	ATA	GAA	GTA	AGC	ACC	AAT	TTA	GGC	AAA	CGC	ACC	TTT	488	
Gln	Pro	Leu	Trp	Ile	Glu	Val	Ser	Thr	Asn	Leu	Gly	Lys	Arg	Thr	Phe		
				135					140					145			
CAG	TTT	TAACCTGCAA	CCAACATTAA	AGAATGCCTT	TAGCATTTTA	AAACCCCTTT	AT	546									
Gln	Phe																
C																547	

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met	Asn	Arg	Met	Asn	Lys	Asn	Tyr	Leu	Leu	Ile	Phe	Leu	Leu	Leu	Ala		
1				5				10						15			
Ser	Leu	Val	Ala	Arg	Glu	Lys	Asp	Ala	Ser	Ser	Asn	Leu	Phe	Asp	Leu		
			20					25					30				
Ile	Asp	Lys	Gly	Ile	Asn	Arg	Glu	Gln	Glu	Leu	Lys	Glu	Gln	Glu	Gln		
		35					40					45					
Lys	Thr	Arg	Leu	Lys	Leu	Ala	Gln	Ser	Pro	Leu	Val	Ala	Leu	Glu	Ile		
	50				55					60							
Val	Pro	Gln	Glu	Thr	Pro	Tyr	Leu	Glu	Trp	Gln	Gly	Ala	Arg	Glu	Ser		
65					70					75				80			
Tyr	Tyr	Leu	Lys	Val	Ser	Ala	Val	Val	Glu	Ser	Val	Val	Ile	Leu	Lys		
				85					90					95			
Ile	Asp	Ile	Asn	Gln	Gly	Arg	Ser	Cys	Ser	Leu	Tyr	Pro	Thr	Pro	Lys		

		100						105						110					
Ser	Val	Ser	Leu	Val	Arg	Asn	Gln	Ser	Val	Ala	Tyr	Glu	Ile	Leu	Cys				
		115					120					125							
Glu	Asn	Gln	Pro	Leu	Trp	Ile	Glu	Val	Ser	Thr	Asn	Leu	Gly	Lys	Arg				
	130					135					140								
Thr	Phe	Gln	Phe																
145																			

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1684 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1631
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

CCTTTCTTTA TTCTCATTCG ATCTTGTTGG ATCATTTTTT TTTTTTATTA ATG CTA	56
Met Leu	
1	
GCT TCC ATC ATC TCA ATT TTA AGG GTT TTT GTT TTG TTA TTC AAC ACG	104
Ala Ser Ile Ile Ser Ile Leu Arg Val Phe Val Leu Leu Phe Asn Thr	
5 10 15	
CCG TTA TTC ATC TTT GCT TTT TTG CCT GTT GGT TTT TTA GGG TAT TTT	152
Pro Leu Phe Ile Phe Ala Phe Leu Pro Val Gly Phe Leu Gly Tyr Phe	
20 25 30	
ATC TTG CAA GCT TAT GCT AAA AAT CCC CTG TTC CCT AAA CTA TGG CTA	200
Ile Leu Gln Ala Tyr Ala Lys Asn Pro Leu Phe Pro Lys Leu Trp Leu	
35 40 45 50	
GTA TTG GCT AGT TTG TTT TTT TAT GCT TTT TGG AAT GTG AAG TAT TTG	248
Val Leu Ala Ser Leu Phe Phe Tyr Ala Phe Trp Asn Val Lys Tyr Leu	
55 60 65	
CCC TTA TTG GTT GGC TCT ATT GTT TTT AAT TAT TTT GTG GCT TTG AAA	296
Pro Leu Leu Val Gly Ser Ile Val Phe Asn Tyr Phe Val Ala Leu Lys	
70 75 80	
ATC CAT CAA ACC CAG CCA AAT GCA TAT AAA AGA TTA TGG CTT ATT TTG	344
Ile His Gln Thr Gln Pro Asn Ala Tyr Lys Arg Leu Trp Leu Ile Leu	
85 90 95	
GGC TTG ATC GCT AAT GTT TCA CTT TTA GGA TTT TTC AAA TAC ACT GAT	392
Gly Leu Ile Ala Asn Val Ser Leu Leu Gly Phe Phe Lys Tyr Thr Asp	
100 105 110	

TTT	TTC	TTA	ACC	AAT	TTC	AAT	CTA	ATA	TGG	AAG	AGC	CAT	TTT	GAA	ACC	440
Phe	Phe	Leu	Thr	Asn	Phe	Asn	Leu	Ile	Trp	Lys	Ser	His	Phe	Glu	Thr	
115					120					125					130	
TTG	CAT	TTA	ATC	TTG	CCT	TTA	GCG	ATC	AGC	TTT	TTC	ACT	TTG	CAA	CAA	488
Leu	His	Leu	Ile	Leu	Pro	Leu	Ala	Ile	Ser	Phe	Phe	Thr	Leu	Gln	Gln	
				135					140					145		
ATC	GCT	TAC	TTG	ATG	GAC	ACT	TAT	AAG	CAA	AAT	CAA	ATC	ATG	CAG	CCC	536
Ile	Ala	Tyr	Leu	Met	Asp	Thr	Tyr	Lys	Gln	Asn	Gln	Ile	Met	Gln	Pro	
			150					155					160			
AAA	ATG	AGA	GAG	AGA	GTG	AGT	GAA	AAC	GCT	CCT	ATT	TTA	TTA	AAT	CCT	584
Lys	Met	Arg	Glu	Arg	Val	Ser	Glu	Asn	Ala	Pro	Ile	Leu	Leu	Asn	Pro	
		165					170					175				
CCC	ACT	TCA	TTT	TTT	TCA	CTT	TCG	CAT	TTT	TTA	GAT	TAC	GCT	TTA	TTT	632
Pro	Thr	Ser	Phe	Phe	Ser	Leu	Ser	His	Phe	Leu	Asp	Tyr	Ala	Leu	Phe	
	180					185					190					
GTG	AGT	TTC	TTC	CCT	CAA	CTC	ATT	GCA	GGG	CCT	ATT	GTG	CAT	CAT	AGC	680
Val	Ser	Phe	Phe	Pro	Gln	Leu	Ile	Ala	Gly	Pro	Ile	Val	His	His	Ser	
195				200					205						210	
GAG	ATG	ATG	CCT	CAA	TTT	AAA	GAT	AAA	AAC	AAT	CAA	TAT	TTG	AAT	TAC	728
Glu	Met	Met	Pro	Gln	Phe	Lys	Asp	Lys	Asn	Asn	Gln	Tyr	Leu	Asn	Tyr	
			215					220					225			
AGA	AAT	ATC	GCT	TTA	GGC	TTG	TTT	ATC	TTT	TCT	ATC	GGT	TTG	TTT	AAA	776
Arg	Asn	Ile	Ala	Leu	Gly	Leu	Phe	Ile	Phe	Ser	Ile	Gly	Leu	Phe	Lys	
			230					235					240			
AAG	GTC	GTG	ATT	GCA	GAT	AAT	ACC	GCT	CAT	TTT	GCT	GAT	TTT	GGA	TTT	824
Lys	Val	Val	Ile	Ala	Asp	Asn	Thr	Ala	His	Phe	Ala	Asp	Phe	Gly	Phe	
		245				250					255					
GAT	AAG	GCG	ACT	AGC	TTA	AGT	TTT	ATT	CAA	GCA	TGG	ATG	ACT	TCT	TTA	872
Asp	Lys	Ala	Thr	Ser	Leu	Ser	Phe	Ile	Gln	Ala	Trp	Met	Thr	Ser	Leu	
	260					265					270					
TCT	TAT	TCG	TTC	CAG	CTG	TAT	TTT	GAT	TTT	AGC	GGT	TAT	TGC	GAT	ATG	920
Ser	Tyr	Ser	Phe	Gln	Leu	Tyr	Phe	Asp	Phe	Ser	Gly	Tyr	Cys	Asp	Met	
275					280					285					290	
GCT	ATA	GGC	ATT	GGC	CTC	TTT	TTT	AAC	ATC	AAA	CTC	CCT	ATC	AAT	TTT	968
Ala	Ile	Gly	Ile	Gly	Leu	Phe	Phe	Asn	Ile	Lys	Leu	Pro	Ile	Asn	Phe	
				295				300						305		
AAT	AGC	CCC	TAT	AAG	GCT	TTG	AAT	ATC	CAA	GAT	TTT	TGG	AGG	AGG	TGG	1016
Asn	Ser	Pro	Tyr	Lys	Ala	Leu	Asn	Ile	Gln	Asp	Phe	Trp	Arg	Arg	Trp	
		310						315				320				
CAT	ATC	ACT	TTG	AGC	CGC	TTC	TTA	AAA	GAG	TAT	TTG	TAT	ATC	CCT	TTA	1064
His	Ile	Thr	Leu	Ser	Arg	Phe	Leu	Lys	Glu	Tyr	Leu	Tyr	Ile	Pro	Leu	
		325					330					335				
GGG	GGT	AAT	AGG	GTG	AAA	GAA	TTA	ATC	GTG	TAT	AGG	AAT	TTA	ATT	TTA	1112
Gly	Gly	Asn	Arg	Val	Lys	Glu	Leu	Ile	Val	Tyr	Arg	Asn	Leu	Ile	Leu	

340	345	350	
GTG TTT TTG ATT GGG GGG TTT TGG CAT GGG GCT GGT TGG ACT TTT ATC			1160
Val Phe Leu Ile Gly Gly Phe Trp His Gly Ala Gly Trp Thr Phe Ile			
355	360	365 370	
ATT TGG GGG CTA TTG CAT GGG ATT GCT TTG AGC GTT CAT AGA GCG TAT			1208
Ile Trp Gly Leu Leu His Gly Ile Ala Leu Ser Val His Arg Ala Tyr			
	375	380 385	
TCT CAT GCC ACT AGA AAA TTC CAT TTC ACT ATG CCA AAG ATT TTA GCA			1256
Ser His Ala Thr Arg Lys Phe His Phe Thr Met Pro Lys Ile Leu Ala			
	390	395 400	
TGG CTC ATC ACT TTT AAT TTT ATC AAT CTC GCA TGG GTG TTT TTT AGA			1304
Trp Leu Ile Thr Phe Asn Phe Ile Asn Leu Ala Trp Val Phe Phe Arg			
	405	410 415	
GCC AAA AAT TTA GAA AGC GCT TTG AAG GTT TTA AAG GGG ATG GTT GGT			1352
Ala Lys Asn Leu Glu Ser Ala Leu Lys Val Leu Lys Gly Met Val Gly			
	420	425 430	
TTG AAT GGT GTT TCG CTT TGT CAT CTT TCA AAA GAG GCA TCA GAG TTT			1400
Leu Asn Gly Val Ser Leu Cys His Leu Ser Lys Glu Ala Ser Glu Phe			
	435	440 445 450	
TTA AAT CGT GTC AAT GAT AAC ATG ATC ATG CAC ACC ATA ATG TAT GCA			1448
Leu Asn Arg Val Asn Asp Asn Met Ile Met His Thr Ile Met Tyr Ala			
	455	460 465	
TCC CCC ACA TTT AAA ATG TGT GTT TTG ATG ATA ATC ATC TCT TTT TGT			1496
Ser Pro Thr Phe Lys Met Cys Val Leu Met Ile Ile Ile Ser Phe Cys			
	470	475 480	
TTA AAA AAT AGT TCC CAT TTA TAC CAA TCC AAT CAA ATG GAT TGG ATT			1544
Leu Lys Asn Ser Ser His Leu Tyr Gln Ser Asn Gln Met Asp Trp Ile			
	485	490 495	
AAA ACA ACA AGC GCT TGT TTG TTG CTC TCT ATA GGT TTT TTA TTT ATT			1592
Lys Thr Thr Ser Ala Cys Leu Leu Leu Ser Ile Gly Phe Leu Phe Ile			
	500	505 510	
TTT GCC AGT TCT CAA TCG GTA TTT TTG TAT TTT AAT TTT TAGGACACTG CT			1643
Phe Ala Ser Ser Gln Ser Val Phe Leu Tyr Phe Asn Phe			
	515	520 525	
ATGGAATTTT ATAAAAACA AACTTTAATC ATTGTTTCTT T			1684

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met	Leu	Ala	Ser	Ile	Ile	Ser	Ile	Leu	Arg	Val	Phe	Val	Leu	Leu	Phe
1				5					10					15	
Asn	Thr	Pro	Leu	Phe	Ile	Phe	Ala	Phe	Leu	Pro	Val	Gly	Phe	Leu	Gly
			20					25					30		
Tyr	Phe	Ile	Leu	Gln	Ala	Tyr	Ala	Lys	Asn	Pro	Leu	Phe	Pro	Lys	Leu
		35					40					45			
Trp	Leu	Val	Leu	Ala	Ser	Leu	Phe	Phe	Tyr	Ala	Phe	Trp	Asn	Val	Lys
	50					55					60				
Tyr	Leu	Pro	Leu	Leu	Val	Gly	Ser	Ile	Val	Phe	Asn	Tyr	Phe	Val	Ala
65					70					75					80
Leu	Lys	Ile	His	Gln	Thr	Gln	Pro	Asn	Ala	Tyr	Lys	Arg	Leu	Trp	Leu
				85					90					95	
Ile	Leu	Gly	Leu	Ile	Ala	Asn	Val	Ser	Leu	Leu	Gly	Phe	Phe	Lys	Tyr
			100						105					110	
Thr	Asp	Phe	Phe	Leu	Thr	Asn	Phe	Asn	Leu	Ile	Trp	Lys	Ser	His	Phe
		115					120					125			
Glu	Thr	Leu	His	Leu	Ile	Leu	Pro	Leu	Ala	Ile	Ser	Phe	Phe	Thr	Leu
	130					135						140			
Gln	Gln	Ile	Ala	Tyr	Leu	Met	Asp	Thr	Tyr	Lys	Gln	Asn	Gln	Ile	Met
145					150					155					160
Gln	Pro	Lys	Met	Arg	Glu	Arg	Val	Ser	Glu	Asn	Ala	Pro	Ile	Leu	Leu
				165					170					175	
Asn	Pro	Pro	Thr	Ser	Phe	Phe	Ser	Leu	Ser	His	Phe	Leu	Asp	Tyr	Ala
			180					185					190		
Leu	Phe	Val	Ser	Phe	Phe	Pro	Gln	Leu	Ile	Ala	Gly	Pro	Ile	Val	His
		195					200					205			
His	Ser	Glu	Met	Met	Pro	Gln	Phe	Lys	Asp	Lys	Asn	Asn	Gln	Tyr	Leu
	210					215					220				
Asn	Tyr	Arg	Asn	Ile	Ala	Leu	Gly	Leu	Phe	Ile	Phe	Ser	Ile	Gly	Leu
225				230					235						240
Phe	Lys	Lys	Val	Val	Ile	Ala	Asp	Asn	Thr	Ala	His	Phe	Ala	Asp	Phe
				245					250					255	
Gly	Phe	Asp	Lys	Ala	Thr	Ser	Leu	Ser	Phe	Ile	Gln	Ala	Trp	Met	Thr
			260					265					270		
Ser	Leu	Ser	Tyr	Ser	Phe	Gln	Leu	Tyr	Phe	Asp	Phe	Ser	Gly	Tyr	Cys
		275					280					285			
Asp	Met	Ala	Ile	Gly	Ile	Gly	Leu	Phe	Phe	Asn	Ile	Lys	Leu	Pro	Ile
	290					295					300				
Asn	Phe	Asn	Ser	Pro	Tyr	Lys	Ala	Leu	Asn	Ile	Gln	Asp	Phe	Trp	Arg
305				310					315						320
Arg	Trp	His	Ile	Thr	Leu	Ser	Arg	Phe	Leu	Lys	Glu	Tyr	Leu	Tyr	Ile
			325						330					335	
Pro	Leu	Gly	Gly	Asn	Arg	Val	Lys	Glu	Leu	Ile	Val	Tyr	Arg	Asn	Leu
			340					345					350		
Ile	Leu	Val	Phe	Leu	Ile	Gly	Gly	Phe	Trp	His	Gly	Ala	Gly	Trp	Thr
		355					360					365			
Phe	Ile	Ile	Trp	Gly	Leu	Leu	His	Gly	Ile	Ala	Leu	Ser	Val	His	Arg
	370					375					380				
Ala	Tyr	Ser	His	Ala	Thr	Arg	Lys	Phe	His	Phe	Thr	Met	Pro	Lys	Ile
385					390				395						400
Leu	Ala	Trp	Leu	Ile	Thr	Phe	Asn	Phe	Ile	Asn	Leu	Ala	Trp	Val	Phe
				405					410					415	
Phe	Arg	Ala	Lys	Asn	Leu	Glu	Ser	Ala	Leu	Lys	Val	Leu	Lys	Gly	Met
			420					425				430			
Val	Gly	Leu	Asn	Gly	Val	Ser	Leu	Cys	His	Leu	Ser	Lys	Glu	Ala	Ser
		435					440					445			

Glu Phe Leu Asn Arg Val Asn Asp Asn Met Ile Met His Thr Ile Met
 450 455 460
 Tyr Ala Ser Pro Thr Phe Lys Met Cys Val Leu Met Ile Ile Ile Ser
 465 470 475 480
 Phe Cys Leu Lys Asn Ser Ser His Leu Tyr Gln Ser Asn Gln Met Asp
 485 490 495
 Trp Ile Lys Thr Ser Ala Cys Leu Leu Ser Ile Gly Phe Leu
 500 505 510
 Phe Ile Phe Ala Ser Ser Gln Ser Val Phe Leu Tyr Phe Asn Phe
 515 520 525

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3973 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic RNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...3920
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

AAAGTCGCAC CCTTTGTGCA AAAATCGTTT TACAAGAAGA AAGGAAAAAA ATG GAA	56
Met Glu	
1	
ATA CAA CAA ACA CAC CGC AAA ATC AAT CGC CCT TTG GTT TCT CTC GCT	104
Ile Gln Gln Thr His Arg Lys Ile Asn Arg Pro Leu Val Ser Leu Ala	
5 10 15	
TTA GTA GGA GCG TTA GTC AGC ATC ACA CCG CAA CAA AGT CAT GCC GCC	152
Leu Val Gly Ala Leu Val Ser Ile Thr Pro Gln Gln Ser His Ala Ala	
20 25 30	
TTT TTC ACA ACC GTG ATC ATT CCA GCC ATT GTT GGG GGG ATT GCT ACA	200
Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile Ala Thr	
35 40 45 50	
GGC GCT GCT GTA GGA ACG GTC TCA GGG CTT CTT GGC TGG GGG CTA AAA	248
Gly Ala Ala Val Gly Thr Val Ser Gly Leu Leu Gly Trp Gly Leu Lys	
55 60 65	
CAA GCC GAA GAA GCC AAT AAA ACC CCA GAT AAA CCC GAT AAA GTT TGG	296
Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys Val Trp	
70 75 80	
CGC ATT CAA GCA GGA AAA GGC TTT AAT GAA TTC CCT AAC AAG GAA TAC	344
Arg Ile Gln Ala Gly Lys Gly Phe Asn Glu Phe Pro Asn Lys Glu Tyr	
85 90 95	

GAC	TTA	TAC	AGA	TCC	CTA	CTA	TCT	AGT	AAG	ATT	GAT	GGA	GGC	TGG	GAT	392
Asp	Leu	Tyr	Arg	Ser	Leu	Leu	Ser	Ser	Lys	Ile	Asp	Gly	Gly	Trp	Asp	
100						105					110					
TGG	GGG	AAT	GCC	GCT	ACG	CAT	TAT	TGG	GTC	AAA	GGC	GGG	CAA	TGG	AAC	440
Trp	Gly	Asn	Ala	Ala	Thr	His	Tyr	Trp	Val	Lys	Gly	Gly	Gln	Trp	Asn	
115					120					125					130	
AAG	CTT	GAA	GTG	GAT	ATG	AAA	GAC	GCT	GTA	GGG	ACT	TAT	AAT	CTC	TCA	488
Lys	Leu	Glu	Val	Asp	Met	Lys	Asp	Ala	Val	Gly	Thr	Tyr	Asn	Leu	Ser	
				135					140					145		
GGG	CTA	AGA	AAC	TTT	ACT	GGT	GGG	GAT	TTA	GAT	GTC	AAT	ATG	CAA	AAA	536
Gly	Leu	Arg	Asn	Phe	Thr	Gly	Gly	Asp	Leu	Asp	Val	Asn	Met	Gln	Lys	
			150					155					160			
GCC	ACT	TTG	CGC	TTG	GGC	CAA	TTC	AAT	GGC	AAT	TCT	TTC	ACA	AGC	TAT	584
Ala	Thr	Leu	Arg	Leu	Gly	Gln	Phe	Asn	Gly	Asn	Ser	Phe	Thr	Ser	Tyr	
		165					170					175				
AAG	GAT	AGC	GCT	GAT	CGC	ACC	ACG	AGA	GTG	GAT	TTC	AAC	GCT	AAA	AAT	632
Lys	Asp	Ser	Ala	Asp	Arg	Thr	Thr	Arg	Val	Asp	Phe	Asn	Ala	Lys	Asn	
	180					185					190					
ATC	TTA	ATT	GAT	AAT	TTT	TTA	GAA	ATC	AAT	AAT	CGT	GTG	GGT	TCT	GGA	680
Ile	Leu	Ile	Asp	Asn	Phe	Leu	Glu	Ile	Asn	Asn	Arg	Val	Gly	Ser	Gly	
195					200					205					210	
GCC	GGG	AGG	AAA	GCC	AGC	TCT	ACG	GTT	TTA	ACT	TTG	CAA	GCT	TCA	GAA	728
Ala	Gly	Arg	Lys	Ala	Ser	Ser	Thr	Val	Leu	Thr	Leu	Gln	Ala	Ser	Glu	
				215					220					225		
GGG	ATT	ACT	AGC	AGT	AAA	AAT	GCG	GAA	ATT	TCT	CTT	TAT	GAT	GGC	GCC	776
Gly	Ile	Thr	Ser	Ser	Lys	Asn	Ala	Glu	Ile	Ser	Leu	Tyr	Asp	Gly	Ala	
			230					235					240			
ACG	CTC	AAT	TTG	GCT	TCA	AAC	AGC	GTT	AAA	TTA	ATG	GGT	AAT	GTG	TGG	824
Thr	Leu	Asn	Leu	Ala	Ser	Asn	Ser	Val	Lys	Leu	Met	Gly	Asn	Val	Trp	
		245					250					255				
ATG	GGC	CGT	TTG	CAA	TAT	GTG	GGA	GCG	TAT	TTG	GCC	CCT	TCA	TAC	AGC	872
Met	Gly	Arg	Leu	Gln	Tyr	Val	Gly	Ala	Tyr	Leu	Ala	Pro	Ser	Tyr	Ser	
	260					265					270					
ACG	ATA	AAC	ACT	TCA	AAA	GTG	ACA	GGG	GAA	GTG	AAT	TTT	AAC	CAT	CTC	920
Thr	Ile	Asn	Thr	Ser	Lys	Val	Thr	Gly	Glu	Val	Asn	Phe	Asn	His	Leu	
275					280					285					290	
ACT	GTG	GGC	GAT	CAC	AAC	GCC	GCT	CAA	GCA	GGC	ATT	ATC	GCT	AGT	AAC	968
Thr	Val	Gly	Asp	His	Asn	Ala	Ala	Gln	Ala	Gly	Ile	Ile	Ala	Ser	Asn	
				295				300					305			
AAG	ACT	CAT	ATT	GGC	ACA	CTG	GAT	TTG	TGG	CAA	AGC	GCG	GGA	CTA	AAC	1016
Lys	Thr	His	Ile	Gly	Thr	Leu	Asp	Leu	Trp	Gln	Ser	Ala	Gly	Leu	Asn	
			310					315					320			
ATT	ATC	GCC	CCT	CCA	GAA	GGC	GGT	TAT	AAG	GAT	AAA	CCT	AAG	GAT	AAA	1064
Ile	Ile	Ala	Pro	Pro	Glu	Gly	Gly	Tyr	Lys	Asp	Lys	Pro	Lys	Asp	Lys	

325					330					335						
CCT	AGT	AAC	ACC	ACG	CAA	AAT	AAT	GCT	AAC	AAC	AAC	CAA	CAA	AAC	AGC	1112
Pro	Ser	Asn	Thr	Thr	Gln	Asn	Asn	Ala	Asn	Asn	Asn	Gln	Gln	Asn	Ser	
340					345					350						
GCT	CAA	AAC	AAT	AGT	AAC	ACT	CAG	GTT	ATT	AAC	CCA	CCC	AAT	AGC	GCG	1160
Ala	Gln	Asn	Asn	Ser	Asn	Thr	Gln	Val	Ile	Asn	Pro	Pro	Asn	Ser	Ala	
355					360					365					370	
CAA	AAA	ACA	GAA	ATT	CAA	CCC	ACG	CAA	GTC	ATT	GAT	GGG	CCT	TTT	GCT	1208
Gln	Lys	Thr	Glu	Ile	Gln	Pro	Thr	Gln	Val	Ile	Asp	Gly	Pro	Phe	Ala	
375					380					385						
GGT	GGC	AAA	GAC	ACG	GTT	GTC	AAT	ATT	GAT	CGC	ATC	AAC	ACT	AAC	GCT	1256
Gly	Gly	Lys	Asp	Thr	Val	Val	Asn	Ile	Asp	Arg	Ile	Asn	Thr	Asn	Ala	
390					395					400						
GAT	GGC	ACG	ATT	AAA	GTG	GGA	GGG	TAT	AAA	GCT	TCT	CTT	ACC	ACC	AAT	1304
Asp	Gly	Thr	Ile	Lys	Val	Gly	Gly	Tyr	Lys	Ala	Ser	Leu	Thr	Thr	Asn	
405					410					415						
GCG	GCT	CAT	TTG	CAT	ATC	GGC	AAA	GGC	GGT	ATC	AAT	CTG	TCC	AAT	CAA	1352
Ala	Ala	His	Leu	His	Ile	Gly	Lys	Gly	Gly	Ile	Asn	Leu	Ser	Asn	Gln	
420					425					430						
GCG	AGC	GGG	CGC	ACC	CTT	TTA	GTG	GAA	AAT	CTA	ACC	GGG	AAT	ATC	ACC	1400
Ala	Ser	Gly	Arg	Thr	Leu	Leu	Val	Glu	Asn	Leu	Thr	Gly	Asn	Ile	Thr	
435					440					445					450	
GTT	GAT	GGG	CCT	TTA	AGA	GTG	AAT	AAT	CAA	GTG	GGT	GGT	TAT	GCT	TTG	1448
Val	Asp	Gly	Pro	Leu	Arg	Val	Asn	Asn	Gln	Val	Gly	Gly	Tyr	Ala	Leu	
455					460					465						
GCA	GGA	TCA	AGC	GCG	AAT	TTT	GAG	TTT	AAG	GCT	GGT	ACG	GAT	ACC	AAA	1496
Ala	Gly	Ser	Ser	Ala	Asn	Phe	Glu	Phe	Lys	Ala	Gly	Thr	Asp	Thr	Lys	
470					475					480						
AAC	GGC	ACA	GCC	ACT	TTT	AAT	AAC	GAT	ATT	AGT	TTG	GGA	AGA	TTT	GTG	1544
Asn	Gly	Thr	Ala	Thr	Phe	Asn	Asn	Asp	Ile	Ser	Leu	Gly	Arg	Phe	Val	
485					490					495						
AAT	TTA	AAA	GTG	GAT	GCT	CAT	ACA	GCT	AAT	TTT	AAA	GGT	ATT	GAT	ACT	1592
Asn	Leu	Lys	Val	Asp	Ala	His	Thr	Ala	Asn	Phe	Lys	Gly	Ile	Asp	Thr	
500					505					510						
GGT	AAT	GGT	GGT	TTC	AAC	ACC	TTA	GAT	TTT	AGT	GGC	GTT	ACA	GGT	AAG	1640
Gly	Asn	Gly	Gly	Phe	Asn	Thr	Leu	Asp	Phe	Ser	Gly	Val	Thr	Gly	Lys	
515					520					525					530	
GTC	AAT	ATC	AAC	AAG	CTC	ATT	ACG	GCT	TCC	ACT	AAT	GTG	GCC	GTT	AAA	1688
Val	Asn	Ile	Asn	Lys	Leu	Ile	Thr	Ala	Ser	Thr	Asn	Val	Ala	Val	Lys	
535					540					545						
AAC	TTC	AAC	ATT	AAT	GAA	TTG	GTT	GTT	AAG	ACC	AAT	GGG	GTG	AGT	GTG	1736
Asn	Phe	Asn	Ile	Asn	Glu	Leu	Val	Val	Lys	Thr	Asn	Gly	Val	Ser	Val	
550					555					560						

GGG Gly	GAA Glu	TAC Tyr	ACT Thr	CAT His	TTT Phe	AGC Ser	GAA Glu	GAT Asp	ATA Ile	GGC Gly	AGT Ser	CAA Gln	TCG Ser	CGC Arg	ATC Ile	1784
565 570 575																
AAT Asn	ACC Thr	GTG Val	CGT Arg	TTG Leu	GAA Glu	ACT Thr	GGC Gly	ACT Thr	AGG Arg	TCA Ser	ATC Ile	TTT Phe	TCT Ser	GGG Gly	GGT Gly	1832
580 585 590																
GTC Val	AAA Lys	TTT Phe	AAA Lys	AGC Ser	GGT Gly	GAA Glu	AAA Lys	CTG Leu	GTT Val	ATA Ile	GAT Asp	GAG Glu	TTT Phe	TAC Tyr	TAT Tyr	1880
595 600 605 610																
AGC Ser	CCT Pro	TGG Trp	AAT Asn	TAT Tyr	TTT Phe	GAC Asp	GCT Ala	AGG Arg	AAT Asn	ATT Ile	AAA Lys	AAT Asn	GTT Val	GAA Glu	ATC Ile	1928
615 620 625																
ACC Thr	AGA Arg	AAA Lys	TTC Phe	GCT Ala	TCT Ser	TCA Ser	ACC Thr	CCA Pro	GAA Glu	AAC Asn	CCT Pro	TGG Trp	GGC Gly	ACA Thr	TCA Ser	1976
630 635 640																
AAG Lys	CTT Leu	ATG Met	TTT Phe	AAT Asn	AAT Asn	CTA Leu	ACC Thr	CTG Leu	GGT Gly	CAA Gln	AAT Asn	GCG Ala	GTC Val	ATG Met	GAC Asp	2024
645 650 655																
TAT Tyr	AGT Ser	CAA Gln	TTT Phe	TCA Ser	AAT Asn	TTA Leu	ACC Thr	ATT Ile	CAG Gln	GGG Gly	GAT Asp	TTC Phe	ATC Ile	AAC Asn	AAT Asn	2072
660 665 670																
CAA Gln	GGC Gly	ACT Thr	ATC Ile	AAT Asn	TAT Tyr	TTG Leu	GTC Val	CGA Arg	GGC Gly	GGG Gly	CAA Gln	GTA Val	GCC Ala	ACC Thr	TTG Leu	2120
675 680 685 690																
AAT Asn	GTA Val	GGC Gly	AAT Asn	GCG Ala	GCA Ala	GCT Ala	ATG Met	TTC Phe	TTT Ser	AGT Ser	AAT Asn	AAT Asn	GTG Val	GAT Asp	AGC Ser	2168
695 700 705																
GCG Ala	ACT Thr	GGG Gly	TTT Phe	TAC Tyr	CAA Gln	CCG Pro	CTC Leu	ATG Met	AAG Lys	ATT Ile	AAC Asn	AGC Ser	GCT Ala	CAA Gln	GAT Asp	2216
710 715 720																
CTC Leu	ATT Ile	AAA Lys	AAT Asn	AAA Lys	GAA Glu	CAT His	GTC Val	TTA Leu	TTG Leu	AAA Lys	GCG Ala	AAA Lys	ATC Ile	ATC Ile	GGT Gly	2264
725 730 735																
TAT Tyr	GGC Gly	AAT Asn	GTT Val	TCT Ser	TTA Leu	GGC Gly	ACT Thr	AAC Asn	AGC Ser	ATT Ile	AGT Ser	AAT Asn	GTT Val	AAT Asn	CTA Leu	2312
740 745 750																
ATA Ile	GAG Glu	CAA Gln	TTC Phe	AAA Lys	GAG Glu	CGC Arg	CTA Leu	GCC Ala	CTT Leu	TAC Tyr	AAC Asn	AAC Asn	AAT Asn	AAC Asn	CGC Arg	2360
755 760 765 770																
ATG Met	GAT Asp	ATT Ile	TGT Cys	GTG Val	GTG Val	CGA Arg	AAT Asn	ACT Thr	GAT Asp	GAC Asp	ATT Ile	AAA Lys	GCA Ala	TGC Cys	GGG Gly	2408
775 780 785																
ACG Thr	GCT Ala	ATC Ile	GGC Gly	AAT Asn	CAA Gln	AGC Ser	ATG Met	GTG Val	AAT Asn	AAC Asn	CCC Pro	GAC Asp	AAT Asn	TAC Tyr	AAG Lys	2456

790										795					800					
TAT	CTT	ATC	GGT	AAA	GCA	TGG	AAG	AAC	ATA	GGG	ATC	AGC	AAA	ACA	GCT	2504				
Tyr	Leu	Ile	Gly	Lys	Ala	Trp	Lys	Asn	Ile	Gly	Ile	Ser	Lys	Thr	Ala					
		805					810					815								
AAT	GGC	TCT	AAA	ATT	TCG	GTG	TAT	TAT	TTA	GGC	AAT	TCT	ACG	CCT	ACT	2552				
Asn	Gly	Ser	Lys	Ile	Ser	Val	Tyr	Tyr	Leu	Gly	Asn	Ser	Thr	Pro	Thr					
	820					825					830									
GAG	AAA	GGT	GGC	AAT	ACC	ACA	AAT	TTA	CCT	ACA	AAC	ACC	ACT	AGC	AAT	2600				
Glu	Lys	Gly	Gly	Asn	Thr	Thr	Asn	Leu	Pro	Thr	Asn	Thr	Thr	Ser	Asn					
835					840					845					850					
GTG	CGT	TCT	GCC	AAC	AAC	GCC	CTT	GCG	CAA	AAC	GCT	CCT	TTC	GCT	CAA	2648				
Val	Arg	Ser	Ala	Asn	Asn	Ala	Leu	Ala	Gln	Asn	Ala	Pro	Phe	Ala	Gln					
				855					860					865						
CCT	AGC	GCC	ACT	CCT	AAT	TTA	GTC	GCT	ATC	AAT	CAG	CAT	GAT	TTT	GGC	2696				
Pro	Ser	Ala	Thr	Pro	Asn	Leu	Val	Ala	Ile	Asn	Gln	His	Asp	Phe	Gly					
			870					875					880							
ACC	ATT	GAA	AGC	GTG	TTT	GAA	TTG	GCT	AAC	CGC	TCT	AAA	GAT	ATT	GAC	2744				
Thr	Ile	Glu	Ser	Val	Phe	Glu	Leu	Ala	Asn	Arg	Ser	Lys	Asp	Ile	Asp					
		885					890					895								
ACG	CTT	TAT	GCT	AAC	TCA	GGC	GCG	CAA	GGC	AGG	GAT	CTC	TTA	CAA	ACC	2792				
Thr	Leu	Tyr	Ala	Asn	Ser	Gly	Ala	Gln	Gly	Arg	Asp	Leu	Leu	Gln	Thr					
	900					905					910									
TTA	TTG	ATT	GAT	AGC	CAT	GAT	GCG	GGT	TAT	GCC	AGA	CAA	ATG	ATT	GAT	2840				
Leu	Leu	Ile	Asp	Ser	His	Asp	Ala	Gly	Tyr	Ala	Arg	Gln	Met	Ile	Asp					
915					920					925					930					
AAC	ACA	AGC	ACC	GGT	GAA	ATC	ACC	AAG	CAA	TTG	AAT	GCG	GCC	ACT	ACC	2888				
Asn	Thr	Ser	Thr	Gly	Glu	Ile	Thr	Lys	Gln	Leu	Asn	Ala	Ala	Thr	Thr					
				935					940					945						
ACT	TTA	AAC	AAC	ATA	GCC	AGT	TTA	GAG	CAT	AAG	ACA	AGC	AGC	TTA	CAA	2936				
Thr	Leu	Asn	Asn	Ile	Ala	Ser	Leu	Glu	His	Lys	Thr	Ser	Ser	Leu	Gln					
				950				955					960							
ACT	TTG	AGC	TTG	AGT	AAT	GCG	ATG	ATC	TTA	AAT	TCT	CGT	TTA	GTC	AAT	2984				
Thr	Leu	Ser	Leu	Ser	Asn	Ala	Met	Ile	Leu	Asn	Ser	Arg	Leu	Val	Asn					
		965					970					975								
CTC	TCC	AGA	AGG	CAC	ACC	AAT	AAT	ATT	GAC	TCA	TTC	GCC	CAA	CGC	TTA	3032				
Leu	Ser	Arg	Arg	His	Thr	Asn	Asn	Ile	Asp	Ser	Phe	Ala	Gln	Arg	Leu					
	980					985					990									
CAA	GCT	TTA	AAA	GAC	CAA	AAA	TTC	GCT	TCT	TTA	GAA	AGC	GCG	GCG	GAA	3080				
Gln	Ala	Leu	Lys	Asp	Gln	Lys	Phe	Ala	Ser	Leu	Glu	Ser	Ala	Ala	Glu					
995					1000					1005					1010					
GTG	TTG	TAT	CAA	TTT	GCC	CCT	AAA	TAT	GAA	AAA	CCT	ACC	AAT	GTT	TGG	3128				
Val	Leu	Tyr	Gln	Phe	Ala	Pro	Lys	Tyr	Glu	Lys	Pro	Thr	Asn	Val	Trp					
			1015						1020					1025						

GCT AAC GCT ATT GGG GGA ACG AGC TTG AAT AAT GGC GGC AAC GCT TCA Ala Asn Ala Ile Gly Gly Thr Ser Leu Asn Asn Gly Gly Asn Ala Ser 1030 1035 1040	3176
TTG TAT GGC ACA AGT GCG GGC GTA GAT GCC TAC CTT AAT GGG GAA GTG Leu Tyr Gly Thr Ser Ala Gly Val Asp Ala Tyr Leu Asn Gly Glu Val 1045 1050 1055	3224
GAA GCC ATT GTG GGC GGT TTT GGA AGC TAT GGT TAT AGC TCT TTT AAT Glu Ala Ile Val Gly Gly Phe Gly Ser Tyr Gly Tyr Ser Ser Phe Asn 1060 1065 1070	3272
AAT CAA GCG AAC TCT CTT AAC TCT GGA GCC AAT AAC ACT AAT TTT GGC Asn Gln Ala Asn Ser Leu Asn Ser Gly Ala Asn Asn Thr Asn Phe Gly 1075 1080 1085 1090	3320
GTG TAT AGC CGT ATC TTT GCT AAC CAG CAT GAA TTT GAT TTT GAA GCT Val Tyr Ser Arg Ile Phe Ala Asn Gln His Glu Phe Asp Phe Glu Ala 1095 1100 1105	3368
CAA GGG GCG CTA GGG AGT GAT CAA TCA AGC TTG AAT TTC AAA AGC GCT Gln Gly Ala Leu Gly Ser Asp Gln Ser Ser Leu Asn Phe Lys Ser Ala 1110 1115 1120	3416
CTA TTG CGA GAT TTG AAT CAA AGC TAT AAT TAC TTA GCC TAT AGC GCT Leu Leu Arg Asp Leu Asn Gln Ser Tyr Asn Tyr Leu Ala Tyr Ser Ala 1125 1130 1135	3464
GCA ACA AGA GCG AGC TAT GGT TAT GAC TTT GCA TTT TTT AGG AAC GCT Ala Thr Arg Ala Ser Tyr Gly Tyr Asp Phe Ala Phe Phe Arg Asn Ala 1140 1145 1150	3512
TTG GTG TTA AAA CCA AGC GTG GGC GTG AGC TAT AAC CAT TTA GGT TCA Leu Val Leu Lys Pro Ser Val Gly Val Ser Tyr Asn His Leu Gly Ser 1155 1160 1165 1170	3560
ACC AAC TTT AAA AGC AAT AGC AAT CAA GTG GCT TTG AAA AAT GGC TCT Thr Asn Phe Lys Ser Asn Ser Asn Gln Val Ala Leu Lys Asn Gly Ser 1175 1180 1185	3608
AGC AGT CAG CAT TTA TTC AAC GCT AGC GCT AAT GTG GAA GCG CGC TAT Ser Ser Gln His Leu Phe Asn Ala Ser Ala Asn Val Glu Ala Arg Tyr 1190 1195 1200	3656
TAT TAT GGG GAC ACT TCA TAC TTC TAT ATG AAC GCT GGA GTT TTA CAA Tyr Tyr Gly Asp Thr Ser Tyr Phe Tyr Met Asn Ala Gly Val Leu Gln 1205 1210 1215	3704
GAA TTT GCT AAC TTT GGT TCT AGC AAT GCG GTA TCT TTA AAC ACC TTT Glu Phe Ala Asn Phe Gly Ser Ser Asn Ala Val Ser Leu Asn Thr Phe 1220 1225 1230	3752
AAA GTG AAT GCC GCA CAC AAT CCT TTA AGT ACC CAT GCC AGA GTG ATG Lys Val Asn Ala Ala His Asn Pro Leu Ser Thr His Ala Arg Val Met 1235 1240 1245 1250	3800
ATG GGT GGG GAA TTA AAA TTA GCT AAA GAA GTG TTT TTG AAT TTG GGC Met Gly Gly Glu Leu Lys Leu Ala Lys Glu Val Phe Leu Asn Leu Gly	3848

1255 1260 1265

TTT GTT TAT TTG CAC AAT TTG ATT TCC AAT ATA GGC CAT TTC GCT TCC 3896
Phe Val Tyr Leu His Asn Leu Ile Ser Asn Ile Gly His Phe Ala Ser
1270 1275 1280

AAT TTA GGA ATG AGG TAT AGT TTC TAAATACCGC TCTTAAACCC ATGCTCAAAG 3950
Asn Leu Gly Met Arg Tyr Ser Phe
1285 1290

CATGGGTTTG AAATCTTACA AAA 3973

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Met Glu Ile Gln Gln Thr His Arg Lys Ile Asn Arg Pro Leu Val Ser
1 5 10 15
Leu Ala Leu Val Gly Ala Leu Val Ser Ile Thr Pro Gln Gln Ser His
20 25 30
Ala Ala Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile
35 40 45
Ala Thr Gly Ala Ala Val Gly Thr Val Ser Gly Leu Leu Gly Trp Gly
50 55 60
Leu Lys Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys
65 70 75 80
Val Trp Arg Ile Gln Ala Gly Lys Gly Phe Asn Glu Phe Pro Asn Lys
85 90 95
Glu Tyr Asp Leu Tyr Arg Ser Leu Leu Ser Ser Lys Ile Asp Gly Gly
100 105 110
Trp Asp Trp Gly Asn Ala Ala Thr His Tyr Trp Val Lys Gly Gly Gln
115 120 125
Trp Asn Lys Leu Glu Val Asp Met Lys Asp Ala Val Gly Thr Tyr Asn
130 135 140
Leu Ser Gly Leu Arg Asn Phe Thr Gly Gly Asp Leu Asp Val Asn Met
145 150 155 160
Gln Lys Ala Thr Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr
165 170 175
Ser Tyr Lys Asp Ser Ala Asp Arg Thr Thr Arg Val Asp Phe Asn Ala
180 185 190
Lys Asn Ile Leu Ile Asp Asn Phe Leu Glu Ile Asn Asn Arg Val Gly
195 200 205
Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala
210 215 220
Ser Glu Gly Ile Thr Ser Ser Lys Asn Ala Glu Ile Ser Leu Tyr Asp
225 230 235 240
Gly Ala Thr Leu Asn Leu Ala Ser Asn Ser Val Lys Leu Met Gly Asn
245 250 255
Val Trp Met Gly Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser

[illegible]

185 1190 1195 1200
 Arg Tyr Tyr Tyr Gly Asp Thr Ser Tyr Phe Tyr Met Asn Ala Gly Val
 1205 1210 1215
 Leu Gln Glu Phe Ala Asn Phe Gly Ser Ser Asn Ala Val Ser Leu Asn
 1220 1225 1230
 Thr Phe Lys Val Asn Ala Ala His Asn Pro Leu Ser Thr His Ala Arg
 1235 1240 1245
 Val Met Met Gly Gly Glu Leu Lys Leu Ala Lys Glu Val Phe Leu Asn
 1250 1255 1260
 Leu Gly Phe Val Tyr Leu His Asn Leu Ile Ser Asn Ile Gly His Phe
 265 1270 1275 1280
 Ala Ser Asn Leu Gly Met Arg Tyr Ser Phe
 1285 1290

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 55...1284
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

TTAGTAGAAA TTGAAGCGAT AGCCATTAAG TAATTTATTA AAGGGACTAT CAGC	ATG	57
	Met	
	1	
AAA AAA GAG GTC GTG GTC ATA GGC GGT GGG ATT GTA GGG CTT TCT TGT		105
Lys Lys Glu Val Val Val Ile Gly Gly Gly Ile Val Gly Leu Ser Cys		
	5 10 15	
GCG TAT TCT ATG CAC AAG TTA GGC CAT AAG GTC TGC GTG ATA GAA AAA		153
Ala Tyr Ser Met His Lys Leu Gly His Lys Val Cys Val Ile Glu Lys		
	20 25 30	
AAC GAT GGC GCA AAC GGC ACT TCT TTT GGG AAT GCT GGG CTT ATT TCT		201
Asn Asp Gly Ala Asn Gly Thr Ser Phe Gly Asn Ala Gly Leu Ile Ser		
	35 40 45	
GCG TTT AAA AAA GCC CCA CTC TCA TGC CCT GGT GTG GTG TTA GAC ACC		249
Ala Phe Lys Lys Ala Pro Leu Ser Cys Pro Gly Val Val Leu Asp Thr		
	50 55 60 65	
CTG AAG CTC ATG CTC AAA AAC CAA GCC CCT TTA AAA TTC CAT TTC GGG		297
Leu Lys Leu Met Leu Lys Asn Gln Ala Pro Leu Lys Phe His Phe Gly		
	70 75 80	
CTT AAT TTA AAG CTC TAT CAA TGG ATT TTA AAA TTT GTA AAA AGC GCG		345

Leu	Asn	Leu	Lys	Leu	Tyr	Gln	Trp	Ile	Leu	Lys	Phe	Val	Lys	Ser	Ala	
			85					90					95			
AAC	GCC	AAA	TCC	ACG	CAC	CGC	ACC	ATG	GCG	TTG	TTT	GAA	CGC	TAC	GGG	393
Asn	Ala	Lys	Ser	Thr	His	Arg	Thr	Met	Ala	Leu	Phe	Glu	Arg	Tyr	Gly	
		100					105					110				
TGG	CTG	AGT	ATT	GAT	ATG	TAT	CAT	CAA	ATG	CTA	AAA	GAC	GGC	ATG	GAC	441
Trp	Leu	Ser	Ile	Asp	Met	Tyr	His	Gln	Met	Leu	Lys	Asp	Gly	Met	Asp	
	115					120					125					
TTT	TGG	TAT	AAA	GAA	GAT	GGG	CTT	TTA	ATG	ATC	TAC	ACT	CTA	GAA	GAA	489
Phe	Trp	Tyr	Lys	Glu	Asp	Gly	Leu	Leu	Met	Ile	Tyr	Thr	Leu	Glu	Glu	
130					135					140					145	
AGT	TTT	GAA	AAA	AAG	CTT	AAA	ACT	TGC	GAT	AAC	AGC	GGC	GCT	TAT	AAA	537
Ser	Phe	Glu	Lys	Lys	Leu	Lys	Thr	Cys	Asp	Asn	Ser	Gly	Ala	Tyr	Lys	
				150					155					160		
ATC	CTT	AGC	GCT	AAA	GAG	ACC	AAA	GAA	TAC	ATG	CCC	GTT	GTT	AAT	GAC	585
Ile	Leu	Ser	Ala	Lys	Glu	Thr	Lys	Glu	Tyr	Met	Pro	Val	Val	Asn	Asp	
			165					170					175			
AAT	ATC	TGC	GGG	AGC	GTG	CTT	TTA	ACC	GAA	AAC	GCG	CAT	GTG	GAT	CCG	633
Asn	Ile	Cys	Gly	Ser	Val	Leu	Leu	Thr	Glu	Asn	Ala	His	Val	Asp	Pro	
		180					185					190				
GGC	GAA	GTG	ATG	CAC	TCT	TTG	CAA	GAA	TAT	TTA	CAA	AAT	GTT	GGC	GTG	681
Gly	Glu	Val	Met	His	Ser	Leu	Gln	Glu	Tyr	Leu	Gln	Asn	Val	Gly	Val	
	195					200					205					
GAG	TTC	CTT	TAT	AAT	GAA	GAA	GTG	ATC	GAT	TTT	GAG	TTT	AAA	AAT	AAC	729
Glu	Phe	Leu	Tyr	Asn	Glu	Glu	Val	Ile	Asp	Phe	Glu	Phe	Lys	Asn	Asn	
210					215					220					225	
CTC	ATT	GAG	GGC	GTT	ATC	ACG	CAC	AAG	GAA	AAA	ATC	CAA	GCA	GAA	ACA	777
Leu	Ile	Glu	Gly	Val	Ile	Thr	His	Lys	Glu	Lys	Ile	Gln	Ala	Glu	Thr	
				230					235					240		
ATC	ATT	CTA	GCC	ACT	GGG	GCT	AAC	CCC	ACT	CTC	ATT	AAA	AAA	ACC	AAG	825
Ile	Ile	Leu	Ala	Thr	Gly	Ala	Asn	Pro	Thr	Leu	Ile	Lys	Lys	Thr	Lys	
			245					250					255			
AAC	GAT	TTT	TTA	ATG	ATG	GGG	GCT	AAA	GGA	TAT	AGC	ATC	ACC	TTT	AAA	873
Asn	Asp	Phe	Leu	Met	Met	Gly	Ala	Lys	Gly	Tyr	Ser	Ile	Thr	Phe	Lys	
		260					265					270				
ATG	CCT	GAA	GAA	TTA	AAA	CCC	AAA	ACC	TCT	TCT	TTA	TTT	GCG	GAT	ATT	921
Met	Pro	Glu	Glu	Leu	Lys	Pro	Lys	Thr	Ser	Ser	Leu	Phe	Ala	Asp	Ile	
	275					280					285					
TTC	ATG	GCG	ATG	ACC	CCA	CGA	AGA	GAC	ACT	GTA	AGG	ATC	ACT	TCT	AAA	969
Phe	Met	Ala	Met	Thr	Pro	Arg	Arg	Asp	Thr	Val	Arg	Ile	Thr	Ser	Lys	
290					295					300					305	
TTA	GAA	TTA	AAC	ACC	AAC	AAC	GCT	CTC	ATT	GAT	AAA	GAG	CAA	ATC	GCT	1017
Leu	Glu	Leu	Asn	Thr	Asn	Asn	Ala	Leu	Ile	Asp	Lys	Glu	Gln	Ile	Ala	
				310					315					320		

AAC ATG AAA AAG AAT TTA GCC GCT TTC ACG CAG CCT TTT GAA ATG AAA	1065
Asn Met Lys Lys Asn Leu Ala Ala Phe Thr Gln Pro Phe Glu Met Lys	
325 330 335	
GAC GCC ATA GAG TGG TGC GGT TTC AGA CCC TTA ACC CCT AAT GAT ATT	1113
Asp Ala Ile Glu Trp Cys Gly Phe Arg Pro Leu Thr Pro Asn Asp Ile	
340 345 350	
CCT TAT TTG GGC TAT GAC AAA CGC TAT AAA AAC TTA ATC CAT GCG ACA	1161
Pro Tyr Leu Gly Tyr Asp Lys Arg Tyr Lys Asn Leu Ile His Ala Thr	
355 360 365	
GGG CTA GGG TGG CTT GGC ATC ACT TTT GGC CCA GCC ATT GGT AAA ATC	1209
Gly Leu Gly Trp Leu Gly Ile Thr Phe Gly Pro Ala Ile Gly Lys Ile	
370 375 380 385	
ATC GCC AAT TTG AGC CAA GAC GGA GCG AAT GAA AAA AAT GCC GAT ATT	1257
Ile Ala Asn Leu Ser Gln Asp Gly Ala Asn Glu Lys Asn Ala Asp Ile	
390 395 400	
ATG CTT TTT TCT GCA TTT TTT AGG GAT TAAGGAATTT CTTTTTTAAA CCCTAGT	1311
Met Leu Phe Ser Ala Phe Phe Arg Asp	
405 410	
TTATTAAGGA GTTTTTATGG AAAC	1335

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Met	Lys	Lys	Glu	Val	Val	Val	Ile	Gly	Gly	Gly	Ile	Val	Gly	Leu	Ser
1				5					10					15	
Cys	Ala	Tyr	Ser	Met	His	Lys	Leu	Gly	His	Lys	Val	Cys	Val	Ile	Glu
			20					25					30		
Lys	Asn	Asp	Gly	Ala	Asn	Gly	Thr	Ser	Phe	Gly	Asn	Ala	Gly	Leu	Ile
		35					40					45			
Ser	Ala	Phe	Lys	Lys	Ala	Pro	Leu	Ser	Cys	Pro	Gly	Val	Val	Leu	Asp
		50				55					60				
Thr	Leu	Lys	Leu	Met	Leu	Lys	Asn	Gln	Ala	Pro	Leu	Lys	Phe	His	Phe
65					70				75					80	
Gly	Leu	Asn	Leu	Lys	Leu	Tyr	Gln	Trp	Ile	Leu	Lys	Phe	Val	Lys	Ser
			85						90					95	
Ala	Asn	Ala	Lys	Ser	Thr	His	Arg	Thr	Met	Ala	Leu	Phe	Glu	Arg	Tyr
			100					105					110		
Gly	Trp	Leu	Ser	Ile	Asp	Met	Tyr	His	Gln	Met	Leu	Lys	Asp	Gly	Met
		115					120					125			
Asp	Phe	Trp	Tyr	Lys	Glu	Asp	Gly	Leu	Leu	Met	Ile	Tyr	Thr	Leu	Glu
	130					135					140				
Glu	Ser	Phe	Glu	Lys	Lys	Leu	Lys	Thr	Cys	Asp	Asn	Ser	Gly	Ala	Tyr

145		150		155		160									
Lys	Ile	Leu	Ser	Ala	Lys	Glu	Thr	Lys	Glu	Tyr	Met	Pro	Val	Val	Asn
				165					170					175	
Asp	Asn	Ile	Cys	Gly	Ser	Val	Leu	Leu	Thr	Glu	Asn	Ala	His	Val	Asp
			180						185					190	
Pro	Gly	Glu	Val	Met	His	Ser	Leu	Gln	Glu	Tyr	Leu	Gln	Asn	Val	Gly
		195					200					205			
Val	Glu	Phe	Leu	Tyr	Asn	Glu	Glu	Val	Ile	Asp	Phe	Glu	Phe	Lys	Asn
	210					215					220				
Asn	Leu	Ile	Glu	Gly	Val	Ile	Thr	His	Lys	Glu	Lys	Ile	Gln	Ala	Glu
225					230					235					240
Thr	Ile	Ile	Leu	Ala	Thr	Gly	Ala	Asn	Pro	Thr	Leu	Ile	Lys	Lys	Thr
				245					250					255	
Lys	Asn	Asp	Phe	Leu	Met	Met	Gly	Ala	Lys	Gly	Tyr	Ser	Ile	Thr	Phe
			260				265						270		
Lys	Met	Pro	Glu	Glu	Leu	Lys	Pro	Lys	Thr	Ser	Ser	Leu	Phe	Ala	Asp
		275					280					285			
Ile	Phe	Met	Ala	Met	Thr	Pro	Arg	Arg	Asp	Thr	Val	Arg	Ile	Thr	Ser
	290					295					300				
Lys	Leu	Glu	Leu	Asn	Thr	Asn	Asn	Ala	Leu	Ile	Asp	Lys	Glu	Gln	Ile
305					310					315					320
Ala	Asn	Met	Lys	Lys	Asn	Leu	Ala	Ala	Phe	Thr	Gln	Pro	Phe	Glu	Met
				325					330					335	
Lys	Asp	Ala	Ile	Glu	Trp	Cys	Gly	Phe	Arg	Pro	Leu	Thr	Pro	Asn	Asp
		340					345					350			
Ile	Pro	Tyr	Leu	Gly	Tyr	Asp	Lys	Arg	Tyr	Lys	Asn	Leu	Ile	His	Ala
		355					360					365			
Thr	Gly	Leu	Gly	Trp	Leu	Gly	Ile	Thr	Phe	Gly	Pro	Ala	Ile	Gly	Lys
	370					375				380					
Ile	Ile	Ala	Asn	Leu	Ser	Gln	Asp	Gly	Ala	Asn	Glu	Lys	Asn	Ala	Asp
385				390						395					400
Ile	Met	Leu	Phe	Ser	Ala	Phe	Phe	Arg	Asp						
				405					410						

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1526
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

AAAAACGCTA TAAGATAGTC AAATACATTC AATAAATGCA AGGGGAAATC ATG GAA	56
Met Glu	
1	
CAT AAA GAA ATC GTT ATA GGG GTT GAT CTA GGC TCT AGA AAG ATT TGC	104

His	Lys	Glu	Ile	Val	Ile	Gly	Val	Asp	Leu	Gly	Ser	Arg	Lys	Ile	Cys	
		5				10						15				
GCG	ATA	GTG	GCT	GAA	TTT	AAA	GAA	GGG	ATT	TTG	CGC	ATC	ATT	GGC	ACG	152
Ala	Ile	Val	Ala	Glu	Phe	Lys	Glu	Gly	Ile	Leu	Arg	Ile	Ile	Gly	Thr	
	20					25					30					
GCC	CAT	CAA	GAC	TCC	AAA	GAA	ATC	AAT	TCA	AAA	GCC	ATT	AAA	AGA	GGG	200
Ala	His	Gln	Asp	Ser	Lys	Glu	Ile	Asn	Ser	Lys	Ala	Ile	Lys	Arg	Gly	
	35				40					45					50	
CGT	ATC	AAT	AGC	CTT	GCT	CAC	GCT	TCC	AAC	GCC	ATT	AAA	GAA	GTG	ATT	248
Arg	Ile	Asn	Ser	Leu	Ala	His	Ala	Ser	Asn	Ala	Ile	Lys	Glu	Val	Ile	
				55					60					65		
AAT	AGC	GCT	AAA	AAA	ATG	GCA	GGT	TTG	AAC	GCT	GAT	GAA	GAC	AGA	AAT	296
Asn	Ser	Ala	Lys	Lys	Met	Ala	Gly	Leu	Asn	Ala	Asp	Glu	Asp	Arg	Asn	
			70					75					80			
AAC	CCC	ATG	CCC	CAT	TTT	GGG	GAA	TAC	CAC	CCT	AAA	ACT	AAG	GCG	ATT	344
Asn	Pro	Met	Pro	His	Phe	Gly	Glu	Tyr	His	Pro	Lys	Thr	Lys	Ala	Ile	
		85				90						95				
GTT	TCT	TTT	TCT	GGG	GCT	TAT	ACT	GAA	AGC	ATT	AGA	GAT	GTT	ACC	GGT	392
Val	Ser	Phe	Ser	Gly	Ala	Tyr	Thr	Glu	Ser	Ile	Arg	Asp	Val	Thr	Gly	
	100					105					110					
GTA	GCG	AGC	ACC	AAA	GAT	AAT	GTG	GTA	ACC	ATT	GAT	GAA	ATC	AAT	CGC	440
Val	Ala	Ser	Thr	Lys	Asp	Asn	Val	Val	Thr	Ile	Asp	Glu	Ile	Asn	Arg	
	115				120					125					130	
GCT	ATC	AAT	AGT	GCA	TGC	GCT	AAA	GCA	GGC	TTA	GAT	AAC	GAC	AAA	CAT	488
Ala	Ile	Asn	Ser	Ala	Cys	Ala	Lys	Ala	Gly	Leu	Asp	Asn	Asp	Lys	His	
				135					140					145		
ATT	TTG	CAT	GCT	CTC	CCC	TAT	CGC	TTC	ACT	TTA	GAC	AAA	CAA	GAA	GTG	536
Ile	Leu	His	Ala	Leu	Pro	Tyr	Arg	Phe	Thr	Leu	Asp	Lys	Gln	Glu	Val	
			150					155					160			
AAT	GAC	CCT	TTA	GGG	ATG	AGC	GGG	ACT	CGC	TTG	GAA	GTC	TTT	ATC	CAC	584
Asn	Asp	Pro	Leu	Gly	Met	Ser	Gly	Thr	Arg	Leu	Glu	Val	Phe	Ile	His	
		165					170					175				
ATT	GTC	TAT	ACA	GAA	AAA	AAC	AAC	ATT	GAA	AAT	TTA	GAA	AAA	ATC	ATG	632
Ile	Val	Tyr	Thr	Glu	Lys	Asn	Asn	Ile	Glu	Asn	Leu	Glu	Lys	Ile	Met	
	180					185					190					
ATC	CAA	TCT	GGG	GTA	GAG	ATT	GAA	AAC	ATC	GTG	ATC	AAT	TCT	TAT	GCA	680
Ile	Gln	Ser	Gly	Val	Glu	Ile	Glu	Asn	Ile	Val	Ile	Asn	Ser	Tyr	Ala	
	195				200					205					210	
GCC	TCG	ATT	GCC	ACC	TTA	TCT	AAT	GAT	GAA	AGG	GAA	TTG	GGC	GTG	GCT	728
Ala	Ser	Ile	Ala	Thr	Leu	Ser	Asn	Asp	Glu	Arg	Glu	Leu	Gly	Val	Ala	
				215					220					225		
TGC	GTG	GAT	ATG	GGC	GGA	GAG	ACA	TGC	AAC	CTT	ACG	ATT	TAT	AGC	GGC	776
Cys	Val	Asp	Met	Gly	Gly	Glu	Thr	Cys	Asn	Leu	Thr	Ile	Tyr	Ser	Gly	
			230					235					240			

AAT TCC ATA CGC TAT AAC AAA TAT TTG CCC GTA GGC TCT CAC CAT TTA	824
Asn Ser Ile Arg Tyr Asn Lys Tyr Leu Pro Val Gly Ser His His Leu	
245 250 255	
ACC ACG GAT TTA TCG CAC ATG CTC AAC ACC CCA TTC CCT TAC GCT GAA	872
Thr Thr Asp Leu Ser His Met Leu Asn Thr Pro Phe Pro Tyr Ala Glu	
260 265 270	
GAA GTT AAG ATC AAA TAC GGG GAT CTT TCT TTT GAA GGC GGC GAA GAA	920
Glu Val Lys Ile Lys Tyr Gly Asp Leu Ser Phe Glu Gly Gly Glu Glu	
275 280 285 290	
ACG CCC TCT CAA AAT GTC CAA ATC CCT ACC ACC GGC TCG GAT GGC CAT	968
Thr Pro Ser Gln Asn Val Gln Ile Pro Thr Thr Gly Ser Asp Gly His	
295 300 305	
GAA AGC CAT ATT GTG CCG CTT AGT GAA ATC CAA ACT ATC ATG AGA GAA	1016
Glu Ser His Ile Val Pro Leu Ser Glu Ile Gln Thr Ile Met Arg Glu	
310 315 320	
AGG GCT TTA GAA ACT TTT AAA ATC ATC CAC AGG AGC ATT CAA GAT AGC	1064
Arg Ala Leu Glu Thr Phe Lys Ile Ile His Arg Ser Ile Gln Asp Ser	
325 330 335	
GGC TTA GAA GAG CAT TTG GGC GGA GGC GTT GTG TTA ACC GGT GGC ATG	1112
Gly Leu Glu Glu His Leu Gly Gly Gly Val Val Leu Thr Gly Gly Met	
340 345 350	
GCT TTA ATG AAA GGG ATC AAA GAA TTA GCC AGA ACC CAT TTC ACT AAT	1160
Ala Leu Met Lys Gly Ile Lys Glu Leu Ala Arg Thr His Phe Thr Asn	
355 360 365 370	
TAC CCG GTG CGT TTG GCA GCC CCT GTG GAA AAA TAC AAT ATC ATG GGC	1208
Tyr Pro Val Arg Leu Ala Ala Pro Val Glu Lys Tyr Asn Ile Met Gly	
375 380 385	
ATG TTT GAA GAT TTG AAA GAC CCT CGC TTT TCA GTC GTA GTT GGC TTG	1256
Met Phe Glu Asp Leu Lys Asp Pro Arg Phe Ser Val Val Val Gly Leu	
390 395 400	
ATT TTA TAC AAA GCA GGG GGG CAT ACC AAT TAT GAA AGA GAC TCT AAA	1304
Ile Leu Tyr Lys Ala Gly Gly His Thr Asn Tyr Glu Arg Asp Ser Lys	
405 410 415	
GGG GTT ATC CGC TAC CAT GAA AGC GAT GAT TAC ACA AGA ACA GCC CAT	1352
Gly Val Ile Arg Tyr His Glu Ser Asp Asp Tyr Thr Arg Thr Ala His	
420 425 430	
CAA TCA AGC CCT ACC CCC CAT ATC CAT TCA TCG CCC ACA GAA AGG AAT	1400
Gln Ser Ser Pro Thr Pro His Ile His Ser Ser Pro Thr Glu Arg Asn	
435 440 445 450	
TTG AGC GAT TTA AAA GCC CCT AGT GCT CCT TTA AAC ACC GCT AAA AAC	1448
Leu Ser Asp Leu Lys Ala Pro Ser Ala Pro Leu Asn Thr Ala Lys Asn	
455 460 465	
GAT GAC TTT TTA CCT ATA AAA CCC ACC GAA CAA AAA GGT TTT TTT AAA	1496
Asp Asp Phe Leu Pro Ile Lys Pro Thr Glu Gln Lys Gly Phe Phe Lys	

470

475

480

AGT TTC CTT GAT AAG ATT TCT AAA TTC TTT TAAGATACAG CCATTTCTTT ATG 1549
 Ser Phe Leu Asp Lys Ile Ser Lys Phe Phe
 485 490

CGATAAAAAC GCCTTGATGG TTATCAAAAG

1579

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met Glu His Lys Glu Ile Val Ile Gly Val Asp Leu Gly Ser Arg Lys
 1 5 10 15
 Ile Cys Ala Ile Val Ala Glu Phe Lys Glu Gly Ile Leu Arg Ile Ile
 20 25 30
 Gly Thr Ala His Gln Asp Ser Lys Glu Ile Asn Ser Lys Ala Ile Lys
 35 40 45
 Arg Gly Arg Ile Asn Ser Leu Ala His Ala Ser Asn Ala Ile Lys Glu
 50 55 60
 Val Ile Asn Ser Ala Lys Lys Met Ala Gly Leu Asn Ala Asp Glu Asp
 65 70 75 80
 Arg Asn Asn Pro Met Pro His Phe Gly Glu Tyr His Pro Lys Thr Lys
 85 90 95
 Ala Ile Val Ser Phe Ser Gly Ala Tyr Thr Glu Ser Ile Arg Asp Val
 100 105 110
 Thr Gly Val Ala Ser Thr Lys Asp Asn Val Val Thr Ile Asp Glu Ile
 115 120 125
 Asn Arg Ala Ile Asn Ser Ala Cys Ala Lys Ala Gly Leu Asp Asn Asp
 130 135 140
 Lys His Ile Leu His Ala Leu Pro Tyr Arg Phe Thr Leu Asp Lys Gln
 145 150 155 160
 Glu Val Asn Asp Pro Leu Gly Met Ser Gly Thr Arg Leu Glu Val Phe
 165 170 175
 Ile His Ile Val Tyr Thr Glu Lys Asn Asn Ile Glu Asn Leu Glu Lys
 180 185 190
 Ile Met Ile Gln Ser Gly Val Glu Ile Glu Asn Ile Val Ile Asn Ser
 195 200 205
 Tyr Ala Ala Ser Ile Ala Thr Leu Ser Asn Asp Glu Arg Glu Leu Gly
 210 215 220
 Val Ala Cys Val Asp Met Gly Gly Glu Thr Cys Asn Leu Thr Ile Tyr
 225 230 235 240
 Ser Gly Asn Ser Ile Arg Tyr Asn Lys Tyr Leu Pro Val Gly Ser His
 245 250 255
 His Leu Thr Thr Asp Leu Ser His Met Leu Asn Thr Pro Phe Pro Tyr
 260 265 270
 Ala Glu Glu Val Lys Ile Lys Tyr Gly Asp Leu Ser Phe Glu Gly Gly
 275 280 285
 Glu Glu Thr Pro Ser Gln Asn Val Gln Ile Pro Thr Thr Gly Ser Asp

290		295		300
Gly His Glu Ser His Ile Val Pro Leu Ser Glu Ile Gln Thr Ile Met				
305		310		320
Arg Glu Arg Ala Leu Glu Thr Phe Lys Ile Ile His Arg Ser Ile Gln				
	325		330	335
Asp Ser Gly Leu Glu Glu His Leu Gly Gly Val Val Leu Thr Gly				
	340		345	350
Gly Met Ala Leu Met Lys Gly Ile Lys Glu Leu Ala Arg Thr His Phe				
	355		360	365
Thr Asn Tyr Pro Val Arg Leu Ala Ala Pro Val Glu Lys Tyr Asn Ile				
	370		375	380
Met Gly Met Phe Glu Asp Leu Lys Asp Pro Arg Phe Ser Val Val Val				
385		390		400
Gly Leu Ile Leu Tyr Lys Ala Gly Gly His Thr Asn Tyr Glu Arg Asp				
	405		410	415
Ser Lys Gly Val Ile Arg Tyr His Glu Ser Asp Asp Tyr Thr Arg Thr				
	420		425	430
Ala His Gln Ser Ser Pro Thr Pro His Ile His Ser Ser Pro Thr Glu				
	435		440	445
Arg Asn Leu Ser Asp Leu Lys Ala Pro Ser Ala Pro Leu Asn Thr Ala				
	450		455	460
Lys Asn Asp Asp Phe Leu Pro Ile Lys Pro Thr Glu Gln Lys Gly Phe				
465		470		480
Phe Lys Ser Phe Leu Asp Lys Ile Ser Lys Phe Phe				
	485		490	

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1987 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1934
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

AGCGCTTGAA ATTTTATGCC ATTTATGACA CGAATTTAGA CGAATTTTAC ATG ATA	56
Met Ile	
1	
AGA GTG GCA GGG CTT AAA CAA CTC TAT GAG CAT AAA ATC GCC TCT AAA	104
Arg Val Ala Gly Leu Lys Gln Leu Tyr Glu His Lys Ile Ala Ser Lys	
5 10 15	
GGC ATT GAT GGC GCA AGC CCT GAA GAA CAA TTA GAA AAA ATC AAG CAT	152
Gly Ile Asp Gly Ala Ser Pro Glu Glu Gln Leu Glu Lys Ile Lys His	
20 25 30	
TAT TTA GCG CAT GAA ATT GAA GAA AGG GAG TTA GAA TTC CAA AAA ATC	200

Tyr 35	Leu	Ala	His	Glu	Ile 40	Glu	Glu	Arg	Glu	Leu 45	Glu	Phe	Gln	Lys	Ile 50	
CAA	GCC	CTA	CTC	TTT	AAA	AAA	GGG	CTT	TGT	ATC	ACC	CCC	TAT	AAT	GAA	248
Gln	Ala	Leu	Leu	Phe 55	Lys	Lys	Gly	Leu	Cys 60	Ile	Thr	Pro	Tyr	Asn 65	Glu	
TTG	AAT	TTA	GAG	CAA	AAA	GCG	AAG	GCT	AAA	ACC	TAT	TTT	AAA	GAG	CAG	296
Leu	Asn	Leu	Glu	Gln	Lys	Ala	Lys	Ala	Lys	Thr	Tyr	Phe	Lys	Glu	Gln	
			70					75					80			
CTT	TAC	GCG	TTA	GTT	TTG	CCT	TTT	AAA	TTG	GAT	TCT	TCA	CAC	ACT	TTC	344
Leu	Tyr	Ala	Leu	Val	Leu	Pro	Phe	Lys	Leu	Asp	Ser	Ser	His	Thr	Phe	
		85					90					95				
CCG	CCT	TTA	GCG	AAT	TTG	ACT	TTC	GCG	CTT	TTT	GCC	CGC	ATC	AAA	GAC	392
Pro	Pro	Leu	Ala	Asn	Leu	Thr	Phe	Ala	Leu	Phe	Ala	Arg	Ile	Lys	Asp	
	100					105					110					
AAA	GAA	ACC	CAA	ATT	ATC	TCC	TAT	GCG	CTC	ATC	AAA	CTC	CCC	TCT	TTT	440
Lys	Glu	Thr	Gln	Ile	Ile	Ser	Tyr	Ala	Leu	Ile	Lys	Leu	Pro	Ser	Phe	
115					120					125					130	
ATC	TTC	CGT	TTT	GTA	GAG	CTA	GAA	AAA	GGC	TTG	TTT	GTG	TTA	GCT	GAA	488
Ile	Phe	Arg	Phe	Val	Glu	Leu	Glu	Lys	Gly	Leu	Phe	Val	Leu	Ala	Glu	
				135					140					145		
GAA	ATC	GTG	GAA	GCG	CAT	TTA	GAA	GAA	TTG	TTT	TTA	GAG	CAT	GAG	ATT	536
Glu	Ile	Val	Glu	Ala	His	Leu	Glu	Glu	Leu	Phe	Leu	Glu	His	Glu	Ile	
			150					155					160			
TTA	GAT	TGC	ATG	GCG	TTT	AGG	GTA	ACT	TGC	GAT	GCG	GAT	ATT	GCT	ATC	584
Leu	Asp	Cys	Met	Ala	Phe	Arg	Val	Thr	Cys	Asp	Ala	Asp	Ile	Ala	Ile	
		165					170					175				
ACT	GAA	GAT	GAA	GCG	CAT	GAT	TAT	GCA	GAT	TTG	ATG	AGT	AAG	AGT	TTG	632
Thr	Glu	Asp	Glu	Ala	His	Asp	Tyr	Ala	Asp	Leu	Met	Ser	Lys	Ser	Leu	
	180					185					190					
AGG	AAA	CGC	AAT	CAA	GGC	GAA	ATC	GTG	CGC	TTG	CAA	ACC	CAA	AAA	GGG	680
Arg	Lys	Arg	Asn	Gln	Gly	Glu	Ile	Val	Arg	Leu	Gln	Thr	Gln	Lys	Gly	
195				200						205					210	
AGT	CAA	GAG	CTT	TTA	AAA	ACC	CTC	TTA	GCG	TCT	TTA	AGG	AGT	TTT	CAA	728
Ser	Gln	Glu	Leu	Leu	Lys	Thr	Leu	Leu	Ala	Ser	Leu	Arg	Ser	Phe	Gln	
			215						220					225		
ACC	CAC	TCT	TAC	AAA	AAG	CAC	AAA	CTC	ACC	GGC	ATG	CAT	ATC	TAT	AAA	776
Thr	His	Ser	Tyr	Lys	Lys	His	Lys	Leu	Thr	Gly	Met	His	Ile	Tyr	Lys	
			230					235					240			
AGC	GCG	ATC	ATG	CTC	AAT	TTA	GGG	GAT	TTG	TGG	GAA	TTA	GTC	AAT	CAT	824
Ser	Ala	Ile	Met	Leu	Asn	Leu	Gly	Asp	Leu	Trp	Glu	Leu	Val	Asn	His	
		245					250					255				
AGC	GAT	TTT	AAA	GCG	CTC	AAA	TCG	CCC	AAT	TTC	ACA	CCC	AAA	ATC	CAC	872
Ser	Asp	Phe	Lys	Ala	Leu	Lys	Ser	Pro	Asn	Phe	Thr	Pro	Lys	Ile	His	
	260					265					270					

CCT CAT TTC AAT GAA AAC GAT CTT TTC AAA TCT ATA GAA AAA CAG GAT	920
Pro His Phe Asn Glu Asn Asp Leu Phe Lys Ser Ile Glu Lys Gln Asp	
275 280 285 290	
CTG TTG CTG TTT CAT CCT TAT GAA AGT TTT GAG CCT GTG ATT GAT TTA	968
Leu Leu Leu Phe His Pro Tyr Glu Ser Phe Glu Pro Val Ile Asp Leu	
295 300 305	
ATA GAG CAA GCC GCT AGC GAT CCA GCC ACC CTT TCT ATC AAA ATG ACG	1016
Ile Glu Gln Ala Ala Ser Asp Pro Ala Thr Leu Ser Ile Lys Met Thr	
310 315 320	
CTT TAT CGT GTG GGC AAG CAT TCC CCC ATT GTC AAA GCT TTG ATT GAA	1064
Leu Tyr Arg Val Gly Lys His Ser Pro Ile Val Lys Ala Leu Ile Glu	
325 330 335	
GCG GCG AGC AAG ATT CAA GTG AGC GTT TTA GTG GAA TTA AAA GCG CGC	1112
Ala Ala Ser Lys Ile Gln Val Ser Val Leu Val Glu Leu Lys Ala Arg	
340 345 350	
TTT GAT GAA GAG AGC AAT CTG CAC TGG GCA AAA GCT TTA GAA AGG GCG	1160
Phe Asp Glu Glu Ser Asn Leu His Trp Ala Lys Ala Leu Glu Arg Ala	
355 360 365 370	
GGC GCG TTA GTC GTT TAT GGC GTT TTC AAA CTC AAA GTG CAT GCT AAA	1208
Gly Ala Leu Val Val Tyr Gly Val Phe Lys Leu Lys Val His Ala Lys	
375 380 385	
ATG CTA TTG ATC ACT AAA AAA ACA GAC AAC CAA TTA CGC CAT TTC ACC	1256
Met Leu Leu Ile Thr Lys Lys Thr Asp Asn Gln Leu Arg His Phe Thr	
390 395 400	
CAT TTA AGC ACG GGC AAT TAC AAC CCT TTG AGC GCT AAA GTC TAT ACC	1304
His Leu Ser Thr Gly Asn Tyr Asn Pro Leu Ser Ala Lys Val Tyr Thr	
405 410 415	
GAT GTG AGT TTT TTT AGC GCT AAA AAT GAA ATC GCT AAC GAC ATT ATC	1352
Asp Val Ser Phe Phe Ser Ala Lys Asn Glu Ile Ala Asn Asp Ile Ile	
420 425 430	
AAG CTT TTC CAT TCC TTG CTC ACT AGC AGC GCG ACT AAT AGC GCA TTA	1400
Lys Leu Phe His Ser Leu Leu Thr Ser Ser Ala Thr Asn Ser Ala Leu	
435 440 445 450	
GAA ACG CTT TTT ATG GCA CCC AAA CAA ATC AAG CCT AAA ATC ATT GAA	1448
Glu Thr Leu Phe Met Ala Pro Lys Gln Ile Lys Pro Lys Ile Ile Glu	
455 460 465	
CTC ATT CAA AAT GAA ATG AAT CAC CAA CAA GAA GGC TAT ATC ATT TTA	1496
Leu Ile Gln Asn Glu Met Asn His Gln Gln Glu Gly Tyr Ile Ile Leu	
470 475 480	
AAA GCC AAC GCC CTA GTG GAT AGC GAA ATC ATT GAA TGG CTC TAT CAA	1544
Lys Ala Asn Ala Leu Val Asp Ser Glu Ile Ile Glu Trp Leu Tyr Gln	
485 490 495	
GCC TCT CAA AAA GGG GTT AAA ATT GAT CTC ATT ATT AGA GGG ATT TGC	1592
Ala Ser Gln Lys Gly Val Lys Ile Asp Leu Ile Ile Arg Gly Ile Cys	

500	505	510	
TGT TTA AAG CCC CAA GTC AAG GGC TTG AGC GAA AAT ATC AGG GTG TAT			1640
Cys Leu Lys Pro Gln Val Lys Gly Leu Ser Glu Asn Ile Arg Val Tyr			
515	520	525	530
TCT ATC GTG GGG AAA TAT TTA GAA CAT GCA CGC ATT TAT TAT TTT AAA			1688
Ser Ile Val Gly Lys Tyr Leu Glu His Ala Arg Ile Tyr Tyr Phe Lys			
	535	540	545
CAT GAA AAT ATT TAT TTT TCT AGC GCG GAT TTA ATG CCC AGG AAT TTA			1736
His Glu Asn Ile Tyr Phe Ser Ser Ala Asp Leu Met Pro Arg Asn Leu			
	550	555	560
GAA AGG CGC GTG GAA TTG CTC ATT CCA GCC ACA AAC CCA AAG ATC GCT			1784
Glu Arg Arg Val Glu Leu Leu Ile Pro Ala Thr Asn Pro Lys Ile Ala			
	565	570	575
CAT AAA TTG TTG CAT ATT TTA GAA ATC CAA CTC AAA GAC ACC TTA AAA			1832
His Lys Leu Leu His Ile Leu Glu Ile Gln Leu Lys Asp Thr Leu Lys			
	580	585	590
CGC TAC GAG TTA AAT TCT AAA GGC CGT TAC ATT AAA GTT TCA AAC CCT			1880
Arg Tyr Glu Leu Asn Ser Lys Gly Arg Tyr Ile Lys Val Ser Asn Pro			
	595	600	605
AAC GAT CCT TTA AAT TCG CAG GAT TAT TTT GAA AAA CAA GCC CTT AAA			1928
Asn Asp Pro Leu Asn Ser Gln Asp Tyr Phe Glu Lys Gln Ala Leu Lys			
	615	620	625
ACC TTT TAAGGGTTAT CGTTCAAATC ATAAAAGATA AGGATTTAAA TGCTTTATTC AT			1986
Thr Phe			
T			1987

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Met	Ile	Arg	Val	Ala	Gly	Leu	Lys	Gln	Leu	Tyr	Glu	His	Lys	Ile	Ala
1				5				10						15	
Ser	Lys	Gly	Ile	Asp	Gly	Ala	Ser	Pro	Glu	Glu	Gln	Leu	Glu	Lys	Ile
		20					25						30		
Lys	His	Tyr	Leu	Ala	His	Glu	Ile	Glu	Glu	Arg	Glu	Leu	Glu	Phe	Gln
		35				40					45				
Lys	Ile	Gln	Ala	Leu	Leu	Phe	Lys	Lys	Gly	Leu	Cys	Ile	Thr	Pro	Tyr
	50					55				60					
Asn	Glu	Leu	Asn	Leu	Glu	Gln	Lys	Ala	Lys	Ala	Lys	Thr	Tyr	Phe	Lys

65					70					75					80
Glu	Gln	Leu	Tyr	Ala	Leu	Val	Leu	Pro	Phe	Lys	Leu	Asp	Ser	Ser	His
				85					90					95	
Thr	Phe	Pro	Pro	Leu	Ala	Asn	Leu	Thr	Phe	Ala	Leu	Phe	Ala	Arg	Ile
			100					105					110		
Lys	Asp	Lys	Glu	Thr	Gln	Ile	Ile	Ser	Tyr	Ala	Leu	Ile	Lys	Leu	Pro
		115					120					125			
Ser	Phe	Ile	Phe	Arg	Phe	Val	Glu	Leu	Glu	Lys	Gly	Leu	Phe	Val	Leu
	130					135					140				
Ala	Glu	Glu	Ile	Val	Glu	Ala	His	Leu	Glu	Glu	Leu	Phe	Leu	Glu	His
145					150					155					160
Glu	Ile	Leu	Asp	Cys	Met	Ala	Phe	Arg	Val	Thr	Cys	Asp	Ala	Asp	Ile
			165						170					175	
Ala	Ile	Thr	Glu	Asp	Glu	Ala	His	Asp	Tyr	Ala	Asp	Leu	Met	Ser	Lys
			180					185					190		
Ser	Leu	Arg	Lys	Arg	Asn	Gln	Gly	Glu	Ile	Val	Arg	Leu	Gln	Thr	Gln
		195					200					205			
Lys	Gly	Ser	Gln	Glu	Leu	Leu	Lys	Thr	Leu	Leu	Ala	Ser	Leu	Arg	Ser
	210					215					220				
Phe	Gln	Thr	His	Ser	Tyr	Lys	Lys	His	Lys	Leu	Thr	Gly	Met	His	Ile
225					230					235					240
Tyr	Lys	Ser	Ala	Ile	Met	Leu	Asn	Leu	Gly	Asp	Leu	Trp	Glu	Leu	Val
			245						250					255	
Asn	His	Ser	Asp	Phe	Lys	Ala	Leu	Lys	Ser	Pro	Asn	Phe	Thr	Pro	Lys
			260					265					270		
Ile	His	Pro	His	Phe	Asn	Glu	Asn	Asp	Leu	Phe	Lys	Ser	Ile	Glu	Lys
		275					280						285		
Gln	Asp	Leu	Leu	Leu	Phe	His	Pro	Tyr	Glu	Ser	Phe	Glu	Pro	Val	Ile
	290					295					300				
Asp	Leu	Ile	Glu	Gln	Ala	Ala	Ser	Asp	Pro	Ala	Thr	Leu	Ser	Ile	Lys
305					310					315					320
Met	Thr	Leu	Tyr	Arg	Val	Gly	Lys	His	Ser	Pro	Ile	Val	Lys	Ala	Leu
				325					330					335	
Ile	Glu	Ala	Ala	Ser	Lys	Ile	Gln	Val	Ser	Val	Leu	Val	Glu	Leu	Lys
			340					345					350		
Ala	Arg	Phe	Asp	Glu	Glu	Ser	Asn	Leu	His	Trp	Ala	Lys	Ala	Leu	Glu
		355					360					365			
Arg	Ala	Gly	Ala	Leu	Val	Val	Tyr	Gly	Val	Phe	Lys	Leu	Lys	Val	His
	370					375				380					
Ala	Lys	Met	Leu	Leu	Ile	Thr	Lys	Lys	Thr	Asp	Asn	Gln	Leu	Arg	His
385					390					395					400
Phe	Thr	His	Leu	Ser	Thr	Gly	Asn	Tyr	Asn	Pro	Leu	Ser	Ala	Lys	Val
				405					410					415	
Tyr	Thr	Asp	Val	Ser	Phe	Phe	Ser	Ala	Lys	Asn	Glu	Ile	Ala	Asn	Asp
			420					425					430		
Ile	Ile	Lys	Leu	Phe	His	Ser	Leu	Leu	Thr	Ser	Ser	Ala	Thr	Asn	Ser
		435					440					445			
Ala	Leu	Glu	Thr	Leu	Phe	Met	Ala	Pro	Lys	Gln	Ile	Lys	Pro	Lys	Ile
	450					455				460					
Ile	Glu	Leu	Ile	Gln	Asn	Glu	Met	Asn	His	Gln	Gln	Glu	Gly	Tyr	Ile
465					470					475					480
Ile	Leu	Lys	Ala	Asn	Ala	Leu	Val	Asp	Ser	Glu	Ile	Ile	Glu	Trp	Leu
				485					490					495	
Tyr	Gln	Ala	Ser	Gln	Lys	Gly	Val	Lys	Ile	Asp	Leu	Ile	Ile	Arg	Gly
			500					505					510		
Ile	Cys	Cys	Leu	Lys	Pro	Gln	Val	Lys	Gly	Leu	Ser	Glu	Asn	Ile	Arg
		515					520					525			
Val	Tyr	Ser	Ile	Val	Gly	Lys	Tyr	Leu	Glu	His	Ala	Arg	Ile	Tyr	Tyr

530		535		540
Phe Lys His Glu Asn Ile Tyr Phe Ser Ser Ala Asp Leu Met Pro Arg				
545		550		555
Asn Leu Glu Arg Arg Val Glu Leu Leu Ile Pro Ala Thr Asn Pro Lys				
	565		570	
Ile Ala His Lys Leu Leu His Ile Leu Glu Ile Gln Leu Lys Asp Thr				
	580		585	
Leu Lys Arg Tyr Glu Leu Asn Ser Lys Gly Arg Tyr Ile Lys Val Ser				
	595		600	
Asn Pro Asn Asp Pro Leu Asn Ser Gln Asp Tyr Phe Glu Lys Gln Ala				
	610		615	
Leu Lys Thr Phe			620	
625				

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...563
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

TATAATATAG ATTTTATTTT AGCTAAAAAT GGCATGGGTT TTAGCAAGGA ATG GGC	56
Met Gly	
1	
TTG AAA AAT CTC TCA ACA CTT CTG GTG TTT TTA TTC TTT TGT TTA GGG	104
Leu Lys Asn Leu Ser Thr Leu Leu Val Phe Leu Phe Phe Cys Leu Gly	
5 10 15	
TGT GTG AGC AAT TTT AAT GAA GAC ACT TAC ACG CTA GAC TTA GTT TTA	152
Cys Val Ser Asn Phe Asn Glu Asp Thr Tyr Thr Leu Asp Leu Val Leu	
20 25 30	
GAA AAA AAG ATC CAA GCC AGC AGG AAA GGT GAA ATC ACC CAA GAT AAT	200
Glu Lys Lys Ile Gln Ala Ser Arg Lys Gly Glu Ile Thr Gln Asp Asn	
35 40 45 50	
GTG CCT ATC ATC ACG GCT ATC GCT ACG CAT TTA AAC GAT GTG GAT AGC	248
Val Pro Ile Ile Thr Ala Ile Ala Thr His Leu Asn Asp Val Asp Ser	
55 60 65	
GGC ACT TAC TAT GAC CAT GAG TAT TTT TTA GTG GAG ATT TTC ACG CAA	296
Gly Thr Tyr Tyr Asp His Glu Tyr Phe Leu Val Glu Ile Phe Thr Gln	
70 75 80	
AAT AAC GAC TGG ATA GAT GAT GGC TAT ATT TCT TAT GAA CTT TTT GGC	344

Asn	Asn	Asp	Trp	Ile	Asp	Asp	Gly	Tyr	Ile	Ser	Tyr	Glu	Leu	Phe	Gly		
		85					90					95					
ACA	AAA	CCT	ATA	GGC	TCA	GAG	CCT	TTA	TGG	GTG	CGA	GAA	ATC	ACA	AAA		392
Thr	Lys	Pro	Ile	Gly	Ser	Glu	Pro	Leu	Trp	Val	Arg	Glu	Ile	Thr	Lys		
	100					105					110						
GAT	GAA	TTT	GAT	GGC	ATT	TTA	GAA	ACC	ACG	AAC	AGG	TGG	AGC	AGA	GCT		440
Asp	Glu	Phe	Asp	Gly	Ile	Leu	Glu	Thr	Thr	Asn	Arg	Trp	Ser	Arg	Ala		
115					120					125					130		
TTT	TTG	CTC	GCT	TTT	AAC	AAA	TTG	GAT	TAT	TTA	GCG	GTT	CAA	GAA	GCC		488
Phe	Leu	Leu	Ala	Phe	Asn	Lys	Leu	Asp	Tyr	Leu	Ala	Val	Gln	Glu	Ala		
				135					140					145			
AAA	CTA	GAG	CTT	GAT	GCC	TAT	AGT	TTG	GGC	AAG	ATT	GTT	TTT	AAT	TTC		536
Lys	Leu	Glu	Leu	Asp	Ala	Tyr	Ser	Leu	Gly	Lys	Ile	Val	Phe	Asn	Phe		
			150					155					160				
GCT	TAT	CAA	GTC	CCC	CTA	CCT	CAA	TTT	TAATGCGCTT	AGATTACGCC	TTATTCA						590
Ala	Tyr	Gln	Val	Pro	Leu	Pro	Gln	Phe									
		165					170										
GTCAGCATT	TT	AGTAA	ATAGC	AGAGAA													616

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Met	Gly	Leu	Lys	Asn	Leu	Ser	Thr	Leu	Leu	Val	Phe	Leu	Phe	Phe	Cys		
1				5					10					15			
Leu	Gly	Cys	Val	Ser	Asn	Phe	Asn	Glu	Asp	Thr	Tyr	Thr	Leu	Asp	Leu		
			20					25					30				
Val	Leu	Glu	Lys	Lys	Ile	Gln	Ala	Ser	Arg	Lys	Gly	Glu	Ile	Thr	Gln		
		35				40						45					
Asp	Asn	Val	Pro	Ile	Ile	Thr	Ala	Ile	Ala	Thr	His	Leu	Asn	Asp	Val		
50					55					60							
Asp	Ser	Gly	Thr	Tyr	Tyr	Asp	His	Glu	Tyr	Phe	Leu	Val	Glu	Ile	Phe		
65				70				75						80			
Thr	Gln	Asn	Asn	Asp	Trp	Ile	Asp	Asp	Gly	Tyr	Ile	Ser	Tyr	Glu	Leu		
			85					90						95			
Phe	Gly	Thr	Lys	Pro	Ile	Gly	Ser	Glu	Pro	Leu	Trp	Val	Arg	Glu	Ile		
			100				105						110				
Thr	Lys	Asp	Glu	Phe	Asp	Gly	Ile	Leu	Glu	Thr	Thr	Asn	Arg	Trp	Ser		
		115				120						125					
Arg	Ala	Phe	Leu	Leu	Ala	Phe	Asn	Lys	Leu	Asp	Tyr	Leu	Ala	Val	Gln		
130					135					140							
Glu	Ala	Lys	Leu	Glu	Leu	Asp	Ala	Tyr	Ser	Leu	Gly	Lys	Ile	Val	Phe		
145					150					155					160		

Asn Phe Ala Tyr Gln Val Pro Leu Pro Gln Phe
165 170

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 966...2291
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

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ATTGTGAATT AGGAGTGAGC GTGAATAGTA ATGGCAATAA AGACAAACAA CAGCAGAATG      60
TAAGCAGTGG GATTTCTCAA ATCTCATTA  AAAAGGTGGC AACTTTTGAT  GAAAATGGGG      120
CGAGTTTGA  GAATTTAAAT TCTATCAACT TTATTTATGG GGCTAATGGG AGCGGTAAGA      180
CAACCACTTC TAGTTTTTTA AAAAATCTAG CTGAAAATGG GATTGAAGAC AAGTTTGCTA      240
ATAGTAAAAAT AGCATGGTAT AACAAATGAGA GTTTAAAGAT TGAAGTTTAT AACAAAGCAAT      300
TTAAAGAAGA  GCAATTGAGA AACTCTCAAG TTAAAGGCAT TTTTACGCTC GGTAACAAAA      360
CGAACGAGAA  TTTAGAAAAA ATTGAAAGCA AGAAAGAATC AATAAACAAA GAGAATGAAA      420
AGAAAAATAA  AAATGAAGCA AGCTTGCAAG TTTTAACACA AAAAAAGGAA AAGGAAGAAA      480
AGGATTTTGC TGATAGGTGT TGGGAAAAAC TTTATAAGAA AAATGAAGAG GATTTTAAAG      540
AAACGCTAGA AGGCTTTAAG CGTAAAGAGA AGTTTAAAGA AAAAATCCTT AAGGAATTTG      600
AAAAACGATA  ATACAATCAA AGCGAAATAG TAGGGTTAGA AAAATTAAAG GAAAAAATTG      660
AGATTGTTTT TGGTGAAAAA CAAACAGAAT TGGCACTATT GGAATGCAAT TTAACAGATT      720
TTGATTTTAT TGAAAAATCAT TCTATTTGGG AACAAAAAAT TGTAGGGAGT GGTGATGCAG      780
CCATTGCAGA TTTAATAAAA  AGATTAAGCA ATGAAGATTG GGTAGCTCAA GGTAGAGAAT      840
ATATAAAGA  TAATAGTATA TGCCCTTTCT GTCAAAAAGA AACCATTACC GAAGAATTTA      900
AAAAACAAC  AGAATCTTAT TTTGATACAA GTTATCAAGA ATCTATTGAA ACGATCAAGG      960
AAAAG ATG GAA GAC TAC GCA AGC AGA ACC GCT GGA GCA CTG GAG CGA CTT      1010
Met Glu Asp Tyr Ala Ser Arg Thr Ala Gly Ala Leu Glu Arg Leu
  1              5              10              15

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GAT AAG ATT GTT GAA ACA GAA CAG AAG AAT CAA CAA ACT AAA TTG GAC      1058
Asp Lys Ile Val Glu Thr Glu Gln Lys Asn Gln Gln Thr Lys Leu Asp
          20              25              30

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ACA GAA AAT TTG AAA ATA ATT ATT GAA ACT TTG AGA AGT AAA ATC AAT      1106
Thr Glu Asn Leu Lys Ile Ile Ile Glu Thr Leu Arg Ser Lys Ile Asn
          35              40              45

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GGG AAT CAG CAA AAG ATG CTT GAT AAA AGT AAA GAA ATG AGC AGA AAT      1154
Gly Asn Gln Gln Lys Met Leu Asp Lys Ser Lys Glu Met Ser Arg Asn
          50              55              60

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TTT AAG CTT GAT AGC ACT AAA AAC GAG ATA GAC GCA ATT AAA GAT TTG      1202
Phe Lys Leu Asp Ser Thr Lys Asn Glu Ile Asp Ala Ile Lys Asp Leu
        65              70              75

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ATT AAA AAG GCT AAT GAG CAA ATA GCC AAT TAT AAT GAG ATG ATA AAG	1250
Ile Lys Lys Ala Asn Glu Gln Ile Ala Asn Tyr Asn Glu Met Ile Lys	
80 85 90 95	
GAT ATT GAA AAA CAG AAA AAG AGT TGT AAG GAA CAA ACT TGG AAA TTT	1298
Asp Ile Glu Lys Gln Lys Lys Ser Cys Lys Glu Gln Thr Trp Lys Phe	
100 105 110	
CTA GTC AAT GAA TTT AAA AGT GAT ATA CAA GAA TAT AAT AAA AAG TAT	1346
Leu Val Asn Glu Phe Lys Ser Asp Ile Gln Glu Tyr Asn Lys Lys Tyr	
115 120 125	
TGC GGT TTG GAG AAA GGA ATA AAC AAT TTA GAG AAA GCA ATT AGT GAA	1394
Cys Gly Leu Glu Lys Gly Ile Asn Asn Leu Glu Lys Ala Ile Ser Glu	
130 135 140	
AAT CAA GAA GAG GTA AAG AAA TTA GAA AAT GAA ATT AAG GAA TTA GAA	1442
Asn Gln Glu Glu Val Lys Lys Leu Glu Asn Glu Ile Lys Glu Leu Glu	
145 150 155	
AAA ACT ATG GTA AGC ATA AAG CCC ATT GTC AAT GAA ATC AAT ACG CTT	1490
Lys Thr Met Val Ser Ile Lys Pro Ile Val Asn Glu Ile Asn Thr Leu	
160 165 170 175	
TTA AAA GGG TAT GGA TTC GCG AAT TTT AGT TTG GCA TGC ACT GAA GAT	1538
Leu Lys Gly Tyr Gly Phe Ala Asn Phe Ser Leu Ala Cys Thr Glu Asp	
180 185 190	
GAA AAA TTT TAT CGT ATT CAA AGA GAA GAT GGT CAA TTA GTA GGA GAA	1586
Glu Lys Phe Tyr Arg Ile Gln Arg Glu Asp Gly Gln Leu Val Gly Glu	
195 200 205	
ACA CTG AGC GAG GGT GAA GTT ACT TTC ATC ACT TTC TTA TAT TAT TAT	1634
Thr Leu Ser Glu Gly Glu Val Thr Phe Ile Thr Phe Leu Tyr Tyr Tyr	
210 215 220	
CAT TTA GCA AAA GGC TCT TTA GAA GAG AAC GAT ATA TCA AAA AAT AAG	1682
His Leu Ala Lys Gly Ser Leu Glu Glu Asn Asp Ile Ser Lys Asn Lys	
225 230 235	
GTT TTA GTG ATT GAT GAC CCC ATT TCA AGT TTG GAT AGC AAT ATA TTG	1730
Val Leu Val Ile Asp Asp Pro Ile Ser Ser Leu Asp Ser Asn Ile Leu	
240 245 250 255	
TTT ATA GTG AGT GTT TTA GTT AAA GAT CTT ATG AAA GAA GCC ATG GAA	1778
Phe Ile Val Ser Val Leu Val Lys Asp Leu Met Lys Glu Ala Met Glu	
260 265 270	
GAA AAA ACA AAC ATC AAG CAA GTT ATT ATA CTA ACC CAC AAC ACA TAT	1826
Glu Lys Thr Asn Ile Lys Gln Val Ile Ile Leu Thr His Asn Thr Tyr	
275 280 285	
TTT TAC AAG GAA ATT ACA TTA GAA TGT GAT TTA AAA CGC TAT CAA GGG	1874
Phe Tyr Lys Glu Ile Thr Leu Glu Cys Asp Leu Lys Arg Tyr Gln Gly	
290 295 300	
AAA TAT TCT TTT TGG ATA ATT AAA AAG GAT AAT AAT GTT TCA AAA ATT	1922
Lys Tyr Ser Phe Trp Ile Ile Lys Lys Asp Asn Asn Val Ser Lys Ile	

305		310		315		
AAA GAT TAT AAA GAA AAT CCC ATT AAA AAT TCC TAT GAA TTG CTA TGG	1970					
Lys Asp Tyr Lys Glu Asn Pro Ile Lys Asn Ser Tyr Glu Leu Leu Trp						
320		325		330		335
CAA GAA GTA AAA CAA GCA AAA GAA AAT AAT GCT TCT TGG GTA TCT TTA	2018					
Gln Glu Val Lys Gln Ala Lys Glu Asn Asn Ala Ser Trp Val Ser Leu						
		340		345		350
CAA AAT GTT ATG CGA AGA ATT ATT GAG TAT TAC TTT AGG ATT TTA GGC	2066					
Gln Asn Val Met Arg Arg Ile Ile Glu Tyr Tyr Phe Arg Ile Leu Gly						
		355		360		365
GGT TTT AAA CAT AAT GAT AGC TTG AGT GAA TGT TTT GAA AAT ATT GAA	2114					
Gly Phe Lys His Asn Asp Ser Leu Ser Glu Cys Phe Glu Asn Ile Glu						
		370		375		380
GAA AAA CGA GTG TGT AAT TCT TTC ATT TCA TGG TTT AAT GAT GGC TCT	2162					
Glu Lys Arg Val Cys Asn Ser Phe Ile Ser Trp Phe Asn Asp Gly Ser						
		385		390		395
CAT GGG ATT TCA GAT GAT TTG TTT ATG CAA AGT CAA GAT ACA AGT ATT	2210					
His Gly Ile Ser Asp Asp Leu Phe Met Gln Ser Gln Asp Thr Ser Ile						
		400		405		410
GAG ACA TAT TTA AAA GTT TTT GAA AAA ATA TTT AAA GAA ACC GGT CAT	2258					
Glu Thr Tyr Leu Lys Val Phe Glu Lys Ile Phe Lys Glu Thr Gly His						
		420		425		430
GAA GCT CAT TAT AAA ATG ATG ATG AGA ATG AAG TAATTGAATT AAAACAAGG	2311					
Glu Ala His Tyr Lys Met Met Met Arg Met Lys						
		435		440		
AATAACATGC GAATCGTATT TATGGGAACG	2341					

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met	Glu	Asp	Tyr	Ala	Ser	Arg	Thr	Ala	Gly	Ala	Leu	Glu	Arg	Leu	Asp
1				5					10					15	
Lys	Ile	Val	Glu	Thr	Glu	Gln	Lys	Asn	Gln	Gln	Thr	Lys	Leu	Asp	Thr
		20						25					30		
Glu	Asn	Leu	Lys	Ile	Ile	Ile	Glu	Thr	Leu	Arg	Ser	Lys	Ile	Asn	Gly
		35				40						45			
Asn	Gln	Gln	Lys	Met	Leu	Asp	Lys	Ser	Lys	Glu	Met	Ser	Arg	Asn	Phe
	50					55				60					
Lys	Leu	Asp	Ser	Thr	Lys	Asn	Glu	Ile	Asp	Ala	Ile	Lys	Asp	Leu	Ile

65					70					75				80
Lys	Lys	Ala	Asn	Glu	Gln	Ile	Ala	Asn	Tyr	Asn	Glu	Met	Ile	Lys
				85					90					95
Ile	Glu	Lys	Gln	Lys	Lys	Ser	Cys	Lys	Glu	Gln	Thr	Trp	Lys	Phe
			100					105					110	Leu
Val	Asn	Glu	Phe	Lys	Ser	Asp	Ile	Gln	Glu	Tyr	Asn	Lys	Lys	Tyr
		115					120					125		Cys
Gly	Leu	Glu	Lys	Gly	Ile	Asn	Asn	Leu	Glu	Lys	Ala	Ile	Ser	Glu
	130					135					140			Asn
Gln	Glu	Glu	Val	Lys	Lys	Leu	Glu	Asn	Glu	Ile	Lys	Glu	Leu	Glu
145					150				155					160
Thr	Met	Val	Ser	Ile	Lys	Pro	Ile	Val	Asn	Glu	Ile	Asn	Thr	Leu
				165					170					175
Lys	Gly	Tyr	Gly	Phe	Ala	Asn	Phe	Ser	Leu	Ala	Cys	Thr	Glu	Asp
		180						185					190	Glu
Lys	Phe	Tyr	Arg	Ile	Gln	Arg	Glu	Asp	Gly	Gln	Leu	Val	Gly	Glu
		195					200					205		Thr
Leu	Ser	Glu	Gly	Glu	Val	Thr	Phe	Ile	Thr	Phe	Leu	Tyr	Tyr	Tyr
	210					215					220			His
Leu	Ala	Lys	Gly	Ser	Leu	Glu	Glu	Asn	Asp	Ile	Ser	Lys	Asn	Lys
225					230				235					240
Leu	Val	Ile	Asp	Asp	Pro	Ile	Ser	Ser	Leu	Asp	Ser	Asn	Ile	Leu
			245						250					255
Ile	Val	Ser	Val	Leu	Val	Lys	Asp	Leu	Met	Lys	Glu	Ala	Met	Glu
			260					265					270	Glu
Lys	Thr	Asn	Ile	Lys	Gln	Val	Ile	Ile	Leu	Thr	His	Asn	Thr	Tyr
		275					280					285		Phe
Tyr	Lys	Glu	Ile	Thr	Leu	Glu	Cys	Asp	Leu	Lys	Arg	Tyr	Gln	Gly
	290					295					300			Lys
Tyr	Ser	Phe	Trp	Ile	Ile	Lys	Lys	Asp	Asn	Asn	Val	Ser	Lys	Ile
305					310				315					320
Asp	Tyr	Lys	Glu	Asn	Pro	Ile	Lys	Asn	Ser	Tyr	Glu	Leu	Leu	Trp
			325						330					335
Glu	Val	Lys	Gln	Ala	Lys	Glu	Asn	Asn	Ala	Ser	Trp	Val	Ser	Leu
			340					345					350	Gln
Asn	Val	Met	Arg	Arg	Ile	Ile	Glu	Tyr	Tyr	Phe	Arg	Ile	Leu	Gly
		355					360					365		Gly
Phe	Lys	His	Asn	Asp	Ser	Leu	Ser	Glu	Cys	Phe	Glu	Asn	Ile	Glu
	370					375				380				Glu
Lys	Arg	Val	Cys	Asn	Ser	Phe	Ile	Ser	Trp	Phe	Asn	Asp	Gly	Ser
385					390					395				400
Gly	Ile	Ser	Asp	Asp	Leu	Phe	Met	Gln	Ser	Gln	Asp	Thr	Ser	Ile
			405					410						415
Thr	Tyr	Leu	Lys	Val	Phe	Glu	Lys	Ile	Phe	Lys	Glu	Thr	Gly	His
		420					425						430	Glu
Ala	His	Tyr	Lys	Met	Met	Met	Arg	Met	Lys					
		435					440							

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...3740
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

TTATGTGGGC TACAACATAG GCTTTTGATT AAACAAATA AGGGAAAAAT ATG ATA	56
Met Ile	
1	
AAA AAA GCT AGA AAA TTC ATA CCA TTC TTT TTA ATT GGC TCC CTC TTA	104
Lys Lys Ala Arg Lys Phe Ile Pro Phe Phe Leu Ile Gly Ser Leu Leu	
5 10 15	
GCT GAA GAC AAT GGC TGG TAT ATG TCT GTA GGC TAT CAA ATC GGT GGC	152
Ala Glu Asp Asn Gly Trp Tyr Met Ser Val Gly Tyr Gln Ile Gly Gly	
20 25 30	
ACG CAA CAA TTC ATC AAT AAC AAA CAA CTT TTA GAA AAT CAA AAT ATC	200
Thr Gln Gln Phe Ile Asn Asn Lys Gln Leu Leu Glu Asn Gln Asn Ile	
35 40 45 50	
ATC AAC AGC GTA ACC CAA AGC GCG ATC AAC ATT GCA GGG CCT ACT ACC	248
Ile Asn Ser Val Thr Gln Ser Ala Ile Asn Ile Ala Gly Pro Thr Thr	
55 60 65	
GGC CTT ATC ACT TTA AGC TCT CAA ACC GTC ATT GAC GCT TTA GGC TAT	296
Gly Leu Ile Thr Leu Ser Ser Gln Thr Val Ile Asp Ala Leu Gly Tyr	
70 75 80	
GGC GTG AGT AAC ACT GTT GGC AAC CAA TTA GAG GGC ATT TCT AAT ATC	344
Gly Val Ser Asn Thr Val Gly Asn Gln Leu Glu Gly Ile Ser Asn Ile	
85 90 95	
TTG AAT CAA ATT GGC AAA AGA AAA GAC TTT TAT TCT AGC CGT CAA ATC	392
Leu Asn Gln Ile Gly Lys Arg Lys Asp Phe Tyr Ser Ser Arg Gln Ile	
100 105 110	
TCT AGC ATT TCC CAA CAA ATC ATA GGG CTT AAA GGA AGC TCT GAT CCC	440
Ser Ser Ile Ser Gln Gln Ile Ile Gly Leu Lys Gly Ser Ser Asp Pro	
115 120 125 130	
TTA AAA GCC CAT TCT TCA CAG ATC ACA GCC AAA CTC CTT TCC AAC ACC	488
Leu Lys Ala His Ser Ser Gln Ile Thr Ala Lys Leu Leu Ser Asn Thr	
135 140 145	
CAA AGC GCG TTT GAT CAG GGC ATC GCG CTA AGC ACT AAC ATC ATT AGC	536
Gln Ser Ala Phe Asp Gln Gly Ile Ala Leu Ser Thr Asn Ile Ile Ser	
150 155 160	
TCT ATC AAT AGC CTA AAC CCT AGC AAC AAC ACC CAA GAG GTT AAA AAA	584
Ser Ile Asn Ser Leu Asn Pro Ser Asn Asn Thr Gln Glu Val Lys Lys	
165 170 175	
CAG CTC CAA AAC ACC GCG CAA TCC ATG ACA GAA TTG TTG CAA CAA ATT	632
Gln Leu Gln Asn Thr Ala Gln Ser Met Thr Glu Leu Leu Gln Gln Ile	

180	185	190	
GAA CAC AGC ATC ACT AAA ACC ACT AGC ACC ACT TAC GCG CAA TCC TTA			680
Glu His Ser Ile Thr Lys Thr Thr Ser Thr Thr Tyr Ala Gln Ser Leu			
195	200	205	210
CTC TCC AAT CTA ACC GAT GCG GTG AAT GCC TCT AGC AAT AAT ACC GCT			728
Leu Ser Asn Leu Thr Asp Ala Val Asn Ala Ser Ser Asn Asn Thr Ala			
	215	220	225
TAT GTG AGC GCT CTT GTT AAC GCT TTA AAC ACT TTA GGG GTA GGG GTT			776
Tyr Val Ser Ala Leu Val Asn Ala Leu Asn Thr Leu Gly Val Gly Val			
	230	235	240
TTC CCC ACC ACA ACC ACA ACG CAT GTG GTG TTA AAC CCA CCG GGA CAA			824
Phe Pro Thr Thr Thr Thr His Val Val Leu Asn Pro Pro Gly Gln			
	245	250	255
GTC GTA TTC TAT CCA ACC AAT TCC ATT TTA GGC TCT ACT TCT TCA AAC			872
Val Val Phe Tyr Pro Thr Asn Ser Ile Leu Gly Ser Thr Ser Ser Asn			
	260	265	270
AGC AAT AAC CAA CAA CAA TAC AAC AAC ACC CTT TTA ATG AAC ACC TTA			920
Ser Asn Asn Gln Gln Gln Tyr Asn Asn Thr Leu Leu Met Asn Thr Leu			
	275	280	285
CAA GGG ACA TTA AGC GCT AAT ACT CAA AAT AAC CCC AAT GGT TGC GCC			968
Gln Gly Thr Leu Ser Ala Asn Thr Gln Asn Asn Pro Asn Gly Cys Ala			
	295	300	305
AAT CAA GTC CAG TGT TTG GAG CAA TTC ATC CAA AAT TTA GCC CCT TTA			1016
Asn Gln Val Gln Cys Leu Glu Gln Phe Ile Gln Asn Leu Ala Pro Leu			
	310	315	320
GCC GCA ACC CCC ACT TCA AAC AAC CAG GCC AAC CAG CAA GTC CAA GCC			1064
Ala Ala Thr Pro Thr Ser Asn Asn Gln Ala Asn Gln Gln Val Gln Ala			
	325	330	335
ATC GCT CAA AAG CTT CAA AGC GTT GCT ATC AAC ACT TTA GAC AAC AAT			1112
Ile Ala Gln Lys Leu Gln Ser Val Ala Ile Asn Thr Leu Asp Asn Asn			
	340	345	350
GCG ATC AAC AAC ACC ACC TAT AAT TTA AAC AAT TTG CAC AAC GCT TTG			1160
Ala Ile Asn Asn Thr Thr Tyr Asn Leu Asn Asn Leu His Asn Ala Leu			
	355	360	365
AAT TTC CAA GCC TAT GAA AGC ACG ATA GAA CAA TAC AAT AAC GCT TTA			1208
Asn Phe Gln Ala Tyr Glu Ser Thr Ile Glu Gln Tyr Asn Asn Ala Leu			
	375	380	385
AAA CAA ATT TCT TGG ATC AGT TTT ACT GAG CCT AAA AAC TTA CTC AAA			1256
Lys Gln Ile Ser Trp Ile Ser Phe Thr Glu Pro Lys Asn Leu Leu Lys			
	390	395	400
AAC ACT TCC AAT AAC TAC CAA ATC GGC ACC GTT ACC AAC GCT CAA GGG			1304
Asn Thr Ser Asn Asn Tyr Gln Ile Gly Thr Val Thr Asn Ala Gln Gly			
	405	410	415

CAA AAT ATC AGC GCC TAT GAT TGC ATG ACT GCT ACC GGA AGC CTT TCT	1352
Gln Asn Ile Ser Ala Tyr Asp Cys Met Thr Ala Thr Gly Ser Leu Ser	
420 425 430	
AGC AAT GCT TCT AGC GGG ATT TCA TGC TCA GCC ACA AGC TCC ACA AGT	1400
Ser Asn Ala Ser Ser Gly Ile Ser Cys Ser Ala Thr Ser Ser Thr Ser	
435 440 445 450	
TCC ACA AAT AGC TTT GAC AAT TCT TTA GTC GCT ACC TCC AAA GTC CAA	1448
Ser Thr Asn Ser Phe Asp Asn Ser Leu Val Ala Thr Ser Lys Val Gln	
455 460 465	
ACC ATC AAC GGC AAA GAG CAG ATC GGC GTG AAT TCT TTT AAC CTT GTC	1496
Thr Ile Asn Gly Lys Glu Gln Ile Gly Val Asn Ser Phe Asn Leu Val	
470 475 480	
TCT CAA GTG TGG AGC GTT TAT AAT TCT TTA AAA ACT TCA GAA GAA AAT	1544
Ser Gln Val Trp Ser Val Tyr Asn Ser Leu Lys Thr Ser Glu Glu Asn	
485 490 495	
TTG CAA AAA AAC GCC AAT ATT TTA TGC GCT AAT GGG ACG CAA TCT GGG	1592
Leu Gln Lys Asn Ala Asn Ile Leu Cys Ala Asn Gly Thr Gln Ser Gly	
500 505 510	
ACA AGC TCA TGC AAT AGC TCT TCA GGG GGT TTG AGC ATC AGC GGG AAC	1640
Thr Ser Ser Cys Asn Ser Ser Ser Gly Gly Leu Ser Ile Ser Gly Asn	
515 520 525 530	
GCC CAA TTG CAA AAT ATT TTA AGC CCT ACT AGT GGG ACT ACC ACT AAT	1688
Ala Gln Leu Gln Asn Ile Leu Ser Pro Thr Ser Gly Thr Thr Thr Asn	
535 540 545	
ACT CAA GCT AAA AGC AAC GCT CCC AAA CTA AAA GCG ATG GTG GTG GTG	1736
Thr Gln Ala Lys Ser Asn Ala Pro Lys Leu Lys Ala Met Val Val Val	
550 555 560	
AAT AAT GAA GAA GAA GCT AAA ACG GCC AAT TTA GCC CAA AGC AGC GGG	1784
Asn Asn Glu Glu Glu Ala Lys Thr Ala Asn Leu Ala Gln Ser Ser Gly	
565 570 575	
ACA ACC ACA CAA TCT CCT AAC AGC ACG GTG ATG GGA GCT TTA AAC ACC	1832
Thr Thr Thr Gln Ser Pro Asn Ser Thr Val Met Gly Ala Leu Asn Thr	
580 585 590	
GTG TTG CAA AAT GTC AGC AAT TTC CAA CAA AGC ATT CAA AAC GCT TTT	1880
Val Leu Gln Asn Val Ser Asn Phe Gln Gln Ser Ile Gln Asn Ala Phe	
595 600 605 610	
CAA AAC CAA GAA AGT AAT ATC CAA GCT TGG GCG AAT GCG ATT TAT AAC	1928
Gln Asn Gln Glu Ser Asn Ile Gln Ala Trp Ala Asn Ala Ile Tyr Asn	
615 620 625	
ACT AAT GGG AGT CAG TCG CAA GAG ATG ACA CCT AAC AAT AAC CAA GAT	1976
Thr Asn Gly Ser Gln Ser Gln Glu Met Thr Pro Asn Asn Asn Gln Asp	
630 635 640	
TTA CGC ATC CAA TTG AGG GCG AAT TTT TAC CAG CTC ATC AAT ACC ATT	2024
Leu Arg Ile Gln Leu Arg Ala Asn Phe Tyr Gln Leu Ile Asn Thr Ile	

645					650					655						
AAC Asn 660	CAG Gln 660	CAA Gln 660	GTG Val 660	CCT Pro 660	ACA Thr 665	GAC Asp 665	ATG Met 665	AAT Asn 665	GCT Ala 670	TTA Leu 670	ATT Ile 670	AAT Asn 670	CAA Gln 670	AGC Ser 670	CAA Gln 670	2072
CAA Gln 675	ACC Thr 675	CAA Gln 675	CAA Gln 675	ACA Thr 680	AGC Ser 680	GGA Gly 680	TCA Ser 685	GCA Ala 685	AGC Ser 685	AAT Asn 685	AAT Asn 685	AAC Asn 685	GCA Ala 690	TGC Cys 690	GCG Ala 690	2120
AGT Ser 695	GGA Gly 695	ATG Met 695	AGT Ser 695	GGG Gly 695	AGT Ser 695	AAT Asn 695	GGT Gly 700	AAC Asn 700	TGG Trp 700	TGC Cys 705	TAT Tyr 705	CAG Gln 705	CAA Gln 705	TGG Trp 705	TCC Ser 705	2168
GAT Asp 710	TCT Ser 710	AAG Lys 710	GCT Ala 710	TAT Tyr 710	TAC Tyr 710	AGC Ser 715	GGG Gly 715	TTG Leu 715	CAA Gln 715	AGC Ser 715	GCT Ala 720	TTA Leu 720	GGG Gly 720	TAT Tyr 720	CAA Gln 720	2216
ACG Thr 725	CAA Gln 725	GCG Ala 725	ACA Thr 725	ACT Thr 725	CAA Gln 725	AGC Ser 730	GGG Gly 730	AGC Ser 730	AAT Asn 735	GGT Gly 735	GGG Gly 735	AAC Asn 735	AGC Ser 735	ATC Ile 735	ACC Thr 735	2264
TAC Tyr 740	AAT Asn 740	GTC Val 740	CAA Gln 740	CAA Gln 740	ATC Ile 745	ACG Thr 745	CTC Leu 745	ACT Thr 745	AGT Ser 745	AAT Asn 750	GGT Gly 750	TTG Leu 750	CTC Leu 750	AAC Asn 750	CAA Gln 750	2312
ATC Ile 755	ATC Ile 755	ACA Thr 755	AAT Asn 755	CTT Leu 760	AAG Lys 760	AGC Ser 760	GTT Val 765	AAT Asn 765	GGA Gly 765	GGC Gly 765	AAT Asn 765	GGC Gly 765	GCG Ala 770	AGT Ser 770	GGT Gly 770	2360
ACA Thr 775	GGC Gly 775	AGT Ser 775	GGG Gly 775	AAT Asn 775	GGC Gly 775	ACC Thr 775	AGT Ser 780	CAA Gln 780	ATC Ile 780	AAC Asn 780	ACA Thr 785	GCC Ala 785	TAC Tyr 785	CAG Gln 785	ATG Met 785	2408
CTC Leu 790	ACA Thr 790	GAC Asp 790	GCC Ala 790	AGC Ser 790	GAT Asp 790	GGG Gly 795	AAA Lys 795	TTA Leu 795	GGG Gly 795	ACT Thr 795	TAT Tyr 800	AGT Ser 800	AGT Ser 800	AGT Ser 800	AGT Ser 800	2456
GGC Gly 805	AGT Ser 805	AAT Asn 805	AAC Asn 805	GGC Gly 805	TAT Tyr 805	ACG Thr 810	CCA Pro 810	TGC Cys 810	AAT Asn 810	AGC Ser 810	ACC Thr 815	AAT Asn 815	GGG Gly 815	AGC Ser 815	AAT Asn 815	2504
AAA Lys 820	ACG Thr 820	AGT Ser 820	GGG Gly 820	AAC Asn 825	AAT Asn 825	TGT Cys 825	TAT Tyr 825	GAA Glu 830	CCC Pro 830	AAC Asn 830	AAA Lys 830	CAA Gln 830	CAA Gln 830	AAC Asn 830	GCC Ala 830	2552
ACC Thr 835	ACC Thr 835	GCA Ala 835	ACC Thr 835	GCC Ala 840	ACA Thr 840	ACC Thr 840	GAC Asp 845	AGC Ser 845	AAT Asn 845	TTA Leu 845	CAA Gln 845	AAA Lys 845	GTC Val 850	TAT Tyr 850	AAT Asn 850	2600
GAC Asp 855	GCC Ala 855	CAA Gln 855	AAA Lys 855	ATA Ile 855	GCC Ala 855	AAC Asn 855	ATT Ile 860	ATC Ile 860	GCC Ala 860	AGC Ser 860	TCT Ser 865	GGG Gly 865	AAC Asn 865	AAT Asn 865	AAA Lys 865	2648
GGC Gly 870	GTT Val 870	GAA Glu 870	AAC Asn 870	GGC Gly 870	TTA Leu 875	AAA Lys 875	CAA Gln 875	TTC Phe 875	TTT Phe 875	GAA Glu 880	GCG Ala 880	TTA Leu 880	AAA Lys 880	AAT Asn 880	AAT Asn 880	2696

AGC Ser	AGC Ser	AGT Ser	CTC Leu	AGT Ser	AAT Asn	TTA Leu	TGT Cys	GGT Gly	AAT Asn	GGT Gly	AGT Ser	AGC Ser	GGT Gly	AGT Ser	AGT Ser	2744
885 890 895																
GGC Gly	ACT Thr	ACT Thr	TGC Cys	TCC Ser	GGT Gly	TGG Trp	CTT Leu	ATC Ile	AAC Asn	CTT Leu	TTA Leu	GGG Gly	GCA Ala	ATC Ile	CCC Pro	2792
900 905 910																
ACC Thr	AAT Asn	GGA Gly	GTG Val	AGC Ser	GAT Asp	ACG Thr	AAT Asn	AAT Asn	TTA Leu	ATT Ile	AAT Asn	CTG Leu	CTC Leu	ACT Thr	GAA Glu	2840
915 920 925 930																
TTC Phe	ATT Ile	AAA Lys	ACC Thr	GCC Ala	GGG Gly	TTT Phe	ATC Ile	CAA Gln	AAT Asn	AAT Asn	GAT Asp	AGT Ser	AGT Ser	GTA Val	TCT Ser	2888
935 940 945																
ACT Thr	AGT Ser	CTT Leu	ACA Thr	AGC Ser	GCT Ala	TTT Phe	CAA Gln	GCC Ala	ATT Ile	ACG Thr	AGC Ser	GCT Ala	ATT Ile	TCT Ser	CAA Gln	2936
950 955 960																
GGG Gly	TTT Phe	CAA Gln	GCC Ala	TTA Leu	CAA Gln	AAC Asn	GAT Asp	ATT Ile	AGC Ser	CCT Pro	AAT Asn	GCG Ala	ATT Ile	TTA Leu	ACC Thr	2984
965 970 975																
TTG Leu	CTC Leu	CAA Gln	GAG Glu	ATT Ile	ACT Thr	TCT Ser	AAC Asn	ACC Thr	ACC Thr	ACC Thr	ATT Ile	CAG Gln	TCA Ser	TTC Phe	TCG Ser	3032
980 985 990																
CAA Gln	ACC Thr	TTA Leu	CGG Arg	CAG Gln	CTT Leu	TTA Leu	GGG Gly	GAT Asp	AAA Lys	ACA Thr	TTC Phe	TTT Phe	ATG Met	GCG Ala	CAA Gln	3080
995 1000 1005 1010																
CAA Gln	AAG Lys	CTC Leu	ATT Ile	GAT Asp	GCG Ala	ATG Met	ATT Ile	AAC Asn	GCC Ala	AGA Arg	AAT Asn	CAG Gln	GTT Val	CAA Gln	AAC Asn	3128
1015 1020 1025																
GCG Ala	CAA Gln	AAT Asn	CAA Gln	GCC Ala	AAT Asn	AAC Asn	TAC Tyr	GGC Gly	TCT Ser	CAA Gln	CCC Pro	GTT Val	TTA Leu	AGC Ser	CAG Gln	3176
1030 1035 1040																
TAT Tyr	GCG Ala	GCC Ala	GCT Ala	AAA Lys	AGC Ser	ACC Thr	CAA Gln	CAT His	GGC Gly	ATG Met	AGC Ser	AAT Asn	GGT Gly	TTA Leu	GGG Gly	3224
1045 1050 1055																
GTT Val	GGT Gly	TTG Leu	GGC Gly	TAT Tyr	AAA Lys	TAC Tyr	TTC Phe	TTT Phe	GGT Gly	AAA Lys	GCG Ala	AGA Arg	AAA Lys	TTA Leu	GGC Gly	3272
1060 1065 1070																
CTT Leu	AGG Arg	CAT His	TAT Tyr	TTT Phe	TTC Phe	TTT Phe	GAT Asp	TAC Tyr	GGC Gly	TTT Phe	AGT Ser	GAA Glu	ATA Ile	GGC Gly	CTA Leu	3320
1075 1080 1085 1090																
GCC Ala	AAT Asn	CAA Gln	AGC Ser	GTG Val	AAA Lys	GCG Ala	AAT Asn	ATC Ile	TTT Phe	GCT Ala	TAT Tyr	GGG Gly	GTA Val	GGC Gly	ACG Thr	3368
1095 1100 1105																
GAT Asp	TTT Phe	TTA Leu	TGG Trp	AAC Asn	TTA Leu	TTC Phe	AGG Arg	AGG Arg	ACT Thr	TAC Tyr	AAC Asn	ACT Thr	AAA Lys	GCG Ala	TTG Leu	3416

1110	1115	1120	
AAT TTT GGG CTA TTT GCT GGG GTC CAA CTG GGC GGC GCA ACC TGG CTT			3464
Asn Phe Gly Leu Phe Ala Gly Val Gln Leu Gly Gly Ala Thr Trp Leu			
1125	1130	1135	
AGC TCC TTA AGG CAA CAA ATC ATT GAC AAC TGG GGG AGT GCT AAT GAC			3512
Ser Ser Leu Arg Gln Gln Ile Ile Asp Asn Trp Gly Ser Ala Asn Asp			
1140	1145	1150	
ATC CAT TCA ACG AAT TTT CAA GTG GCG CTG AAT TTT GGG GTG CGC ACC			3560
Ile His Ser Thr Asn Phe Gln Val Ala Leu Asn Phe Gly Val Arg Thr			
1155	1160	1165	1170
AAC TTC GCG GAG TTT AAG CGT TTT GCT AAG AAA TTC CAC AAT CAA GGG			3608
Asn Phe Ala Glu Phe Lys Arg Phe Ala Lys Lys Phe His Asn Gln Gly			
1175	1180	1185	
GTC ATC AGC CAA AAG AGC GTG GAA TTT GGG ATC AAA GTG CCT CTC ATC			3656
Val Ile Ser Gln Lys Ser Val Glu Phe Gly Ile Lys Val Pro Leu Ile			
1190	1195	1200	
AAT CAA GCG TAT TTG AAT AGC GCT GGA GCT GAT GTG AGT TAC AGG AGG			3704
Asn Gln Ala Tyr Leu Asn Ser Ala Gly Ala Asp Val Ser Tyr Arg Arg			
1205	1210	1215	
CTT TAT ACT TTT TAT ATC AAT TAC ATC ATG GGG TTT TAAAAAAGGG TGTGTC			3756
Leu Tyr Thr Phe Tyr Ile Asn Tyr Ile Met Gly Phe			
1220	1225	1230	
ATGGAAATCT TACAATTCAT CGGCTATGGG AATATGG			3793

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1230 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Met	Ile	Lys	Lys	Ala	Arg	Lys	Phe	Ile	Pro	Phe	Phe	Leu	Ile	Gly	Ser
1				5					10					15	
Leu	Leu	Ala	Glu	Asp	Asn	Gly	Trp	Tyr	Met	Ser	Val	Gly	Tyr	Gln	Ile
			20					25					30		
Gly	Gly	Thr	Gln	Gln	Phe	Ile	Asn	Asn	Lys	Gln	Leu	Leu	Glu	Asn	Gln
			35				40					45			
Asn	Ile	Ile	Asn	Ser	Val	Thr	Gln	Ser	Ala	Ile	Asn	Ile	Ala	Gly	Pro
	50					55					60				
Thr	Thr	Gly	Leu	Ile	Thr	Leu	Ser	Ser	Gln	Thr	Val	Ile	Asp	Ala	Leu
65					70				75					80	
Gly	Tyr	Gly	Val	Ser	Asn	Thr	Val	Gly	Asn	Gln	Leu	Glu	Gly	Ile	Ser
			85					90					95		
Asn	Ile	Leu	Asn	Gln	Ile	Gly	Lys	Arg	Lys	Asp	Phe	Tyr	Ser	Ser	Arg

[REDACTED]

				565					570					575			
Ser	Gly	Thr	Thr	Thr	Gln	Ser	Pro	Asn	Ser	Thr	Val	Met	Gly	Ala	Leu		
			580					585					590				
Asn	Thr	Val	Leu	Gln	Asn	Val	Ser	Asn	Phe	Gln	Gln	Ser	Ile	Gln	Asn		
		595					600					605					
Ala	Phe	Gln	Asn	Gln	Glu	Ser	Asn	Ile	Gln	Ala	Trp	Ala	Asn	Ala	Ile		
	610						615				620						
Tyr	Asn	Thr	Asn	Gly	Ser	Gln	Ser	Gln	Glu	Met	Thr	Pro	Asn	Asn	Asn		
625					630					635					640		
Gln	Asp	Leu	Arg	Ile	Gln	Leu	Arg	Ala	Asn	Phe	Tyr	Gln	Leu	Ile	Asn		
			645						650					655			
Thr	Ile	Asn	Gln	Gln	Val	Pro	Thr	Asp	Met	Asn	Ala	Leu	Ile	Asn	Gln		
		660						665					670				
Ser	Gln	Gln	Thr	Gln	Gln	Thr	Ser	Gly	Ser	Ala	Ser	Asn	Asn	Asn	Ala		
		675					680					685					
Cys	Ala	Ser	Gly	Met	Ser	Gly	Ser	Asn	Gly	Asn	Trp	Cys	Tyr	Gln	Gln		
	690					695					700						
Trp	Ser	Asp	Ser	Lys	Ala	Tyr	Tyr	Ser	Gly	Leu	Gln	Ser	Ala	Leu	Gly		
705				710					715						720		
Tyr	Gln	Thr	Gln	Ala	Thr	Thr	Gln	Ser	Gly	Ser	Asn	Gly	Gly	Asn	Ser		
			725					730						735			
Ile	Thr	Tyr	Asn	Val	Gln	Gln	Ile	Thr	Leu	Thr	Ser	Asn	Gly	Leu	Leu		
		740						745					750				
Asn	Gln	Ile	Ile	Thr	Asn	Leu	Lys	Ser	Val	Asn	Gly	Gly	Asn	Gly	Ala		
	755					760						765					
Ser	Gly	Thr	Gly	Ser	Gly	Asn	Gly	Thr	Ser	Gln	Ile	Asn	Thr	Ala	Tyr		
	770					775					780						
Gln	Met	Leu	Thr	Asp	Ala	Ser	Asp	Gly	Lys	Leu	Gly	Thr	Tyr	Ser	Ser		
785				790					795						800		
Ser	Ser	Gly	Ser	Asn	Asn	Gly	Tyr	Thr	Pro	Cys	Asn	Ser	Thr	Asn	Gly		
			805					810						815			
Ser	Asn	Lys	Thr	Ser	Gly	Asn	Asn	Cys	Tyr	Glu	Pro	Asn	Lys	Gln	Gln		
		820						825					830				
Asn	Ala	Thr	Thr	Ala	Thr	Ala	Thr	Thr	Asp	Ser	Asn	Leu	Gln	Lys	Val		
	835						840					845					
Tyr	Asn	Asp	Ala	Gln	Lys	Ile	Ala	Asn	Ile	Ile	Ala	Ser	Ser	Gly	Asn		
	850					855					860						
Asn	Lys	Gly	Val	Glu	Asn	Gly	Leu	Lys	Gln	Phe	Phe	Glu	Ala	Leu	Lys		
865				870					875						880		
Asn	Asn	Ser	Ser	Ser	Leu	Ser	Asn	Leu	Cys	Gly	Asn	Gly	Ser	Ser	Gly		
			885					890						895			
Ser	Ser	Gly	Thr	Thr	Cys	Ser	Gly	Trp	Leu	Ile	Asn	Leu	Leu	Gly	Ala		
		900						905					910				
Ile	Pro	Thr	Asn	Gly	Val	Ser	Asp	Thr	Asn	Asn	Leu	Ile	Asn	Leu	Leu		
	915						920					925					
Thr	Glu	Phe	Ile	Lys	Thr	Ala	Gly	Phe	Ile	Gln	Asn	Asn	Asp	Ser	Ser		
	930					935					940						
Val	Ser	Thr	Ser	Leu	Thr	Ser	Ala	Phe	Gln	Ala	Ile	Thr	Ser	Ala	Ile		
945				950					955						960		
Ser	Gln	Gly	Phe	Gln	Ala	Leu	Gln	Asn	Asp	Ile	Ser	Pro	Asn	Ala	Ile		
			965					970						975			
Leu	Thr	Leu	Leu	Gln	Glu	Ile	Thr	Ser	Asn	Thr	Thr	Thr	Ile	Gln	Ser		
		980						985					990				
Phe	Ser	Gln	Thr	Leu	Arg	Gln	Leu	Gly	Asp	Lys	Thr	Phe	Phe	Met			
	995					1000					1005						
Ala	Gln	Gln	Lys	Leu	Ile	Asp	Ala	Met	Ile	Asn	Ala	Arg	Asn	Gln	Val		
	1010					1015					1020						
Gln	Asn	Ala	Gln	Asn	Gln	Ala	Asn	Asn	Tyr	Gly	Ser	Gln	Pro	Val	Leu		

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025          1030          1035          1040
Ser Gln Tyr Ala Ala Ala Lys Ser Thr Gln His Gly Met Ser Asn Gly
          1045          1050          1055
Leu Gly Val Gly Leu Gly Tyr Lys Tyr Phe Phe Gly Lys Ala Arg Lys
          1060          1065          1070
Leu Gly Leu Arg His Tyr Phe Phe Phe Asp Tyr Gly Phe Ser Glu Ile
          1075          1080          1085
Gly Leu Ala Asn Gln Ser Val Lys Ala Asn Ile Phe Ala Tyr Gly Val
          1090          1095          1100
Gly Thr Asp Phe Leu Trp Asn Leu Phe Arg Arg Thr Tyr Asn Thr Lys
105          1110          1115          1120
Ala Leu Asn Phe Gly Leu Phe Ala Gly Val Gln Leu Gly Gly Ala Thr
          1125          1130          1135
Trp Leu Ser Ser Leu Arg Gln Gln Ile Ile Asp Asn Trp Gly Ser Ala
          1140          1145          1150
Asn Asp Ile His Ser Thr Asn Phe Gln Val Ala Leu Asn Phe Gly Val
          1155          1160          1165
Arg Thr Asn Phe Ala Glu Phe Lys Arg Phe Ala Lys Lys Phe His Asn
          1170          1175          1180
Gln Gly Val Ile Ser Gln Lys Ser Val Glu Phe Gly Ile Lys Val Pro
185          1190          1195          1200
Leu Ile Asn Gln Ala Tyr Leu Asn Ser Ala Gly Ala Asp Val Ser Tyr
          1205          1210          1215
Arg Arg Leu Tyr Thr Phe Tyr Ile Asn Tyr Ile Met Gly Phe
          1220          1225          1230

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(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 48...1226
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

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TAAGGATAAA ATCAAGCGAT TAGCCCGAAT TTTAAGAGAG TATTAAG ATG AAT AAA      56
                                     Met Asn Lys
                                     1

AAA GCG TAT TTT GGG GAG TTT GGA GGG AGT TTT GTT TCG GAG TTG TTA      104
Lys Ala Tyr Phe Gly Glu Phe Gly Gly Ser Phe Val Ser Glu Leu Leu
5          10          15

GTG CCT GCA TTA AGA GAA TTA GAA CAG GCG TTT GAT GCG TGT TTG AAA      152
Val Pro Ala Leu Arg Glu Leu Glu Gln Ala Phe Asp Ala Cys Leu Lys
20          25          30          35

GAT GAA AAA TTC CAA AAA GAA TAT TTT CGT CTT TTA AAG GAT TTT GTG      200

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Asp	Glu	Lys	Phe	Gln	Lys	Glu	Tyr	Phe	Arg	Leu	Leu	Lys	Asp	Phe	Val	
				40					45					50		
GGC	CGT	CCT	AGC	CCT	TTA	ACC	TTG	TGT	CAA	AAT	ATC	GTT	TCT	AAC	CCT	248
Gly	Arg	Pro	Ser	Pro	Leu	Thr	Leu	Cys	Gln	Asn	Ile	Val	Ser	Asn	Pro	
			55					60					65			
AAA	GTC	AAG	CTT	TAT	TTA	AAA	CGA	GAG	GAT	TTA	ATC	CAT	GGC	GGG	GCG	296
Lys	Val	Lys	Leu	Tyr	Leu	Lys	Arg	Glu	Asp	Leu	Ile	His	Gly	Gly	Ala	
		70					75					80				
CAT	AAG	ACT	AAT	CAA	GCC	TTA	GGG	CAA	GCC	CTT	TTA	GCG	AAA	AAA	ATG	344
His	Lys	Thr	Asn	Gln	Ala	Leu	Gly	Gln	Ala	Leu	Leu	Ala	Lys	Lys	Met	
	85					90					95					
GGT	AAA	ACA	AGG	ATC	ATC	GCT	GAA	ACA	GGC	GCC	GGT	CAG	CAT	GGC	GTG	392
Gly	Lys	Thr	Arg	Ile	Ile	Ala	Glu	Thr	Gly	Ala	Gly	Gln	His	Gly	Val	
100					105					110					115	
GCG	ACG	GCT	ATC	GCT	TGC	GCA	TTA	TTG	AAC	TTA	AAA	TGC	GTG	GTT	TTT	440
Ala	Thr	Ala	Ile	Ala	Cys	Ala	Leu	Leu	Asn	Leu	Lys	Cys	Val	Val	Phe	
				120					125					130		
ATG	GGA	TCT	AAA	GAC	ATC	AAG	CGC	CAG	GAA	ATG	AAT	GTT	TTT	AGA	ATG	488
Met	Gly	Ser	Lys	Asp	Ile	Lys	Arg	Gln	Glu	Met	Asn	Val	Phe	Arg	Met	
			135					140					145			
CAC	TTA	TTA	GGC	GCT	GAA	GTG	AGA	GAG	GTT	AAT	TCA	GGG	AGC	GCG	ACG	536
His	Leu	Leu	Gly	Ala	Glu	Val	Arg	Glu	Val	Asn	Ser	Gly	Ser	Ala	Thr	
		150					155					160				
CTT	AAA	GAC	GCT	GTG	AAT	GAA	GCC	TTA	AGA	GAT	TGG	GCG	AGC	AGT	TAC	584
Leu	Lys	Asp	Ala	Val	Asn	Glu	Ala	Leu	Arg	Asp	Trp	Ala	Ser	Ser	Tyr	
	165					170					175					
AAG	GAC	ACG	CAT	TAT	TTG	CTA	GGC	ACA	GCC	GCC	GGG	CCA	CAC	CCT	TAC	632
Lys	Asp	Thr	His	Tyr	Leu	Leu	Gly	Thr	Ala	Ala	Gly	Pro	His	Pro	Tyr	
180					185					190					195	
CCC	ACA	ATG	GTT	AAA	ACC	TTT	CAA	AAA	ATG	ATA	GGC	GAT	GAG	GTT	AAA	680
Pro	Thr	Met	Val	Lys	Thr	Phe	Gln	Lys	Met	Ile	Gly	Asp	Glu	Val	Lys	
				200					205					210		
AGC	CAG	ATT	TTA	GAA	AAA	GAA	AAC	CGC	TTG	CCT	GAT	TAT	GTG	ATC	GCA	728
Ser	Gln	Ile	Leu	Glu	Lys	Glu	Asn	Arg	Leu	Pro	Asp	Tyr	Val	Ile	Ala	
			215					220					225			
TGC	GTT	GGA	GGG	GGG	TCT	AAC	GCT	ATA	GGG	ATA	TTC	AGC	GCA	TTT	TTA	776
Cys	Val	Gly	Gly	Gly	Ser	Asn	Ala	Ile	Gly	Ile	Phe	Ser	Ala	Phe	Leu	
		230					235					240				
AAC	GAC	AAA	GAA	GTT	AAA	CTC	ATA	GGC	GTA	GAG	CCG	GCG	GGT	TTA	GGG	824
Asn	Asp	Lys	Glu	Val	Lys	Leu	Ile	Gly	Val	Glu	Pro	Ala	Gly	Leu	Gly	
	245					250					255					
CTA	GAA	ACC	AAT	AAG	CAT	GGG	GCG	ACT	TTG	AAT	AAG	GGG	CGT	GTG	GGG	872
Leu	Glu	Thr	Asn	Lys	His	Gly	Ala	Thr	Leu	Asn	Lys	Gly	Arg	Val	Gly	
260					265					270					275	

ATT TTG CAT GGG AAT AAA ACC TAT CTT TTA CAA GAT GAT GAA GGC CAG	920
Ile Leu His Gly Asn Lys Thr Tyr Leu Leu Gln Asp Asp Glu Gly Gln	
280 285 290	
ATT GCA GAA AGC CAT AGC ATT AGC GCC GGG CTT GAT TAT CCA GGA GTG	968
Ile Ala Glu Ser His Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val	
295 300 305	
GGG CCA GAA CAC AGC TAT TTA AAA GAA AGT GGG CGT GCG GTT TAT GAA	1016
Gly Pro Glu His Ser Tyr Leu Lys Glu Ser Gly Arg Ala Val Tyr Glu	
310 315 320	
AGC GCA AGC GAT GCT GAA GCG CTA GAA GCC TTC AAG TTG TTG TGC CAA	1064
Ser Ala Ser Asp Ala Glu Ala Leu Glu Ala Phe Lys Leu Leu Cys Gln	
325 330 335	
AAA GAA GGC ATT ATC CCA GCG CTA GAA AGC TCA CAC GCC TTA GCG TAT	1112
Lys Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala Leu Ala Tyr	
340 345 350 355	
GCC TTA AAG CTC GCT CAA AAA TGC GAA GAA GAA AGC ATC ATC GTA GTG	1160
Ala Leu Lys Leu Ala Gln Lys Cys Glu Glu Glu Ser Ile Ile Val Val	
360 365 370	
AAT TTA AGC GGC AGA GGG GAT AAG GAT TTA AGC ACC GTT TAT AAC GCT	1208
Asn Leu Ser Gly Arg Gly Asp Lys Asp Leu Ser Thr Val Tyr Asn Ala	
375 380 385	
TTA AAA GGA GGT TTA AAA TGAGGTATCA AAACATGTTT GAAACCTTAA AAA	1259
Leu Lys Gly Gly Leu Lys	
390	

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Met Asn Lys Lys Ala Tyr Phe Gly Glu Phe Gly Gly Ser Phe Val Ser	
1 5 10 15	
Glu Leu Leu Val Pro Ala Leu Arg Glu Leu Glu Gln Ala Phe Asp Ala	
20 25 30	
Cys Leu Lys Asp Glu Lys Phe Gln Lys Glu Tyr Phe Arg Leu Leu Lys	
35 40 45	
Asp Phe Val Gly Arg Pro Ser Pro Leu Thr Leu Cys Gln Asn Ile Val	
50 55 60	
Ser Asn Pro Lys Val Lys Leu Tyr Leu Lys Arg Glu Asp Leu Ile His	
65 70 75 80	
Gly Gly Ala His Lys Thr Asn Gln Ala Leu Gly Gln Ala Leu Leu Ala	
85 90 95	

Lys	Lys	Met	Gly	Lys	Thr	Arg	Ile	Ile	Ala	Glu	Thr	Gly	Ala	Gly	Gln	
			100					105					110			
His	Gly	Val	Ala	Thr	Ala	Ile	Ala	Cys	Ala	Leu	Leu	Asn	Leu	Lys	Cys	
		115					120					125				
Val	Val	Phe	Met	Gly	Ser	Lys	Asp	Ile	Lys	Arg	Gln	Glu	Met	Asn	Val	
	130					135					140					
Phe	Arg	Met	His	Leu	Leu	Gly	Ala	Glu	Val	Arg	Glu	Val	Asn	Ser	Gly	
145					150					155					160	
Ser	Ala	Thr	Leu	Lys	Asp	Ala	Val	Asn	Glu	Ala	Leu	Arg	Asp	Trp	Ala	
			165						170					175		
Ser	Ser	Tyr	Lys	Asp	Thr	His	Tyr	Leu	Leu	Gly	Thr	Ala	Ala	Gly	Pro	
		180						185					190			
His	Pro	Tyr	Pro	Thr	Met	Val	Lys	Thr	Phe	Gln	Lys	Met	Ile	Gly	Asp	
		195					200					205				
Glu	Val	Lys	Ser	Gln	Ile	Leu	Glu	Lys	Glu	Asn	Arg	Leu	Pro	Asp	Tyr	
	210					215					220					
Val	Ile	Ala	Cys	Val	Gly	Gly	Gly	Ser	Asn	Ala	Ile	Gly	Ile	Phe	Ser	
225					230					235					240	
Ala	Phe	Leu	Asn	Asp	Lys	Glu	Val	Lys	Leu	Ile	Gly	Val	Glu	Pro	Ala	
			245						250					255		
Gly	Leu	Gly	Leu	Glu	Thr	Asn	Lys	His	Gly	Ala	Thr	Leu	Asn	Lys	Gly	
			260					265					270			
Arg	Val	Gly	Ile	Leu	His	Gly	Asn	Lys	Thr	Tyr	Leu	Leu	Gln	Asp	Asp	
	275						280						285			
Glu	Gly	Gln	Ile	Ala	Glu	Ser	His	Ser	Ile	Ser	Ala	Gly	Leu	Asp	Tyr	
	290					295					300					
Pro	Gly	Val	Gly	Pro	Glu	His	Ser	Tyr	Leu	Lys	Glu	Ser	Gly	Arg	Ala	
305					310					315					320	
Val	Tyr	Glu	Ser	Ala	Ser	Asp	Ala	Glu	Ala	Leu	Glu	Ala	Phe	Lys	Leu	
			325						330					335		
Leu	Cys	Gln	Lys	Glu	Gly	Ile	Ile	Pro	Ala	Leu	Glu	Ser	Ser	His	Ala	
			340					345					350			
Leu	Ala	Tyr	Ala	Leu	Lys	Leu	Ala	Gln	Lys	Cys	Glu	Glu	Glu	Ser	Ile	
		355					360					365				
Ile	Val	Val	Asn	Leu	Ser	Gly	Arg	Gly	Asp	Lys	Asp	Leu	Ser	Thr	Val	
	370					375					380					
Tyr	Asn	Ala	Leu	Lys	Gly	Gly	Leu	Lys								
385					390											

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 197...547
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

TGGTGATGCA AAACCAAAAC AAGCGCATCA TGAATTACAT TCCTATTAAG TTGAATTTAA 60
 GTGGGGTGAT CCCCCTATT TTCGCTTCAG CTTTGCTCGT GTTCCCTTCT ACGATTTTGC 120
 AGCAAGCCAC AAGCAACAAA ACCTTGCAAG CGGTTGCGNA TTTTTTAAGC CCGCAAGGTA 180
 TGCCTATAAT ATTTTG ATG TTC TTG CTC ATC ATC TTT TTT GCT TAC TTT TAT 232
 Met Phe Leu Leu Ile Ile Phe Phe Ala Tyr Phe Tyr
 1 5 10

TCT TCT ATT GTG TTC AAT TCT AAG GAT ATT GCG GAT AAT TTG AGG CGT 280
 Ser Ser Ile Val Phe Asn Ser Lys Asp Ile Ala Asp Asn Leu Arg Arg
 15 20 25

AAT GGC GGG TAT ATT CCA GGG CTT AGG CCT GGA GAG GGG ACT TCA TCG 328
 Asn Gly Gly Tyr Ile Pro Gly Leu Arg Pro Gly Glu Gly Thr Ser Ser
 30 35 40

TTT TTA AAT TCT GTA GCG AGT AAG CTC ACT TTG TGG GGT TCA TTG TAT 376
 Phe Leu Asn Ser Val Ala Ser Lys Leu Thr Leu Trp Gly Ser Leu Tyr
 45 50 55 60

TTA GCG CTC ATT TCT ACC GTG CCT TGG ATT TTG GTT AAG GCT ATG GGC 424
 Leu Ala Leu Ile Ser Thr Val Pro Trp Ile Leu Val Lys Ala Met Gly
 65 70 75

GTG CCT TTT TAC TTT GGA GGC ACA GCG GTG CTG ATT GTG GTT CAA GTC 472
 Val Pro Phe Tyr Phe Gly Gly Thr Ala Val Leu Ile Val Val Gln Val
 80 85 90

GCT ATT GAC ACC ATG AAA AAG ATT GAA GCG CAA ATT TAT ATG AGC AAG 520
 Ala Ile Asp Thr Met Lys Lys Ile Glu Ala Gln Ile Tyr Met Ser Lys
 95 100 105

TAT AAA ACT TTA AGC GCG GTA GGC TTT TAATGGCAAT CTCTATTAAA AGCCCAA 574
 Tyr Lys Thr Leu Ser Ala Val Gly Phe
 110 115

AAGAAATCAA AGCTCTAAGA AAAGCCG 601

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Met Phe Leu Leu Ile Ile Phe Phe Ala Tyr Phe Tyr Ser Ser Ile Val
 1 5 10 15
 Phe Asn Ser Lys Asp Ile Ala Asp Asn Leu Arg Arg Asn Gly Tyr
 20 25 30
 Ile Pro Gly Leu Arg Pro Gly Glu Gly Thr Ser Ser Phe Leu Asn Ser
 35 40 45
 Val Ala Ser Lys Leu Thr Leu Trp Gly Ser Leu Tyr Leu Ala Leu Ile
 50 55 60

Ser	Thr	Val	Pro	Trp	Ile	Leu	Val	Lys	Ala	Met	Gly	Val	Pro	Phe	Tyr	
65					70				75						80	
Phe	Gly	Gly	Thr	Ala	Val	Leu	Ile	Val	Val	Gln	Val	Ala	Ile	Asp	Thr	
			85						90					95		
Met	Lys	Lys	Ile	Glu	Ala	Gln	Ile	Tyr	Met	Ser	Lys	Tyr	Lys	Thr	Leu	
			100					105					110			
Ser	Ala	Val	Gly	Phe												
			115													

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 64...675
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GAAAACAGGA	TAACGCATGA	AACATGTGAG	TAGGGATTTT	GATACCGGTT	GGGTTGCGTA	60
TCA ATG ACT CTA GGC ATT GAT GAA GCG GGT AGG GGG TGT TTG GCC GGT	108					
Met Thr Leu Gly Ile Asp Glu Ala Gly Arg Gly Cys Leu Ala Gly						
1 5 10 15						
TCG CTT TTT GTG GCT GGG GTG GCG TGT AAT GAA AAA ACA GCC TTA GAA	156					
Ser Leu Phe Val Ala Gly Val Ala Cys Asn Glu Lys Thr Ala Leu Glu						
20 25 30						
TTT CTA AAA ATG GGT TTA AAA GAC AGC AAG AAG CTC AGC CTA AAA AAG	204					
Phe Leu Lys Met Gly Leu Lys Asp Ser Lys Lys Leu Ser Leu Lys Lys						
35 40 45						
CGC TTT TTC TTA GAA TAT AAG ATC AAA ACG CAT GGT GAG GTG GGG TTT	252					
Arg Phe Phe Leu Glu Tyr Lys Ile Lys Thr His Gly Glu Val Gly Phe						
50 55 60						
TTC GTG GTT AAA AAA AGC GCA AAT GAA ATT GAT AGC TTG GGC TTA GGG	300					
Phe Val Val Lys Lys Ser Ala Asn Glu Ile Asp Ser Leu Gly Leu Gly						
65 70 75						
GCG TGT TTG AAA CTC GCT GTG CAA GAA ATT TTA GAA AAT GGT TGC TCT	348					
Ala Cys Leu Lys Leu Ala Val Gln Glu Ile Leu Glu Asn Gly Cys Ser						
80 85 90 95						
TTA GTT GAT GAA ATA AAA ATA GAC GGC AAC ACG GCG TTT GGC TTG AAC	396					
Leu Val Asp Glu Ile Lys Ile Asp Gly Asn Thr Ala Phe Gly Leu Asn						
100 105 110						
AAA CGC TAC CCC CAT ATA CAA ACC ATC ATC AAG GGC GAT GAA ACA ATC	444					

Lys	Arg	Tyr	Pro	His	Ile	Gln	Thr	Ile	Ile	Lys	Gly	Asp	Glu	Thr	Ile		
			115					120					125				
GCT	CAA	ATC	GCT	ATG	GCG	TCT	GTT	TTG	GCG	AAA	GCT	TTT	AAG	GAC	AGA	492	
Ala	Gln	Ile	Ala	Met	Ala	Ser	Val	Leu	Ala	Lys	Ala	Phe	Lys	Asp	Arg		
		130					135					140					
GAA	ATG	CTA	GAG	TTG	CAC	GCT	TTG	TTT	AAG	GAA	TAC	GGC	TGG	GAT	AAG	540	
Glu	Met	Leu	Glu	Leu	His	Ala	Leu	Phe	Lys	Glu	Tyr	Gly	Trp	Asp	Lys		
		145				150					155						
AAT	TGC	GGG	TAT	GGG	ACT	AAA	CAA	CAT	ATA	GAA	GCG	ATC	ATT	AAG	CTA	588	
Asn	Cys	Gly	Tyr	Gly	Thr	Lys	Gln	His	Ile	Glu	Ala	Ile	Ile	Lys	Leu		
160					165				170						175		
GGG	GCT	ACG	CCT	TTT	CAT	CGG	CAT	AGC	TTC	ACG	CTT	AAA	AAC	CGC	ATC	636	
Gly	Ala	Thr	Pro	Phe	His	Arg	His	Ser	Phe	Thr	Leu	Lys	Asn	Arg	Ile		
				180					185					190			
TTA	AAT	CCC	AAA	CTC	TTA	GAG	GTG	GAA	CAA	CGC	CTT	ATT	TAAAAGGGCG	CT	687		
Leu	Asn	Pro	Lys	Leu	Leu	Glu	Val	Glu	Gln	Arg	Leu	Ile					
			195					200									
GAGATGGGTA	GCGCTCGCTG	AAGAAAGGTC	GATGCGTT													725	

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Met	Thr	Leu	Gly	Ile	Asp	Glu	Ala	Gly	Arg	Gly	Cys	Leu	Ala	Gly	Ser		
1				5					10					15			
Leu	Phe	Val	Ala	Gly	Val	Ala	Cys	Asn	Glu	Lys	Thr	Ala	Leu	Glu	Phe		
			20					25					30				
Leu	Lys	Met	Gly	Leu	Lys	Asp	Ser	Lys	Lys	Leu	Ser	Leu	Lys	Lys	Arg		
		35				40					45						
Phe	Phe	Leu	Glu	Tyr	Lys	Ile	Lys	Thr	His	Gly	Glu	Val	Gly	Phe	Phe		
	50					55				60							
Val	Val	Lys	Lys	Ser	Ala	Asn	Glu	Ile	Asp	Ser	Leu	Gly	Leu	Gly	Ala		
65					70				75						80		
Cys	Leu	Lys	Leu	Ala	Val	Gln	Glu	Ile	Leu	Glu	Asn	Gly	Cys	Ser	Leu		
				85					90					95			
Val	Asp	Glu	Ile	Lys	Ile	Asp	Gly	Asn	Thr	Ala	Phe	Gly	Leu	Asn	Lys		
			100				105						110				
Arg	Tyr	Pro	His	Ile	Gln	Thr	Ile	Ile	Lys	Gly	Asp	Glu	Thr	Ile	Ala		
		115				120						125					
Gln	Ile	Ala	Met	Ala	Ser	Val	Leu	Ala	Lys	Ala	Phe	Lys	Asp	Arg	Glu		
		130				135					140						
Met	Leu	Glu	Leu	His	Ala	Leu	Phe	Lys	Glu	Tyr	Gly	Trp	Asp	Lys	Asn		
145					150					155					160		

His	Ala	Lys	Lys	Phe	Leu	Glu	Ile	Gln	Lys	Asn	Glu	Phe	Leu	Gln	Leu	
115						120					125					
GGT	GTT	TTG	GGG	GAT	TTT	GAA	GAT	CCT	TAT	AAA	ACC	ATG	GAT	TTT	AAA	492
Gly	Val	Leu	Gly	Asp	Phe	Glu	Asp	Pro	Tyr	Lys	Thr	Met	Asp	Phe	Lys	
130					135					140					145	
TTT	GAA	GCG	AGC	ATT	TAT	AGA	GCC	TTA	GTG	GAA	GTG	GCT	AAA	AAA	GGG	540
Phe	Glu	Ala	Ser	Ile	Tyr	Arg	Ala	Leu	Val	Glu	Val	Ala	Lys	Lys	Gly	
				150					155						160	
CTT	TTG	AAA	GAG	CGC	CAC	AAG	CCT	ATT	TAT	TGG	AGT	TAT	GCA	TGC	GAG	588
Leu	Leu	Lys	Glu	Arg	His	Lys	Pro	Ile	Tyr	Trp	Ser	Tyr	Ala	Cys	Glu	
			165					170					175			
AGC	GCT	TTA	GCG	GAA	GCT	GAA	GTG	GAA	TAC	AAA	ATG	AAA	AAA	TCG	CCC	636
Ser	Ala	Leu	Ala	Glu	Ala	Glu	Val	Glu	Tyr	Lys	Met	Lys	Lys	Ser	Pro	
		180					185					190				
TCC	ATT	TTC	GTG	GCG	TTT	GGT	TTG	AAA	AAG	GAG	AGT	TTA	GAA	AAA	TTA	684
Ser	Ile	Phe	Val	Ala	Phe	Gly	Leu	Lys	Lys	Glu	Ser	Leu	Glu	Lys	Leu	
	195					200					205					
AAA	GTC	AAA	AAA	GCG	AGC	TTG	GTG	ATT	TGG	ACG	ACC	ACG	CCT	TGG	ACT	732
Lys	Val	Lys	Lys	Ala	Ser	Leu	Val	Ile	Trp	Thr	Thr	Thr	Pro	Trp	Thr	
210					215					220					225	
TTG	TAT	GCG	AAT	GTA	GCG	ATC	GCT	TTG	AAA	AAA	GAC	GCT	GTT	TAT	GCG	780
Leu	Tyr	Ala	Asn	Val	Ala	Ile	Ala	Leu	Lys	Lys	Asp	Ala	Val	Tyr	Ala	
				230					235					240		
CTC	ACC	CAA	AAA	GGC	TAT	TTA	GTC	GCT	AAA	GCC	TTG	CAT	GAA	AAA	TTA	828
Leu	Thr	Gln	Lys	Gly	Tyr	Leu	Val	Ala	Lys	Ala	Leu	His	Glu	Lys	Leu	
			245					250					255			
GCC	GCT	TTA	GGG	GTG	GTG	GAT	AAT	GAG	ATC	ACA	CAT	GAA	TTC	AAT	TCC	876
Ala	Ala	Leu	Gly	Val	Val	Asp	Asn	Glu	Ile	Thr	His	Glu	Phe	Asn	Ser	
		260					265					270				
AAT	GAT	TTA	GAA	TAT	TTA	GTG	GCT	ACA	AAC	CCG	CTC	AAT	CAA	AGG	GAT	924
Asn	Asp	Leu	Glu	Tyr	Leu	Val	Ala	Thr	Asn	Pro	Leu	Asn	Gln	Arg	Asp	
	275					280					285					
TCG	CTG	GTG	GCT	TTA	GGA	GAG	CAT	GTC	GGT	TTA	GAA	GAT	GGC	ACA	GGA	972
Ser	Leu	Val	Ala	Leu	Gly	Glu	His	Val	Gly	Leu	Glu	Asp	Gly	Thr	Gly	
290				295						300					305	
GCC	GTG	CAT	ACC	GCA	CCT	GGG	CAT	GGT	GAA	GAG	GAC	TAT	TAT	TTA	GGC	1020
Ala	Val	His	Thr	Ala	Pro	Gly	His	Gly	Glu	Glu	Asp	Tyr	Tyr	Leu	Gly	
				310					315					320		
TTA	AGA	TAT	AAT	TTA	GAA	GTG	TTA	ATG	TCT	GTA	GAT	GAG	AAA	GGT	TGC	1068
Leu	Arg	Tyr	Asn	Leu	Glu	Val	Leu	Met	Ser	Val	Asp	Glu	Lys	Gly	Cys	
			325					330					335			
TAT	GAT	GAG	GGC	ATT	ATC	CAT	AAC	CAA	CTA	TTA	GAT	GAA	AGC	TAT	CTG	1116
Tyr	Asp	Glu	Gly	Ile	Ile	His	Asn	Gln	Leu	Leu	Asp	Glu	Ser	Tyr	Leu	
		340					345					350				

GGC	GAG	CAT	GTT	TTT	AAG	GCT	CAA	AAA	CGC	ATT	ATA	GAG	CAA	TTG	GGC	1164
Gly	Glu	His	Val	Phe	Lys	Ala	Gln	Lys	Arg	Ile	Ile	Glu	Gln	Leu	Gly	
355						360					365					
GAT	TCT	TTA	TTG	CTA	GAG	CAA	GAG	ATT	GAG	CAT	TCT	TAT	CCG	CAT	TGC	1212
Asp	Ser	Leu	Leu	Leu	Glu	Gln	Glu	Ile	Glu	His	Ser	Tyr	Pro	His	Cys	
370					375				380						385	
TGG	AGG	ACG	CAC	AAG	CCT	GTG	ATT	TAC	AGA	GCG	ACT	ACG	CAA	TGG	TTT	1260
Trp	Arg	Thr	His	Lys	Pro	Val	Ile	Tyr	Arg	Ala	Thr	Thr	Gln	Trp	Phe	
				390					395					400		
ATT	TTA	ATG	GAT	GAG	CCT	TTT	ATC	CAA	AAT	GAT	GGC	TCT	CAA	AAA	ACC	1308
Ile	Leu	Met	Asp	Glu	Pro	Phe	Ile	Gln	Asn	Asp	Gly	Ser	Gln	Lys	Thr	
			405					410					415			
TTA	AGA	GAA	GTG	GCT	TTA	GAT	GCG	ATT	GAA	AAG	GTG	GAA	TTT	GTG	CCA	1356
Leu	Arg	Glu	Val	Ala	Leu	Asp	Ala	Ile	Glu	Lys	Val	Glu	Phe	Val	Pro	
		420					425					430				
AGC	AGC	GGG	AAA	AAC	CGC	CTA	AAA	ACC	ATG	ATA	GAA	AAC	CGC	CCT	GAT	1404
Ser	Ser	Gly	Lys	Asn	Arg	Leu	Lys	Thr	Met	Ile	Glu	Asn	Arg	Pro	Asp	
		435				440					445					
TGG	TGC	TTG	AGC	CGG	CAA	AGA	AAA	TGG	GGC	GTG	CCA	CTG	GCC	TTT	TTC	1452
Trp	Cys	Leu	Ser	Arg	Gln	Arg	Lys	Trp	Gly	Val	Pro	Leu	Ala	Phe	Phe	
450					455				460					465		
ATA	GAC	AAA	CGC	ACG	AAT	AAG	CCT	TGT	TTT	GAA	AGC	GAA	GTT	TTA	GAG	1500
Ile	Asp	Lys	Arg	Thr	Asn	Lys	Pro	Cys	Phe	Glu	Ser	Glu	Val	Leu	Glu	
				470					475					480		
CAT	GTG	GCC	AAT	CTT	TTT	GAG	AAA	AAA	GGC	TGT	GAT	GTG	TGG	TGG	GAG	1548
His	Val	Ala	Asn	Leu	Phe	Glu	Lys	Lys	Gly	Cys	Asp	Val	Trp	Trp	Glu	
			485					490					495			
TAT	AGC	GTG	AAA	GAT	TTA	TTG	CCC	CCT	AGC	TAT	CAA	GAG	GAC	GCC	AAG	1596
Tyr	Ser	Val	Lys	Asp	Leu	Leu	Pro	Pro	Ser	Tyr	Gln	Glu	Asp	Ala	Lys	
		500					505					510				
CAT	TAT	GAG	AAA	ATC	ATG	CAC	ATT	TTA	GAC	GTG	TGG	TTT	GAT	AGT	GGT	1644
His	Tyr	Glu	Lys	Ile	Met	His	Ile	Leu	Asp	Val	Trp	Phe	Asp	Ser	Gly	
		515				520					525					
AGC	ACC	TTT	AAG	GCG	GTT	TTA	GAA	GAC	TAT	CAT	GGA	GAA	AAA	GGG	CAA	1692
Ser	Thr	Phe	Lys	Ala	Val	Leu	Glu	Asp	Tyr	His	Gly	Glu	Lys	Gly	Gln	
530					535					540					545	
AGC	CCT	AGC	GAT	GTG	ATC	TTA	GAA	GGG	AGC	GAT	CAG	CAT	AGG	GGG	TGG	1740
Ser	Pro	Ser	Asp	Val	Ile	Leu	Glu	Gly	Ser	Asp	Gln	His	Arg	Gly	Trp	
				550					555					560		
TTT	CAA	AGC	TCG	CTT	CTA	ATC	GGT	TGT	GTT	TTA	AAC	AAC	CAA	GCC	CCT	1788
Phe	Gln	Ser	Ser	Leu	Leu	Ile	Gly	Cys	Val	Leu	Asn	Asn	Gln	Ala	Pro	
			565					570					575			
TTT	AAA	AAG	GTC	ATT	ACG	CAT	GGC	TTT	ATC	GTA	GAT	GAA	AAG	GGC	GAA	1836
Phe	Lys	Lys	Val	Ile	Thr	His	Gly	Phe	Ile	Val	Asp	Glu	Lys	Gly	Glu	

580					585					590						
AAA	ATG	AGT	AAA	TCT	AAG	GGC	AAT	GTG	GTG	TCT	TTG	GAC	AAG	CTG	CTC	1884
Lys	Met	Ser	Lys	Ser	Lys	Gly	Asn	Val	Val	Ser	Leu	Asp	Lys	Leu	Leu	
595					600					605						
AAA	ACG	CAT	GGG	AGC	GAT	GTG	GTG	CGT	TTG	TGG	GTA	GCG	TTT	AAT	GAC	1932
Lys	Thr	His	Gly	Ser	Asp	Val	Val	Arg	Leu	Trp	Val	Ala	Phe	Asn	Asp	
610					615					620					625	
TAT	CAA	AAC	GAT	TTG	AGA	GTC	TCT	CAA	ACC	TTT	TTC	ACT	CAA	ACA	GAA	1980
Tyr	Gln	Asn	Asp	Leu	Arg	Val	Ser	Gln	Thr	Phe	Phe	Thr	Gln	Thr	Glu	
630					635					640						
CAA	CAT	TAT	AAA	AAA	TTC	CGC	AAC	ACC	CTG	AAA	TTC	TTA	CTC	GCT	AAT	2028
Gln	His	Tyr	Lys	Lys	Phe	Arg	Asn	Thr	Leu	Lys	Phe	Leu	Leu	Ala	Asn	
645					650					655						
TTT	AGC	GAT	ATG	GAT	CTC	AAG	AAT	TTA	GAA	CGC	CCC	CAT	AAC	TTC	AGC	2076
Phe	Ser	Asp	Met	Asp	Leu	Lys	Asn	Leu	Glu	Arg	Pro	His	Asn	Phe	Ser	
660					665					670						
CCT	TTA	GAT	CAT	TTT	ATG	TTA	GAG	ACT	TTA	GAA	ACC	ATA	AGC	GCT	GGA	2124
Pro	Leu	Asp	His	Phe	Met	Leu	Glu	Thr	Leu	Glu	Thr	Ile	Ser	Ala	Gly	
675					680					685						
GTC	AAT	AGC	GCG	TTT	GAA	GAG	CAT	GAT	TTT	GTG	AAA	GGC	TTG	AAT	ATT	2172
Val	Asn	Ser	Ala	Phe	Glu	Glu	His	Asp	Phe	Val	Lys	Gly	Leu	Asn	Ile	
690					695					700					705	
TTA	ATG	GCG	TTT	GTT	ACC	AAT	GAA	TTG	AGC	GGG	ATT	TAT	TTA	GAC	GCT	2220
Leu	Met	Ala	Phe	Val	Thr	Asn	Glu	Leu	Ser	Gly	Ile	Tyr	Leu	Asp	Ala	
710					715					720						
TGC	AAG	GAT	AGC	TTG	TAT	TGC	GAT	AGC	AAA	AAC	AAT	GAA	AAA	CGC	CAA	2268
Cys	Lys	Asp	Ser	Leu	Tyr	Cys	Asp	Ser	Lys	Asn	Asn	Glu	Lys	Arg	Gln	
725					730					735						
GCC	ATT	CAA	ATG	GTT	TTA	CTC	GCT	ACA	GCT	AGT	AAG	TTG	TGC	TAC	TTT	2316
Ala	Ile	Gln	Met	Val	Leu	Leu	Ala	Thr	Ala	Ser	Lys	Leu	Cys	Tyr	Phe	
740					745					750						
TTA	GCC	CCG	ATT	TTA	ACG	CAC	ACG	ATT	GAA	GAA	GTT	TTA	GAG	CAT	AGC	2364
Leu	Ala	Pro	Ile	Leu	Thr	His	Thr	Ile	Glu	Glu	Val	Leu	Glu	His	Ser	
755					760					765						
CAA	GCG	CTT	CGC	ATT	TTT	TTA	CAA	GCC	AAA	GAT	GTG	TTT	GAT	TTA	AAA	2412
Gln	Ala	Leu	Arg	Ile	Phe	Leu	Gln	Ala	Lys	Asp	Val	Phe	Asp	Leu	Lys	
770					775					780					785	
GAC	ATT	AGC	GTT	TCA	GAA	AAA	CTC	CAC	CTC	AAA	GAG	TTT	AAA	AAA	CCA	2460
Asp	Ile	Ser	Val	Ser	Glu	Lys	Leu	His	Leu	Lys	Glu	Phe	Lys	Lys	Pro	
790					795					800						
GAA	AAT	TTT	GAA	GCC	GTT	TTA	GCC	TTG	CGT	TCT	GCC	TTT	AAT	GAA	GAG	2508
Glu	Asn	Phe	Glu	Ala	Val	Leu	Ala	Leu	Arg	Ser	Ala	Phe	Asn	Glu	Glu	
805					810					815						

TTA GAC CGA TTG AAA AAA GAA GGC GTC ATT AAA AAT TCG TTA GAG TGC 2556
 Leu Asp Arg Leu Lys Lys Glu Gly Val Ile Lys Asn Ser Leu Glu Cys
 820 825 830

GCT ATT GAA GTA AAA GAA AAA GCG TTG GAT GAA AAT TTA GTA GAA GAG 2604
 Ala Ile Glu Val Lys Glu Lys Ala Leu Asp Glu Asn Leu Val Glu Glu
 835 840 845

TTG CTG ATG GTA AGC TTT GTG GGG ATT GCA AAA GAA AAA TTG AGT GAA 2652
 Leu Leu Met Val Ser Phe Val Gly Ile Ala Lys Glu Lys Leu Ser Glu
 850 855 860 865

ACG CCA GCA TTC ACG CTC TTT AAA GCC CCC TTT TAT AAA TGC CCC AGG 2700
 Thr Pro Ala Phe Thr Leu Phe Lys Ala Pro Phe Tyr Lys Cys Pro Arg
 870 875 880

TGT TGG CGT TTT AAA AGC GAG CTA GAA AAC ACC CCT TGC AAG CGT TGC 2748
 Cys Trp Arg Phe Lys Ser Glu Leu Glu Asn Thr Pro Cys Lys Arg Cys
 885 890 895

GAA CAG GTT TTA AAA GAG CGA TGATAAAAGG ATAGGGCTTT TGAAAACCTTT ACAA 2803
 Glu Gln Val Leu Lys Glu Arg
 900

ACCCATAGAG TTTTACAA 2821

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Met Lys Gly Asn Leu Ser Val Asn Glu Pro Lys Thr Tyr Ala Lys Trp
 1 5 10 15
 Gln Glu Gln Gln Ala Phe Lys Arg Met Gln Ala Arg Lys Asp Asn His
 20 25 30
 Gly Asp Phe Thr Leu His Asp Gly Pro Pro Tyr Ala Asn Gly His Leu
 35 40 45
 His Leu Gly His Ala Leu Asn Lys Ile Leu Lys Asp Ile Val Val Lys
 50 55 60
 Arg Glu Tyr Phe Lys Gly Lys Lys Ile Tyr Tyr Thr Pro Gly Trp Asp
 65 70 75 80
 Cys His Gly Leu Pro Ile Glu Gln Gln Ile Leu Glu Arg Leu Glu Lys
 85 90 95
 Glu Lys Thr Ser Leu Glu Asn Pro Thr Leu Phe Arg Glu Lys Cys Arg
 100 105 110
 Asp His Ala Lys Lys Phe Leu Glu Ile Gln Lys Asn Glu Phe Leu Gln
 115 120 125
 Leu Gly Val Leu Gly Asp Phe Glu Asp Pro Tyr Lys Thr Met Asp Phe
 130 135 140
 Lys Phe Glu Ala Ser Ile Tyr Arg Ala Leu Val Glu Val Ala Lys Lys

145					150					155					160
Gly	Leu	Leu	Lys	Glu	Arg	His	Lys	Pro	Ile	Tyr	Trp	Ser	Tyr	Ala	Cys
				165					170					175	
Glu	Ser	Ala	Leu	Ala	Glu	Ala	Glu	Val	Glu	Tyr	Lys	Met	Lys	Lys	Ser
			180					185					190		
Pro	Ser	Ile	Phe	Val	Ala	Phe	Gly	Leu	Lys	Lys	Glu	Ser	Leu	Glu	Lys
		195					200					205			
Leu	Lys	Val	Lys	Lys	Ala	Ser	Leu	Val	Ile	Trp	Thr	Thr	Thr	Pro	Trp
	210					215					220				
Thr	Leu	Tyr	Ala	Asn	Val	Ala	Ile	Ala	Leu	Lys	Lys	Asp	Ala	Val	Tyr
225				230						235				240	
Ala	Leu	Thr	Gln	Lys	Gly	Tyr	Leu	Val	Ala	Lys	Ala	Leu	His	Glu	Lys
			245						250					255	
Leu	Ala	Ala	Leu	Gly	Val	Val	Asp	Asn	Glu	Ile	Thr	His	Glu	Phe	Asn
			260					265					270		
Ser	Asn	Asp	Leu	Glu	Tyr	Leu	Val	Ala	Thr	Asn	Pro	Leu	Asn	Gln	Arg
		275					280					285			
Asp	Ser	Leu	Val	Ala	Leu	Gly	Glu	His	Val	Gly	Leu	Glu	Asp	Gly	Thr
	290					295				300					
Gly	Ala	Val	His	Thr	Ala	Pro	Gly	His	Gly	Glu	Glu	Asp	Tyr	Tyr	Leu
305				310						315				320	
Gly	Leu	Arg	Tyr	Asn	Leu	Glu	Val	Leu	Met	Ser	Val	Asp	Glu	Lys	Gly
			325						330					335	
Cys	Tyr	Asp	Glu	Gly	Ile	Ile	His	Asn	Gln	Leu	Leu	Asp	Glu	Ser	Tyr
		340						345				350			
Leu	Gly	Glu	His	Val	Phe	Lys	Ala	Gln	Lys	Arg	Ile	Ile	Glu	Gln	Leu
		355					360					365			
Gly	Asp	Ser	Leu	Leu	Leu	Glu	Gln	Glu	Ile	Glu	His	Ser	Tyr	Pro	His
	370					375				380					
Cys	Trp	Arg	Thr	His	Lys	Pro	Val	Ile	Tyr	Arg	Ala	Thr	Thr	Gln	Trp
385				390						395				400	
Phe	Ile	Leu	Met	Asp	Glu	Pro	Phe	Ile	Gln	Asn	Asp	Gly	Ser	Gln	Lys
			405						410					415	
Thr	Leu	Arg	Glu	Val	Ala	Leu	Asp	Ala	Ile	Glu	Lys	Val	Glu	Phe	Val
		420						425					430		
Pro	Ser	Ser	Gly	Lys	Asn	Arg	Leu	Lys	Thr	Met	Ile	Glu	Asn	Arg	Pro
		435					440					445			
Asp	Trp	Cys	Leu	Ser	Arg	Gln	Arg	Lys	Trp	Gly	Val	Pro	Leu	Ala	Phe
	450					455				460					
Phe	Ile	Asp	Lys	Arg	Thr	Asn	Lys	Pro	Cys	Phe	Glu	Ser	Glu	Val	Leu
465				470						475				480	
Glu	His	Val	Ala	Asn	Leu	Phe	Glu	Lys	Lys	Gly	Cys	Asp	Val	Trp	Trp
			485						490					495	
Glu	Tyr	Ser	Val	Lys	Asp	Leu	Leu	Pro	Ser	Tyr	Gln	Glu	Asp	Ala	
			500					505				510			
Lys	His	Tyr	Glu	Lys	Ile	Met	His	Ile	Leu	Asp	Val	Trp	Phe	Asp	Ser
		515					520					525			
Gly	Ser	Thr	Phe	Lys	Ala	Val	Leu	Glu	Asp	Tyr	His	Gly	Glu	Lys	Gly
	530					535				540					
Gln	Ser	Pro	Ser	Asp	Val	Ile	Leu	Glu	Gly	Ser	Asp	Gln	His	Arg	Gly
545				550						555				560	
Trp	Phe	Gln	Ser	Ser	Leu	Leu	Ile	Gly	Cys	Val	Leu	Asn	Asn	Gln	Ala
			565						570					575	
Pro	Phe	Lys	Lys	Val	Ile	Thr	His	Gly	Phe	Ile	Val	Asp	Glu	Lys	Gly
		580						585				590			
Glu	Lys	Met	Ser	Lys	Ser	Lys	Gly	Asn	Val	Val	Ser	Leu	Asp	Lys	Leu
		595					600					605			
Leu	Lys	Thr	His	Gly	Ser	Asp	Val	Val	Arg	Leu	Trp	Val	Ala	Phe	Asn

610	Asp Tyr Gln Asn Asp	615	Leu Arg Val Ser Gln Thr	620	Phe Phe Thr Gln Thr
625	Glu Gln His Tyr Lys	630	Lys Phe Arg Asn Thr	635	Leu Lys Phe Leu Leu
	645	650	Asn Leu Glu Arg Pro	655	His Asn Phe
Asn Phe Ser Asp Met	660	665	Leu Glu Thr Leu Glu	670	Thr Ile Ser Ala
Ser Pro Leu Asp His	675	680	Phe Met Leu Glu Thr	685	Val Lys Gly Leu Asn
Gly Val Asn Ser Ala	690	695	Phe Glu Glu His Asp	700	Gly Ile Tyr Leu Asp
Ile Leu Met Ala Phe	710	715	Val Thr Asn Glu Leu	720	Ser Gly Ile Tyr Leu
705	725	730	Ala Cys Lys Asp Ser	735	Leu Tyr Leu Asp
Ala Cys Lys Asp Ser	740	745	Leu Tyr Cys Asp Ser	750	Asn Asn Glu Lys Arg
Gln Ala Ile Gln Met	755	760	Val Leu Leu Ala Thr	765	Ala Ser Lys Leu Cys
Phe Leu Ala Pro Ile	770	775	Leu Thr His Thr Ile	780	Glu Glu Val Leu Glu
Ser Gln Ala Leu Arg	785	790	Ile Phe Leu Gln Ala	795	Lys Asp Val Phe Asp
Lys Asp Ile Ser Val	805	810	Ser Glu Lys Leu His	815	Leu Lys Glu Phe Lys
Pro Glu Asn Phe Glu	820	825	Ala Val Leu Ala Leu	830	Arg Ser Ala Phe Asn
Glu Leu Asp Arg Leu	835	840	Lys Lys Glu Gly Val	845	Ile Lys Asn Ser Leu
Cys Ala Ile Glu Val	850	855	Lys Glu Lys Ala Leu	860	Asp Glu Asn Leu Val
Glu Leu Leu Met Val	865	870	Ser Phe Val Gly Ile	875	Ala Lys Glu Lys Leu
Glu Thr Pro Ala Phe	885	890	Thr Leu Phe Lys Ala	895	Pro Phe Tyr Lys Cys
Arg Cys Trp Arg Phe			885		Pro Cys Lys Arg
Cys Glu Gln Val Leu					
	900				

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 70...288
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

TGTAGAATGA AATCCTAGCC AGTGAGCTAG AATTTAAATT TTTAATCAAA GGAGTCATCA

60

TGGCACACC ATG AAG AAC AAC ACG GCG GGC ACC ACC ACC ACC ATC ACC ACA 111
 Met Lys Asn Asn Thr Ala Gly Thr Thr Thr Thr Ile Thr Thr
 1 5 10

CAC ACC ACC ACC ACT ATC ATG GCG GTG AAC ACC ACC ATC ACC ACC ACA 159
 His Thr Thr Thr Thr Ile Met Ala Val Asn Thr Thr Thr Thr Thr Thr
 15 20 25 30

GCT CTC ATC ATG AAG AAG GTT GTT GCA GCA CTA GCG ACA GTC ATC ATC 207
 Ala Leu Ile Met Lys Lys Val Val Ala Ala Leu Ala Thr Val Ile Ile
 35 40 45

AAG AAG AAG GTT GCT GCC ACG GGC ATC ACG AGT AAT ATC GGT GTG GCT 255
 Lys Lys Lys Val Ala Ala Thr Gly Ile Thr Ser Asn Ile Gly Val Ala
 50 55 60

AGG GGC AAC TTG ACT AGG GTT GTC TCT GGC TTT TGACTTTAAA ATACAATCAT 308
 Arg Gly Asn Leu Thr Arg Val Val Ser Gly Phe
 65 70

TCCATTCTAA CCCATTCTGA TCAAACCCGT T 339

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Met Lys Asn Asn Thr Ala Gly Thr Thr Thr Thr Ile Thr Thr His Thr
 1 5 10 15
 Thr Thr Thr Ile Met Ala Val Asn Thr Thr Thr Thr Thr Thr Ala Leu
 20 25 30
 Ile Met Lys Lys Val Val Ala Ala Leu Ala Thr Val Ile Ile Lys Lys
 35 40 45
 Lys Val Ala Ala Thr Gly Ile Thr Ser Asn Ile Gly Val Ala Arg Gly
 50 55 60
 Asn Leu Thr Arg Val Val Ser Gly Phe
 65 70

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

(B) LOCATION: 51...734
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GTTTTCTACT TATGATTTTG TGGAAGAATA TTGCAAATTA AAGGAAATGC	ATG CTT	56
	Met Leu	
	1	
GAA AAA GTG TTT CAA GAA ATT ACC AAT AAA AGA AAG TTT TTT GCA AGT		104
Glu Lys Val Phe Gln Glu Ile Thr Asn Lys Arg Lys Phe Phe Ala Ser		
5 10 15		
TCT AGC ACA GGG GAG CAG TTT GAA AAC CAA TTT AGG AAT GAA TTA AAA		152
Ser Ser Thr Gly Glu Gln Phe Glu Asn Gln Phe Arg Asn Glu Leu Lys		
20 25 30		
AAA CAC TTT AGC GAA ATC AAT GGC GAT TTA ACA GAA GAA TTA AGC CAT		200
Lys His Phe Ser Glu Ile Asn Gly Asp Leu Thr Glu Glu Leu Ser His		
35 40 45 50		
ATT GAA GAA AAG CCT AAT AAA GAA ATC AAA ACC ACT TTT AAC CAA CTC		248
Ile Glu Glu Lys Pro Asn Lys Glu Ile Lys Thr Thr Phe Asn Gln Leu		
55 60 65		
AAA AAG CAA GTT TTA GAA AAA AAT CAC CCG CAC ACC CTT AAA AAC CCT		296
Lys Lys Gln Val Leu Glu Lys Asn His Pro His Thr Leu Lys Asn Pro		
70 75 80		
TTT TCA AAC CTT ACA AGC CAT TTT TTA TAC CAG CCT TTT GGC TCA CAA		344
Phe Ser Asn Leu Thr Ser His Phe Leu Tyr Gln Pro Phe Gly Ser Gln		
85 90 95		
AAT TAC CCT GAT TTT TTG GTT TTT ATT TTT GAC TAT GTG GTG GGG ATT		392
Asn Tyr Pro Asp Phe Leu Val Phe Ile Phe Asp Tyr Val Val Gly Ile		
100 105 110		
GAA ATC AAG TTT TCT AAA AAC GAT AAG GGT GAA AAA AAT CTT CAA ACA		440
Glu Ile Lys Phe Ser Lys Asn Asp Lys Gly Glu Lys Asn Leu Gln Thr		
115 120 125 130		
TCT CGC CCC ATG TGG AAT TCA AAC CTG CCT AAA CCC AAT GCG ATT TAT		488
Ser Arg Pro Met Trp Asn Ser Asn Leu Pro Lys Pro Asn Ala Ile Tyr		
135 140 145		
GTG TAT GGA GTC GCT AAT GCA AAC ATC ACT TTT TTT AAA GGC TCA GAT		536
Val Tyr Gly Val Ala Asn Ala Asn Ile Thr Phe Phe Lys Gly Ser Asp		
150 155 160		
ATT TTG AGT TAT GAA ACC AGA GAG GTC TTG CTC AAG TAT TTT GAT ATT		584
Ile Leu Ser Tyr Glu Thr Arg Glu Val Leu Leu Lys Tyr Phe Asp Ile		
165 170 175		
TTA GAT AAA GAT GAA AGA AGT TTG AAA AAC GCC TTA AAG GAT TTA GAA		632
Leu Asp Lys Asp Glu Arg Ser Leu Lys Asn Ala Leu Lys Asp Leu Glu		
180 185 190		

AAC CCT TTT GGG TTT GCC CCC TAC ATC AGA AAA GCT TAT GAG CAT AAA 680
 Asn Pro Phe Gly Phe Ala Pro Tyr Ile Arg Lys Ala Tyr Glu His Lys
 195 200 205 210

AGG AAT TTT CTA ACC ACC ACC AGA TTG AAA GCT TCT TTT CGC CCA ACC 728
 Arg Asn Phe Leu Thr Thr Arg Leu Lys Ala Ser Phe Arg Pro Thr
 215 220 225

ACA TTT TAAGAGAGCG GAATGTCTTG GAATTTTGA AAACGCTCAC TCATTAGCGT AT 786
 Thr Phe

T 787

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Met Leu Glu Lys Val Phe Gln Glu Ile Thr Asn Lys Arg Lys Phe Phe
 1 5 10 15
 Ala Ser Ser Ser Thr Gly Glu Gln Phe Glu Asn Gln Phe Arg Asn Glu
 20 25 30
 Leu Lys Lys His Phe Ser Glu Ile Asn Gly Asp Leu Thr Glu Glu Leu
 35 40 45
 Ser His Ile Glu Glu Lys Pro Asn Lys Glu Ile Lys Thr Thr Phe Asn
 50 55 60
 Gln Leu Lys Lys Gln Val Leu Glu Lys Asn His Pro His Thr Leu Lys
 65 70 75 80
 Asn Pro Phe Ser Asn Leu Thr Ser His Phe Leu Tyr Gln Pro Phe Gly
 85 90 95
 Ser Gln Asn Tyr Pro Asp Phe Leu Val Phe Ile Phe Asp Tyr Val Val
 100 105 110
 Gly Ile Glu Ile Lys Phe Ser Lys Asn Asp Lys Gly Glu Lys Asn Leu
 115 120 125
 Gln Thr Ser Arg Pro Met Trp Asn Ser Asn Leu Pro Lys Pro Asn Ala
 130 135 140
 Ile Tyr Val Tyr Gly Val Ala Asn Ala Asn Ile Thr Phe Phe Lys Gly
 145 150 155 160
 Ser Asp Ile Leu Ser Tyr Glu Thr Arg Glu Val Leu Leu Lys Tyr Phe
 165 170 175
 Asp Ile Leu Asp Lys Asp Glu Arg Ser Leu Lys Asn Ala Leu Lys Asp
 180 185 190
 Leu Glu Asn Pro Phe Gly Phe Ala Pro Tyr Ile Arg Lys Ala Tyr Glu
 195 200 205
 His Lys Arg Asn Phe Leu Thr Thr Arg Leu Lys Ala Ser Phe Arg
 210 215 220
 Pro Thr Thr Phe
 225

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 53...493
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CCAAACCTT	TTGAAACT	TGCTACTAA	CCCATTATAA	GCCGCAAAAA	CC	ATG	CTC		58							
						Met	Leu									
						1										
TCT	TTA	AAA	CAA	GAT	TCC	TTT	TTT	TTC	TTA	TGT	TTA	GGA	ATC	CTG	GGG	106
Ser	Leu	Lys	Gln	Asp	Ser	Phe	Phe	Phe	Leu	Cys	Leu	Gly	Ile	Leu	Gly	
		5						10				15				
TTT	TAT	TTT	TAT	AGC	CTT	TTG	AGG	GAT	TTA	ATG	CCT	TTT	TTA	CCC	CCA	154
Phe	Tyr	Phe	Tyr	Ser	Leu	Leu	Arg	Asp	Leu	Met	Pro	Phe	Leu	Pro	Pro	
	20					25				30						
ATG	ATT	GGG	TTT	TTA	TTC	TTG	TTT	TAT	GCG	AAA	AAA	TAC	GAT	CAT	TTT	202
Met	Ile	Gly	Phe	Leu	Phe	Leu	Phe	Tyr	Ala	Lys	Lys	Tyr	Asp	His	Phe	
35					40				45					50		
TTA	CCC	AGT	TTG	AGC	GTG	TTT	GGT	TGT	TTG	TTT	TGG	TTT	GAG	AGC	ATG	250
Leu	Pro	Ser	Leu	Ser	Val	Phe	Gly	Cys	Leu	Phe	Trp	Phe	Glu	Ser	Met	
				55				60					65			
CAT	TTA	AAG	ACT	TTA	GGC	GTT	TTA	GCT	TTA	TTG	TTT	TTA	ATC	TAC	CAT	298
His	Leu	Lys	Thr	Leu	Gly	Val	Leu	Ala	Leu	Leu	Phe	Leu	Ile	Tyr	His	
			70				75						80			
CAA	ATC	GCC	TAT	AAA	AAC	TCT	TTA	AAG	CTT	TTT	AAT	GAC	GGC	TTT	TTA	346
Gln	Ile	Ala	Tyr	Lys	Asn	Ser	Leu	Lys	Leu	Phe	Asn	Asp	Gly	Phe	Leu	
	85						90					95				
TTC	AAA	ACT	TTG	CAT	GTT	TTT	TTG	GTT	TAT	TAC	CTT	TAT	TTA	TCG	CGC	394
Phe	Lys	Thr	Leu	His	Val	Phe	Leu	Val	Tyr	Tyr	Leu	Tyr	Leu	Ser	Arg	
	100					105					110					
TTT	TTT	TCG	ATG	TCT	TTG	AGT	TTG	AAA	ATA	CTC	GGC	TTT	CTC	GCT	CTT	442
Phe	Phe	Ser	Met	Ser	Leu	Ser	Leu	Lys	Ile	Leu	Gly	Phe	Leu	Ala	Leu	
115					120					125				130		
TTT	GCT	TTA	ATA	GAA	AGC	GCT	TTG	TGG	GGT	TTG	TAT	GAA	AAA	TCT	TCG	490
Phe	Ala	Leu	Ile	Glu	Ser	Ala	Leu	Trp	Gly	Leu	Tyr	Glu	Lys	Ser	Ser	
				135					140					145		

CTA TAAGCTTTTG CTCTTTGTTT TTATAGGGTT TTGGGGGTTA CTAGCCT
Leu

540

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Met	Leu	Ser	Leu	Lys	Gln	Asp	Ser	Phe	Phe	Phe	Leu	Cys	Leu	Gly	Ile
1				5					10					15	
Leu	Gly	Phe	Tyr	Phe	Tyr	Ser	Leu	Leu	Arg	Asp	Leu	Met	Pro	Phe	Leu
			20					25					30		
Pro	Pro	Met	Ile	Gly	Phe	Leu	Phe	Leu	Phe	Tyr	Ala	Lys	Lys	Tyr	Asp
		35				40						45			
His	Phe	Leu	Pro	Ser	Leu	Ser	Val	Phe	Gly	Cys	Leu	Phe	Trp	Phe	Glu
	50					55					60				
Ser	Met	His	Leu	Lys	Thr	Leu	Gly	Val	Leu	Ala	Leu	Leu	Phe	Leu	Ile
65					70				75						80
Tyr	His	Gln	Ile	Ala	Tyr	Lys	Asn	Ser	Leu	Lys	Leu	Phe	Asn	Asp	Gly
			85					90					95		
Phe	Leu	Phe	Lys	Thr	Leu	His	Val	Phe	Leu	Val	Tyr	Tyr	Leu	Tyr	Leu
			100					105					110		
Ser	Arg	Phe	Phe	Ser	Met	Ser	Leu	Ser	Leu	Lys	Ile	Leu	Gly	Phe	Leu
		115				120						125			
Ala	Leu	Phe	Ala	Leu	Ile	Glu	Ser	Ala	Leu	Trp	Gly	Leu	Tyr	Glu	Lys
	130					135					140				
Ser	Ser	Leu													
145															

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1835
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

CACTAAAGTC AATCCAAGCG CAAGTTGGAT GAAAAAATAA GAAGGAAGTT ATG AAA
Met Lys

56

1

AAG	TCA	TTC	AAA	AAA	TTA	GGC	TTT	GTC	TCT	TTA	GCG	GCT	AGT	GGC	GTG	104
Lys	Ser	Phe	Lys	Lys	Leu	Gly	Phe	Val	Ser	Leu	Ala	Ala	Ser	Gly	Val	
		5					10					15				
CTT	TTA	GGG	AGC	ATG	AAC	GCT	ACC	GAT	TTA	GAA	ACC	TAC	GCA	GCA	TTG	152
Leu	Leu	Gly	Ser	Met	Asn	Ala	Thr	Asp	Leu	Glu	Thr	Tyr	Ala	Ala	Leu	
	20					25					30					
CAA	AAA	TCA	TCG	CAT	GTT	TTT	GGT	AAT	TAT	GCT	GAA	AAG	GAT	AAG	GAT	200
Gln	Lys	Ser	Ser	His	Val	Phe	Gly	Asn	Tyr	Ala	Glu	Lys	Asp	Lys	Asp	
35					40					45					50	
AGT	AAA	TTA	ACA	AGC	GAT	TCA	CCA	ACG	CAA	CAA	CAA	GAT	CAA	AAA	GTA	248
Ser	Lys	Leu	Thr	Ser	Asp	Ser	Pro	Thr	Gln	Gln	Gln	Asp	Gln	Lys	Val	
				55					60					65		
GCC	CAA	AAC	ACC	GCT	TCA	AAC	GAC	AGC	CAA	GAA	GCG	ACA	ACA	CTT	GAA	296
Ala	Gln	Asn	Thr	Ala	Ser	Asn	Asp	Ser	Gln	Glu	Ala	Thr	Thr	Leu	Glu	
			70				75						80			
AAC	ACC	GCT	TCT	ACT	GAC	AAC	ACA	ACC	GCC	ACA	ACT	GAT	GAA	ACT	TAT	344
Asn	Thr	Ala	Ser	Thr	Asp	Asn	Thr	Thr	Ala	Thr	Thr	Asp	Glu	Thr	Tyr	
		85					90					95				
ACA	AAA	AGC	ACT	GAC	ACT	ACT	GTA	GCT	GGT	GCG	GCT	CAA	AAA	GTA	GAA	392
Thr	Lys	Ser	Thr	Asp	Thr	Thr	Val	Ala	Gly	Ala	Ala	Gln	Lys	Val	Glu	
	100					105					110					
ACC	GAT	AAC	ACA	GCC	GTT	CAA	AGC	GCT	GAA	CAA	ACT	TTA	AAA	ACA	GAT	440
Thr	Asp	Asn	Thr	Ala	Val	Gln	Ser	Ala	Glu	Gln	Thr	Leu	Lys	Thr	Asp	
115					120					125					130	
GTA	GCT	AAA	GTT	CAA	GCT	GAT	GCT	AGT	GCT	AAA	GAT	TTT	GAT	GAA	ACC	488
Val	Ala	Lys	Val	Gln	Ala	Asp	Ala	Ser	Ala	Lys	Asp	Phe	Asp	Glu	Thr	
				135					140					145		
ACT	TTT	CAA	GCC	GAT	CAA	GCA	GCA	GAG	CAA	ACC	GCT	GAA	AAA	GCT	TTA	536
Thr	Phe	Gln	Ala	Asp	Gln	Ala	Ala	Glu	Gln	Thr	Ala	Glu	Lys	Ala	Leu	
			150					155					160			
CAA	CAG	GCT	GAG	AGC	AAA	CTC	AAC	ACC	GAT	CAA	CAG	ACT	TTA	AAC	ACA	584
Gln	Gln	Ala	Glu	Ser	Lys	Leu	Asn	Thr	Asp	Gln	Gln	Thr	Leu	Asn	Thr	
		165					170					175				
GCG	TTA	CAA	GAT	CAG	ACG	AAA	ACA	CCA	ACC	CCA	TCA	ACC	CCA	CCA	ACT	632
Ala	Leu	Gln	Asp	Gln	Thr	Lys	Thr	Pro	Thr	Pro	Ser	Thr	Pro	Pro	Thr	
	180					185					190					
AAA	GAG	GAA	CCA	AAA	CAC	ACC	GCT	TCA	AGC	GGC	ACA	CCA	CCA	GCT	CCA	680
Lys	Glu	Glu	Pro	Lys	His	Thr	Ala	Ser	Ser	Gly	Thr	Pro	Pro	Ala	Pro	
195					200					205					210	
GAA	AGC	CCA	CCA	GCT	AAA	AAA	GAT	GAA	ACA	AGT	GGC	ACA	CCA	AGT	GCT	728
Glu	Ser	Pro	Pro	Ala	Lys	Lys	Asp	Glu	Thr	Ser	Gly	Thr	Pro	Ser	Ala	
				215					220					225		

AGT	GGG	AGT	TCT	GTG	GCA	AGC	CAG	CTA	ACC	AAA	GAT	ACC	ACT	ATG	GTT	776
Ser	Gly	Ser	Ser	Val	Ala	Ser	Gln	Leu	Thr	Lys	Asp	Thr	Thr	Met	Val	
			230					235					240			
AAT	AAT	CTT	AAG	AGT	GTG	AGC	GTG	AGC	GCG	ATG	AAC	ACC	ACT	TTA	AGT	824
Asn	Asn	Leu	Lys	Ser	Val	Ser	Val	Ser	Ala	Met	Asn	Thr	Thr	Leu	Ser	
		245					250					255				
GGA	GTA	GAA	ACC	ATG	TCT	CAA	CAA	ACT	GCA	ACG	ATT	GGC	AAC	CTT	TTG	872
Gly	Val	Glu	Thr	Met	Ser	Gln	Gln	Thr	Ala	Thr	Ile	Gly	Asn	Leu	Leu	
	260					265					270					
AAT	AGT	AGC	ACC	GAT	TTA	AGC	AGT	GTG	ATT	CCC	AAC	GCT	CAA	GGG	CTA	920
Asn	Ser	Ser	Thr	Asp	Leu	Ser	Ser	Val	Ile	Pro	Asn	Ala	Gln	Gly	Leu	
275					280					285					290	
AAC	AGC	GCG	TTT	AGC	ACA	TTA	GAA	AGC	GCT	CAA	AAC	ACT	CTA	AAA	GGC	968
Asn	Ser	Ala	Phe	Ser	Thr	Leu	Glu	Ser	Ala	Gln	Asn	Thr	Leu	Lys	Gly	
			295						300					305		
TAT	TTA	AAT	TCT	TCT	AGC	GCG	ACG	ATT	GGG	CAA	TTG	ACA	AAC	GGA	TCT	1016
Tyr	Leu	Asn	Ser	Ser	Ser	Ala	Thr	Ile	Gly	Gln	Leu	Thr	Asn	Gly	Ser	
			310					315					320			
AAT	GCG	GTT	GTG	GGC	GCG	TTA	GAT	AAA	GCT	ATC	AAT	CAA	GTG	GAT	ATG	1064
Asn	Ala	Val	Val	Gly	Ala	Leu	Asp	Lys	Ala	Ile	Asn	Gln	Val	Asp	Met	
		325					330					335				
GCT	TTG	GCC	GAT	CTT	AGT	GCA	GCT	GAT	ACG	CAA	AAA	ACG	CAA	GCC	GTT	1112
Ala	Leu	Ala	Asp	Leu	Ser	Ala	Ala	Asp	Thr	Gln	Lys	Thr	Gln	Ala	Val	
	340					345					350					
ACG	CTT	GCA	ACT	GCT	AGT	GAT	AGT	CCA	ACG	ACA	ACG	ACA	GAT	GCC	ATC	1160
Thr	Leu	Ala	Thr	Ala	Ser	Asp	Ser	Pro	Thr	Thr	Thr	Thr	Asp	Ala	Ile	
355					360					365					370	
AAT	TTC	TTA	AAC	GCG	CTA	AAA	AGC	AAT	CTA	ATG	GCT	CAA	AAA	GAC	GCT	1208
Asn	Phe	Leu	Asn	Ala	Leu	Lys	Ser	Asn	Leu	Met	Ala	Gln	Lys	Asp	Ala	
			375					380					385			
TTT	TTG	AAT	GTG	CAT	AAA	AAC	ATT	CAA	ACC	GCT	GTC	GCT	CAA	GCC	CAG	1256
Phe	Leu	Asn	Val	His	Lys	Asn	Ile	Gln	Thr	Ala	Val	Ala	Gln	Ala	Gln	
			390				395						400			
GAA	ACC	TAC	ACG	CCA	AGC	GTG	ATC	AAC	ACC	AAT	AAT	TAC	GGG	CAA	ATG	1304
Glu	Thr	Tyr	Thr	Pro	Ser	Val	Ile	Asn	Thr	Asn	Asn	Tyr	Gly	Gln	Met	
		405					410					415				
TAT	GGG	GTA	GAT	GCG	ATG	GCA	GGG	TAT	AAG	TGG	TTC	TTT	GGC	AAA	ACC	1352
Tyr	Gly	Val	Asp	Ala	Met	Ala	Gly	Tyr	Lys	Trp	Phe	Phe	Gly	Lys	Thr	
	420					425				430						
AAA	CGC	TTT	GGC	TTT	AGG	TCT	TAT	GGA	TAC	TAC	AGC	TAT	AAC	CAT	GCG	1400
Lys	Arg	Phe	Gly	Phe	Arg	Ser	Tyr	Gly	Tyr	Tyr	Ser	Tyr	Asn	His	Ala	
435					440					445					450	
AAT	TTA	AGC	TTT	GTG	GGG	AGC	CAG	CTT	GGA	ATC	ATG	GAG	GGC	GCG	TCT	1448
Asn	Leu	Ser	Phe	Val	Gly	Ser	Gln	Leu	Gly	Ile	Met	Glu	Gly	Ala	Ser	

455										460					465					
CAA	GTG	AAT	AAC	TTC	ACT	TAT	GGC	GTG	GGC	TTT	GAT	GTG	CTC	TAT	AAC	1496				
Gln	Val	Asn	Asn	Phe	Thr	Tyr	Gly	Val	Gly	Phe	Asp	Val	Leu	Tyr	Asn					
			470						475						480					
TTC	TAT	GAA	AGC	AAA	GAG	GGC	TAT	AAC	ACA	GCA	GGG	TTG	TTC	TTA	GGC	1544				
Phe	Tyr	Glu	Ser	Lys	Glu	Gly	Tyr	Asn	Thr	Ala	Gly	Leu	Phe	Leu	Gly					
			485					490							495					
TTT	GGG	TTA	GGA	GGG	GAT	TCG	TTT	ATC	GTT	CAA	GGA	GAG	AGC	TAC	TTG	1592				
Phe	Gly	Leu	Gly	Gly	Asp	Ser	Phe	Ile	Val	Gln	Gly	Glu	Ser	Tyr	Leu					
		500					505					510								
AAA	TCT	CAA	ATG	CAC	ATT	TGC	AAC	AAC	ACC	GCC	GGC	TGT	TCA	GCG	AGC	1640				
Lys	Ser	Gln	Met	His	Ile	Cys	Asn	Asn	Thr	Ala	Gly	Cys	Ser	Ala	Ser					
					520					525					530					
ATG	AAC	ACA	AGC	TAC	TTC	CAA	ATG	CCT	GTT	GAA	TTT	GGT	TTT	AGG	AGC	1688				
Met	Asn	Thr	Ser	Tyr	Phe	Gln	Met	Pro	Val	Glu	Phe	Gly	Phe	Arg	Ser					
					535					540					545					
AAT	TTC	TCT	AAA	CAC	AGC	GGG	ATT	GAA	GTG	GGC	TTT	AAA	TTG	CCT	TTA	1736				
Asn	Phe	Ser	Lys	His	Ser	Gly	Ile	Glu	Val	Gly	Phe	Lys	Leu	Pro	Leu					
			550					555					560							
TTC	ACC	AAC	CAA	TTC	TAT	AAA	GAA	AGG	GGC	GTA	GAT	GGA	TCG	GTA	GAT	1784				
Phe	Thr	Asn	Gln	Phe	Tyr	Lys	Glu	Arg	Gly	Val	Asp	Gly	Ser	Val	Asp					
			565					570					575							
GTG	TTC	TAT	AAA	AGG	AAT	TTC	TCT	ATT	TAT	TTT	AAC	TAC	ATG	ATC	AAC	1832				
Val	Phe	Tyr	Lys	Arg	Asn	Phe	Ser	Ile	Tyr	Phe	Asn	Tyr	Met	Ile	Asn					
			580					585							590					
TTC	TAAGCCTTTC	TATTCTTTCC	AATAGAGGGT	TTTCTCTCTG	TTGTTTCTTT	TTT										1888				
Phe																				
595																				

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Met	Lys	Lys	Ser	Phe	Lys	Lys	Leu	Gly	Phe	Val	Ser	Leu	Ala	Ala	Ser
1				5					10					15	
Gly	Val	Leu	Leu	Gly	Ser	Met	Asn	Ala	Thr	Asp	Leu	Glu	Thr	Tyr	Ala
			20					25					30		
Ala	Leu	Gln	Lys	Ser	Ser	His	Val	Phe	Gly	Asn	Tyr	Ala	Glu	Lys	Asp
		35					40					45			
Lys	Asp	Ser	Lys	Leu	Thr	Ser	Asp	Ser	Pro	Thr	Gln	Gln	Gln	Asp	Gln

50		55		60
Lys Val Ala Gln Asn Thr	Ala Ser Asn Asp Ser	Gln Glu Ala Thr Thr		
65		70		80
Leu Glu Asn Thr	Ala Ser Thr Asp Asn Thr	Thr Ala Thr Thr Asp Glu		
	85	90		95
Thr Tyr Thr	Lys Ser Thr Asp Thr	Thr Val Ala Gly Ala Ala Gln Lys		
	100	105		110
Val Glu Thr	Asp Asn Thr Ala Val Gln Ser Ala	Glu Gln Thr Leu Lys		
	115	120		125
Thr Asp Val	Ala Lys Val Gln Ala Asp Ala Ser	Ala Lys Asp Phe Asp		
	130	135		140
Glu Thr Thr	Phe Gln Ala Asp Gln Ala Ala	Glu Gln Thr Ala Glu Lys		
145		150		160
Ala Leu Gln Gln	Ala Glu Ser Lys Leu Asn Thr	Asp Gln Gln Thr Leu		
	165	170		175
Asn Thr Ala	Leu Gln Asp Gln Thr Lys Thr	Pro Thr Pro Ser Thr Pro		
	180	185		190
Pro Thr Lys	Glu Glu Pro Lys His Thr Ala Ser	Ser Ser Gly Thr Pro Pro		
	195	200		205
Ala Pro Glu	Ser Pro Pro Ala Lys Lys Asp	Glu Thr Ser Gly Thr Pro		
	210	215		220
Ser Ala Ser	Gly Ser Ser Val Ala Ser Gln	Leu Thr Lys Asp Thr Thr		
225		230		240
Met Val Asn	Asn Leu Lys Ser Val Ser Val	Ser Ala Met Asn Thr Thr		
	245	250		255
Leu Ser Gly	Val Glu Thr Met Ser Gln Thr	Ala Thr Ile Gly Asn		
	260	265		270
Leu Leu Asn	Ser Ser Thr Asp Leu Ser Ser	Val Ile Pro Asn Ala Gln		
	275	280		285
Gly Leu Asn	Ser Ala Phe Ser Thr Leu Glu	Ser Ala Gln Asn Thr Leu		
	290	295		300
Lys Gly Tyr	Leu Asn Ser Ser Ser Ala Thr	Ile Gly Gln Leu Thr Asn		
305		310		320
Gly Ser Asn	Ala Val Val Gly Ala Leu Asp	Lys Ala Ile Asn Gln Val		
	325	330		335
Asp Met Ala	Leu Ala Asp Leu Ser Ala	Ala Asp Thr Gln Lys Thr Gln		
	340	345		350
Ala Val Thr	Leu Ala Thr Ala Ser Asp Ser	Pro Thr Thr Thr Thr Asp		
	355	360		365
Ala Ile Asn	Phe Leu Asn Ala Leu Lys Ser	Asn Leu Met Ala Gln Lys		
	370	375		380
Asp Ala Phe	Leu Asn Val His Lys Asn Ile	Gln Thr Ala Val Ala Gln		
385		390		400
Ala Gln Glu	Thr Tyr Thr Pro Ser Val	Ile Asn Thr Asn Asn Tyr Gly		
	405	410		415
Gln Met Tyr	Gly Val Asp Ala Met Ala	Gly Tyr Lys Trp Phe Phe Gly		
	420	425		430
Lys Thr Lys	Arg Phe Gly Phe Arg Ser Tyr	Gly Tyr Tyr Ser Tyr Asn		
	435	440		445
His Ala Asn	Leu Ser Phe Val Gly Ser Gln	Leu Gly Ile Met Glu Gly		
	450	455		460
Ala Ser Gln	Val Asn Asn Phe Thr Tyr Gly	Val Gly Phe Asp Val Leu		
465		470		480
Tyr Asn Phe	Tyr Glu Ser Lys Glu Gly Tyr	Asn Thr Ala Gly Leu Phe		
	485	490		495
Leu Gly Phe	Gly Leu Gly Gly Asp Ser Phe	Ile Val Gln Gly Glu Ser		
	500	505		510
Tyr Leu Lys	Ser Gln Met His Ile Cys Asn	Asn Thr Ala Gly Cys Ser		

[illegible]

(2) INFORMATION FOR SEO ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1470 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 46...1416
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

TTTAAGAAAC	TATTTGCGCA	TTTGATGTTA	AGGTTTCTCT	AAAGC	ATG	CGT	TAT	TTT									57
												Met	Arg	Tyr	Phe		
												1					
CTT	GTA	GTT	TTC	TTG	TTT	TTG	TTT	GTG	GGT	TGC	ACA	AAA	AAG	GAT	TTC		105
Leu	Val	Val	Phe	Leu	Phe	Leu	Phe	Val	Gly	Cys	Thr	Lys	Lys	Asp	Phe		
5					10					15					20		
ACG	CTC	AAA	GAT	TTA	TCC	TTG	CCC	CAA	GAG	GCT	TCA	AGC	TAT	CTT	GCA		153
Thr	Leu	Lys	Asp	Leu	Ser	Leu	Pro	Gln	Glu	Ala	Ser	Ser	Tyr	Leu	Ala		
				25					30					35			
AGC	TCT	CAA	AAT	GGC	AGT	AAC	AAC	AAC	CAA	AGC	ATT	GAC	CCC	CAA	GCG		201
Ser	Ser	Gln	Asn	Gly	Ser	Asn	Asn	Asn	Gln	Ser	Ile	Asp	Pro	Gln	Ala		
			40					45					50				
TTA	AGA	GAA	AAT	CTG	AAA	GAG	AGC	TAT	CTC	AAA	GCG	TGG	TAT	TCC	CCA		249
Leu	Arg	Glu	Asn	Leu	Lys	Glu	Ser	Tyr	Leu	Lys	Ala	Trp	Tyr	Ser	Pro		
		55				60						65					
TGG	CTA	GAT	ATG	AAA	GTC	AAA	AGC	AAT	AAA	AAA	GAA	GTG	TTT	TGG	ATC		297
Trp	Leu	Asp	Met	Lys	Val	Lys	Ser	Asn	Lys	Lys	Glu	Val	Phe	Trp	Ile		
	70					75					80						
CTT	AAG	GAG	ATG	AAT	AAA	TCC	ACC	GGT	TAT	GGC	GAA	GAT	CTA	AAA	CCC		345
Leu	Lys	Glu	Met	Asn	Lys	Ser	Thr	Gly	Tyr	Gly	Glu	Asp	Leu	Lys	Pro		
85					90					95					100		

AAC GCA AAA GCT TTC AAT GAC GCA CTC ATT AAG AGC ATG GAT ATT GAG	393
Asn Ala Lys Ala Phe Asn Asp Ala Leu Ile Lys Ser Met Asp Ile Glu	
105 110 115	
CAT TAC CCT AGC GTT AAG ATT AGG GCT GTT GTA GCG CGA GAT AGC GAT	441
His Tyr Pro Ser Val Lys Ile Arg Ala Val Val Ala Arg Asp Ser Asp	
120 125 130	
GTG AGG GCT GTG CCT ACT AAC AAA CCT TAT TAT CTT TCT CAA AAA GGC	489
Val Arg Ala Val Pro Thr Asn Lys Pro Tyr Tyr Leu Ser Gln Lys Gly	
135 140 145	
TAT CCT TTT GAT AGG TAT CAA AAT TCG CTG ATT TTT CAA GGC ACG CCG	537
Tyr Pro Phe Asp Arg Tyr Gln Asn Ser Leu Ile Phe Gln Gly Thr Pro	
150 155 160	
GTT TTA ATC ACG CAT TTT AAT CTA GAT AAA ACT TAT GCC CAC ATT CAA	585
Val Leu Ile Thr His Phe Asn Leu Asp Lys Thr Tyr Ala His Ile Gln	
165 170 175 180	
AGC AGT TTT GTT TAT GGC TGG ATC AAA GTT AGC GAT TTA GTC TAC ATG	633
Ser Ser Phe Val Tyr Gly Trp Ile Lys Val Ser Asp Leu Val Tyr Met	
185 190 195	
CAC GAT AAA GAC ATA GAG CTT TTA ACC CAT CTT AAA GAT TAT GTC ATG	681
His Asp Lys Asp Ile Glu Leu Leu Thr His Leu Lys Asp Tyr Val Met	
200 205 210	
CCT ATA AAA GAT AAA ATC CCC CTT TAT ACA GAC TAT GGG GAT TTT TAC	729
Pro Ile Lys Asp Lys Ile Pro Leu Tyr Thr Asp Tyr Gly Asp Phe Tyr	
215 220 225	
ACC AAC GCC AGA GTG GGC GAA TTG TTC GCT CTC ATC CCC CAA AGT CAA	777
Thr Asn Ala Arg Val Gly Glu Leu Phe Ala Leu Ile Pro Gln Ser Gln	
230 235 240	
AAA ACA CCT CAA AAA CCC CAA AAA AAG GAA TTG AAA GCC TAT GGT TTT	825
Lys Thr Pro Gln Lys Pro Gln Lys Lys Glu Leu Lys Ala Tyr Gly Phe	
245 250 255 260	
TTG AGA GAC GCT AAG GGT TAT GCA GCT TTA CAA AGC GTG ATC TTA GAA	873
Leu Arg Asp Ala Lys Gly Tyr Ala Ala Leu Gln Ser Val Ile Leu Glu	
265 270 275	
GAA AAG GAT TTT TTT GTT TTC CCT AAG GCT TTT AAC AGC GAG AAC ATG	921
Glu Lys Asp Phe Phe Val Phe Pro Lys Ala Phe Asn Ser Glu Asn Met	
280 285 290	
GCG TAT TTT ATA GAC ACC ATG TTA GGG CAA AAA TAC GGC TGG GGC GGC	969
Ala Tyr Phe Ile Asp Thr Met Leu Gly Gln Lys Tyr Gly Trp Gly Gly	
295 300 305	
CTA TTG GGT AAT AGG GAT TGC TCG GCT TTC ACC AGA GAT AGT TTT GCT	1017
Leu Leu Gly Asn Arg Asp Cys Ser Ala Phe Thr Arg Asp Ser Phe Ala	
310 315 320	
AAT TTT GGT ATT TTG CTC CCC AGA AAT TCC TAT GCG CAA AGC CGT TAT	1065
Asn Phe Gly Ile Leu Leu Pro Arg Asn Ser Tyr Ala Gln Ser Arg Tyr	

325	330	335	340	
GCG AAC AAT TAT GTG GAT TTA AGC TCT ATG AAA GCC AAA GAA AAA GAA				1113
Ala Asn Asn Tyr Val Asp Leu Ser Ser Met Lys Ala Lys Glu Lys Glu	345	350	355	
GAC TAC ATC CTT AAA AAC GCC ACG CCT TTT GGA ACG CTC ATC TAT TTA				1161
Asp Tyr Ile Leu Lys Asn Ala Thr Pro Phe Gly Thr Leu Ile Tyr Leu	360	365	370	
AAA GGG CAT ATC ATG CTT TAT TTA GGC GCA CAC AAC CAT CAA GCG ATA				1209
Lys Gly His Ile Met Leu Tyr Leu Gly Ala His Asn His Gln Ala Ile	375	380	385	
GTC GCT CAC AGC ATT TGG TCG GTG CAA ACC CAA AAG CAT TTT AAA ACC				1257
Val Ala His Ser Ile Trp Ser Val Gln Thr Gln Lys His Phe Lys Thr	390	395	400	
TTG AGC CAT AAA ATA GGA GGC GTG GTG ATC ACT TCG TTA TGG TTA GCT				1305
Leu Ser His Lys Ile Gly Gly Val Val Ile Thr Ser Leu Trp Leu Ala	405	410	415	420
GAA GAG CAT AAT GGG GCG TTT TCT AAA AAG AAA TTA TTG ATT GAT AGG				1353
Glu Glu His Asn Gly Ala Phe Ser Lys Lys Lys Leu Leu Ile Asp Arg	425	430	435	
GTG CTT GGA ATG AGC GAT TTG AAA GAT TTT GTC AAT AAA ACT TCA AGC				1401
Val Leu Gly Met Ser Asp Leu Lys Asp Phe Val Asn Lys Thr Ser Ser	440	445	450	
CCT TTA AAT GCG AAT TGATTTTCTT ATATTATGAT TACGATTTAT CAATTTAAAA C				1457
Pro Leu Asn Ala Asn	455			
ATTTGGAGAA AGA				1470

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Met	Arg	Tyr	Phe	Leu	Val	Val	Phe	Leu	Phe	Leu	Phe	Val	Gly	Cys	Thr
1				5				10						15	
Lys	Lys	Asp	Phe	Thr	Leu	Lys	Asp	Leu	Ser	Leu	Pro	Gln	Glu	Ala	Ser
			20					25					30		
Ser	Tyr	Leu	Ala	Ser	Ser	Gln	Asn	Gly	Ser	Asn	Asn	Asn	Gln	Ser	Ile
		35					40					45			
Asp	Pro	Gln	Ala	Leu	Arg	Glu	Asn	Leu	Lys	Glu	Ser	Tyr	Leu	Lys	Ala
	50					55				60					
Trp	Tyr	Ser	Pro	Trp	Leu	Asp	Met	Lys	Val	Lys	Ser	Asn	Lys	Lys	Glu

65					70					75					80
Val	Phe	Trp	Ile	Leu	Lys	Glu	Met	Asn	Lys	Ser	Thr	Gly	Tyr	Gly	Glu
			85						90					95	
Asp	Leu	Lys	Pro	Asn	Ala	Lys	Ala	Phe	Asn	Asp	Ala	Leu	Ile	Lys	Ser
			100					105					110		
Met	Asp	Ile	Glu	His	Tyr	Pro	Ser	Val	Lys	Ile	Arg	Ala	Val	Val	Ala
			115					120				125			
Arg	Asp	Ser	Asp	Val	Arg	Ala	Val	Pro	Thr	Asn	Lys	Pro	Tyr	Tyr	Leu
			130			135					140				
Ser	Gln	Lys	Gly	Tyr	Pro	Phe	Asp	Arg	Tyr	Gln	Asn	Ser	Leu	Ile	Phe
			145			150			155					160	
Gln	Gly	Thr	Pro	Val	Leu	Ile	Thr	His	Phe	Asn	Leu	Asp	Lys	Thr	Tyr
			165						170					175	
Ala	His	Ile	Gln	Ser	Ser	Phe	Val	Tyr	Gly	Trp	Ile	Lys	Val	Ser	Asp
			180					185					190		
Leu	Val	Tyr	Met	His	Asp	Lys	Asp	Ile	Glu	Leu	Leu	Thr	His	Leu	Lys
			195				200					205			
Asp	Tyr	Val	Met	Pro	Ile	Lys	Asp	Lys	Ile	Pro	Leu	Tyr	Thr	Asp	Tyr
			210			215					220				
Gly	Asp	Phe	Tyr	Thr	Asn	Ala	Arg	Val	Gly	Glu	Leu	Phe	Ala	Leu	Ile
			225		230				235					240	
Pro	Gln	Ser	Gln	Lys	Thr	Pro	Gln	Lys	Pro	Gln	Lys	Lys	Glu	Leu	Lys
			245						250					255	
Ala	Tyr	Gly	Phe	Leu	Arg	Asp	Ala	Lys	Gly	Tyr	Ala	Ala	Leu	Gln	Ser
			260				265						270		
Val	Ile	Leu	Glu	Glu	Lys	Asp	Phe	Val	Phe	Pro	Lys	Ala	Phe	Asn	
			275				280				285				
Ser	Glu	Asn	Met	Ala	Tyr	Phe	Ile	Asp	Thr	Met	Leu	Gly	Gln	Lys	Tyr
			290			295					300				
Gly	Trp	Gly	Gly	Leu	Leu	Gly	Asn	Arg	Asp	Cys	Ser	Ala	Phe	Thr	Arg
			305		310				315					320	
Asp	Ser	Phe	Ala	Asn	Phe	Gly	Ile	Leu	Leu	Pro	Arg	Asn	Ser	Tyr	Ala
			325					330						335	
Gln	Ser	Arg	Tyr	Ala	Asn	Asn	Tyr	Val	Asp	Leu	Ser	Ser	Met	Lys	Ala
			340					345					350		
Lys	Glu	Lys	Glu	Asp	Tyr	Ile	Leu	Lys	Asn	Ala	Thr	Pro	Phe	Gly	Thr
			355				360					365			
Leu	Ile	Tyr	Leu	Lys	Gly	His	Ile	Met	Leu	Tyr	Leu	Gly	Ala	His	Asn
			370			375					380				
His	Gln	Ala	Ile	Val	Ala	His	Ser	Ile	Trp	Ser	Val	Gln	Thr	Gln	Lys
			385		390				395					400	
His	Phe	Lys	Thr	Leu	Ser	His	Lys	Ile	Gly	Gly	Val	Val	Ile	Thr	Ser
			405						410					415	
Leu	Trp	Leu	Ala	Glu	Glu	His	Asn	Gly	Ala	Phe	Ser	Lys	Lys	Lys	Leu
			420					425					430		
Leu	Ile	Asp	Arg	Val	Leu	Gly	Met	Ser	Asp	Leu	Lys	Asp	Phe	Val	Asn
			435				440					445			
Lys	Thr	Ser	Ser	Pro	Leu	Asn	Ala	Asn							
			450			455									

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...182
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

```
CTTTTACTTT ATAATTATCG TTGGCATT TT AATATTCAAA GGAGCTTGAA ATG AGA      56
                                     Met Arg
                                     1

ATT TCT CTT TTA GCT GTA ATT TTA GCG TTA TTG TTT GTG GCT TGC CAC      104
Ile Ser Leu Leu Ala Val Ile Leu Ala Leu Leu Phe Val Ala Cys His
      5                      10                      15

GAA ACT AAA AAA CAA ATC TTA CAA AAC GAA GCC GAT AGC ACC CCT TCA      152
Glu Thr Lys Lys Gln Ile Leu Gln Asn Glu Ala Asp Ser Thr Pro Ser
      20                      25                      30

GAA AAA ACC ATT TGG CAA CCT GAA CAA AAA TAAAAATTGT AAAAATACTC AAA      205
Glu Lys Thr Ile Trp Gln Pro Glu Gln Lys
      35                      40

GGCATT TTTT AAAATAAACG CAATAAAAAA      235
```

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

```
Met Arg Ile Ser Leu Ala Val Ile Leu Ala Leu Leu Phe Val Ala
  1                      5                      10                      15
Cys His Glu Thr Lys Lys Gln Ile Leu Gln Asn Glu Ala Asp Ser Thr
      20                      25                      30
Pro Ser Glu Lys Thr Ile Trp Gln Pro Glu Gln Lys
      35                      40
```

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...1298
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

CCAGCGATGC	GTCCTGTTAA	AAACGATTTT	AATGTGGAGA	GTGAAGAATA	ATG GCG	56
					Met Ala	
					1	
TAT TTT TTA GAA CAA ACG GAT AGT GAA ATT TTT GAG CTT ATC TTT GAA	104					
Tyr Phe Leu Glu Gln Thr Asp Ser Glu Ile Phe Glu Leu Ile Phe Glu						
5 10 15						
GAA TAC AAG CGG CAA AAT GAG CAT TTA GAA ATG ATA GCG AGC GAG AAT	152					
Glu Tyr Lys Arg Gln Asn Glu His Leu Glu Met Ile Ala Ser Glu Asn						
20 25 30						
TAC ACT TTT GCA AGC GTT ATG GAG GCT ATG GGG AGT GTT TTA ACG AAT	200					
Tyr Thr Phe Ala Ser Val Met Glu Ala Met Gly Ser Val Leu Thr Asn						
35 40 45 50						
AAA TAC GCT GAA GGC TAC CCT AAC AAG CGC TAT TAT GGA GGC TGT GAA	248					
Lys Tyr Ala Glu Gly Tyr Pro Asn Lys Arg Tyr Tyr Gly Gly Cys Glu						
55 60 65						
GTG GTG GAT AAA ATA GAA AGC CTA GCC ATA GAA AGG GCT AAA AAG CTT	296					
Val Val Asp Lys Ile Glu Ser Leu Ala Ile Glu Arg Ala Lys Lys Leu						
70 75 80						
TTT AAT TGC CAG TTC GCT AAC GTG CAA GCG CAT TCA GGC TCA CAA GCC	344					
Phe Asn Cys Gln Phe Ala Asn Val Gln Ala His Ser Gly Ser Gln Ala						
85 90 95						
AAT AAC GCT GTC TAT CAC GCT CTT TTA AAG CCT TAT GAC AAG ATT TTA	392					
Asn Asn Ala Val Tyr His Ala Leu Leu Lys Pro Tyr Asp Lys Ile Leu						
100 105 110						
GGC ATG GAT TTA AGC TGT GGA GGG CAT TTA ACG CAT GGC GCT AAA GTG	440					
Gly Met Asp Leu Ser Cys Gly Gly His Leu Thr His Gly Ala Lys Val						
115 120 125 130						
AGT TTA ACC GGC AAG CAT TAT CAG AGC TTT TCT TAT GGC GTG AAT TTG	488					
Ser Leu Thr Gly Lys His Tyr Gln Ser Phe Ser Tyr Gly Val Asn Leu						
135 140 145						
GAT GGC TAT ATT GAT TAT GAA GAG GCG CTA AAA ATC GCT CAA AGC GTT	536					
Asp Gly Tyr Ile Asp Tyr Glu Glu Ala Leu Lys Ile Ala Gln Ser Val						
150 155 160						
AAG CCA GAA ATC ATC GTG TGC GGG TTT TCA GCC TAT CCA AGG GAG ATT	584					
Lys Pro Glu Ile Ile Val Cys Gly Phe Ser Ala Tyr Pro Arg Glu Ile						
165 170 175						
GAT TTT AAG AAA TTT AGA GAA ATC GCT GAT GAA GTG GGG GCG TTA CTA	632					

Asp	Phe	Lys	Lys	Phe	Arg	Glu	Ile	Ala	Asp	Glu	Val	Gly	Ala	Leu	Leu	
180						185					190					
TTA	GGC	GAT	ATA	GCC	CAT	GTG	GCA	GGG	CTT	GTG	GTA	ACC	GGT	GAG	CAT	680
Leu	Gly	Asp	Ile	Ala	His	Val	Ala	Gly	Leu	Val	Val	Thr	Gly	Glu	His	
195					200					205					210	
GCC	CAT	CCT	TTC	CCG	CAT	TGC	CAT	GTG	GTT	TCA	AGC	ACC	ACT	CAT	AAG	728
Ala	His	Pro	Phe	Pro	His	Cys	His	Val	Val	Ser	Ser	Thr	Thr	His	Lys	
				215					220					225		
ACC	TTA	AGA	GGG	CCT	AGA	GGG	GGG	ATT	ATT	TTA	ACT	AAT	GAT	GAA	GAG	776
Thr	Leu	Arg	Gly	Pro	Arg	Gly	Gly	Ile	Ile	Leu	Thr	Asn	Asp	Glu	Glu	
			230					235					240			
ATA	GCG	GCT	AAG	ATT	GAC	AAA	GCG	ATT	TTT	CCA	GGA	ACT	CAA	GGC	GGG	824
Ile	Ala	Ala	Lys	Ile	Asp	Lys	Ala	Ile	Phe	Pro	Gly	Thr	Gln	Gly	Gly	
			245				250					255				
CCT	TTG	ATG	CAT	GTG	ATT	GCT	GCT	AAA	GCG	GTG	GGT	TTT	AAA	GAG	AAT	872
Pro	Leu	Met	His	Val	Ile	Ala	Ala	Lys	Ala	Val	Gly	Phe	Lys	Glu	Asn	
	260					265					270					
CTA	AAA	CCA	GAA	TTT	AAA	GCT	TAT	GCA	CAA	TTA	GTG	AAA	TCT	AAC	ATG	920
Leu	Lys	Pro	Glu	Phe	Lys	Ala	Tyr	Ala	Gln	Leu	Val	Lys	Ser	Asn	Met	
275					280					285					290	
CAA	GTT	TTG	GCT	AAA	GCG	TTA	AAA	GAA	AAA	AAC	CAT	AAG	TTA	GTG	AGT	968
Gln	Val	Leu	Ala	Lys	Ala	Leu	Lys	Glu	Lys	Asn	His	Lys	Leu	Val	Ser	
				295				300						305		
GGT	GGC	ACT	TCT	AAC	CAT	TTG	CTT	TTA	ATG	GAT	TTT	TTA	GAT	AAG	CCT	1016
Gly	Gly	Thr	Ser	Asn	His	Leu	Leu	Leu	Met	Asp	Phe	Leu	Asp	Lys	Pro	
			310				315					320				
TAT	AGC	GGG	AAA	GAC	GCT	GAT	ATT	GCA	TTA	GGG	AAT	GCC	GGA	ATC	ACC	1064
Tyr	Ser	Gly	Lys	Asp	Ala	Asp	Ile	Ala	Leu	Gly	Asn	Ala	Gly	Ile	Thr	
		325					330					335				
GTG	AAT	AAA	AAC	ACC	ATT	CCT	GGT	GAA	ACG	CGC	AGC	CCT	TTT	GTA	ACG	1112
Val	Asn	Lys	Asn	Thr	Ile	Pro	Gly	Glu	Thr	Arg	Ser	Pro	Phe	Val	Thr	
	340					345					350					
AGC	GGG	ATA	AGG	ATT	GGC	TCA	GCG	GCA	TTG	AGC	GCA	AGG	GGC	ATG	GGA	1160
Ser	Gly	Ile	Arg	Ile	Gly	Ser	Ala	Ala	Leu	Ser	Ala	Arg	Gly	Met	Gly	
355					360					365					370	
GCT	AAG	GAA	TTT	GAA	ATC	ATA	GGG	AAT	AAA	ATA	TCA	GAT	ATT	TTG	AAT	1208
Ala	Lys	Glu	Phe	Glu	Ile	Ile	Gly	Asn	Lys	Ile	Ser	Asp	Ile	Leu	Asn	
				375					380					385		
GAT	ATT	AAT	AAT	GTT	AGT	TTG	CAA	TTG	CAT	GTG	AAA	GAA	GAA	TTG	AAA	1256
Asp	Ile	Asn	Asn	Val	Ser	Leu	Gln	Leu	His	Val	Lys	Glu	Glu	Leu	Lys	
			390					395					400			
GCC	ATG	GTC	AAT	CAA	TTC	CCT	GTG	TAC	CAC	CAA	CCT	ATT	TTT	TAAGGGAGT	1307	
Ala	Met	Val	Asn	Gln	Phe	Pro	Val	Tyr	His	Gln	Pro	Ile	Phe			
		405					410					415				

CAAGATGACA GAAATGGAAT TAAAGCTCAT TAAGATAGAC ACAA

1351

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met	Ala	Tyr	Phe	Leu	Glu	Gln	Thr	Asp	Ser	Glu	Ile	Phe	Glu	Leu	Ile	1	5	10	15
Phe	Glu	Glu	Tyr	Lys	Arg	Gln	Asn	Glu	His	Leu	Glu	Met	Ile	Ala	Ser	20	25	30	
Glu	Asn	Tyr	Thr	Phe	Ala	Ser	Val	Met	Glu	Ala	Met	Gly	Ser	Val	Leu	35	40	45	
Thr	Asn	Lys	Tyr	Ala	Glu	Gly	Tyr	Pro	Asn	Lys	Arg	Tyr	Tyr	Gly	Gly	50	55	60	
Cys	Glu	Val	Val	Asp	Lys	Ile	Glu	Ser	Leu	Ala	Ile	Glu	Arg	Ala	Lys	65	70	75	80
Lys	Leu	Phe	Asn	Cys	Gln	Phe	Ala	Asn	Val	Gln	Ala	His	Ser	Gly	Ser	85	90	95	
Gln	Ala	Asn	Asn	Ala	Val	Tyr	His	Ala	Leu	Leu	Lys	Pro	Tyr	Asp	Lys	100	105	110	
Ile	Leu	Gly	Met	Asp	Leu	Ser	Cys	Gly	Gly	His	Leu	Thr	His	Gly	Ala	115	120	125	
Lys	Val	Ser	Leu	Thr	Gly	Lys	His	Tyr	Gln	Ser	Phe	Ser	Tyr	Gly	Val	130	135	140	
Asn	Leu	Asp	Gly	Tyr	Ile	Asp	Tyr	Glu	Glu	Ala	Leu	Lys	Ile	Ala	Gln	145	150	155	160
Ser	Val	Lys	Pro	Glu	Ile	Ile	Val	Cys	Gly	Phe	Ser	Ala	Tyr	Pro	Arg	165	170	175	
Glu	Ile	Asp	Phe	Lys	Lys	Phe	Arg	Glu	Ile	Ala	Asp	Glu	Val	Gly	Ala	180	185	190	
Leu	Leu	Leu	Gly	Asp	Ile	Ala	His	Val	Ala	Gly	Leu	Val	Val	Thr	Gly	195	200	205	
Glu	His	Ala	His	Pro	Phe	Pro	His	Cys	His	Val	Val	Ser	Ser	Thr	Thr	210	215	220	
His	Lys	Thr	Leu	Arg	Gly	Pro	Arg	Gly	Gly	Ile	Leu	Thr	Asn	Asp		225	230	235	240
Glu	Glu	Ile	Ala	Ala	Lys	Ile	Asp	Lys	Ala	Ile	Phe	Pro	Gly	Thr	Gln	245	250	255	
Gly	Gly	Pro	Leu	Met	His	Val	Ile	Ala	Ala	Lys	Ala	Val	Gly	Phe	Lys	260	265	270	
Glu	Asn	Leu	Lys	Pro	Glu	Phe	Lys	Ala	Tyr	Ala	Gln	Leu	Val	Lys	Ser	275	280	285	
Asn	Met	Gln	Val	Leu	Ala	Lys	Ala	Leu	Lys	Glu	Lys	Asn	His	Lys	Leu	290	295	300	
Val	Ser	Gly	Gly	Thr	Ser	Asn	His	Leu	Leu	Leu	Met	Asp	Phe	Leu	Asp	305	310	315	320
Lys	Pro	Tyr	Ser	Gly	Lys	Asp	Ala	Asp	Ile	Ala	Leu	Gly	Asn	Ala	Gly	325	330	335	
Ile	Thr	Val	Asn	Lys	Asn	Thr	Ile	Pro	Gly	Glu	Thr	Arg	Ser	Pro	Phe				

(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION:

235

Ala	Asn	Leu	Glu	Gln	Ser	Leu	Gly	Ile	Leu	Gly	Lys	Leu	Leu	Asp	Leu	
100						105					110					
TCC	CAA	CAA	TAC	GCT	AGT	CAG	GGT	GTC	ATT	AAG	CCT	TTG	GTG	GTG	GAT	440
Ser	Gln	Gln	Tyr	Ala	Ser	Gln	Gly	Val	Ile	Lys	Pro	Leu	Val	Val	Asp	
115					120					125					130	
GTG	GGG	AAA	GAA	CAA	ATC	GGT	ATC	ACG	GAT	AGC	ATG	CTC	TTG	GTG	GCT	488
Val	Gly	Lys	Glu	Gln	Ile	Gly	Ile	Thr	Asp	Ser	Met	Leu	Leu	Val	Ala	
				135					140					145		
CAA	AAC	ATC	GTT	TTA	GCT	TTA	GGG	CAA	GTG	GAT	TTG	AGC	AAA	ATC	CAA	536
Gln	Asn	Ile	Val	Leu	Ala	Leu	Gly	Gln	Val	Asp	Leu	Ser	Lys	Ile	Gln	
			150					155					160			
CAA	AAC	AAT	AAC	GAA	CAG	CTA	TAC	GAA	AAT	ATT	ATG	AAA	GTC	ATG	CTT	584
Gln	Asn	Asn	Asn	Glu	Gln	Leu	Tyr	Glu	Asn	Ile	Met	Lys	Val	Met	Leu	
		165					170					175				
TTA	GGC	GCG	GGC	GGG	ACT	AAT	GGG	GCG	TAT	AAT	GGC	GTG	AGT	GTG	GGC	632
Leu	Gly	Ala	Gly	Gly	Thr	Asn	Gly	Ala	Tyr	Asn	Gly	Val	Ser	Val	Gly	
	180					185					190					
GAC	ATT	GCC	ACG	GGC	ATG	CAA	AAT	TTT	TCT	TCG	CAA	ACG	GGC	TTG	ATA	680
Asp	Ile	Ala	Thr	Gly	Met	Gln	Asn	Phe	Ser	Ser	Gln	Thr	Gly	Leu	Ile	
195					200					205					210	
GGG	GCT	AAT	TCT	ACG	GTT	AGC	GAG	CTG	AAT	GCT	TTG	ATT	AAG	AGC	GGG	728
Gly	Ala	Asn	Ser	Thr	Val	Ser	Glu	Leu	Asn	Ala	Leu	Ile	Lys	Ser	Gly	
				215					220					225		
ATT	TCT	TTG	GAT	CGT	GAG	ACT	TTG	GGG	TTA	GGG	AGT	TTT	ATT	GAA	AAA	776
Ile	Ser	Leu	Asp	Arg	Glu	Thr	Leu	Gly	Leu	Gly	Ser	Phe	Ile	Glu	Lys	
			230					235					240			
AAT	ATC	TGT	AGC	GGT	GCA	TCG	TCT	TGT	TTT	AGT	GGG	AAT	CAG	CTT	ATC	824
Asn	Ile	Cys	Ser	Gly	Ala	Ser	Ser	Cys	Phe	Ser	Gly	Asn	Gln	Leu	Ile	
		245					250					255				
TAT	AAG	AAA	GGG	CTA	GAC	AGA	ACC	ATA	AAC	ATC	ATT	AAT	ACG	GTA	TTA	872
Tyr	Lys	Lys	Gly	Leu	Asp	Arg	Thr	Ile	Asn	Ile	Ile	Asn	Thr	Val	Leu	
	260					265					270					
GGT	CAG	TTT	GAA	TCT	TCG	GCT	AGT	TCT	CTT	TAT	AAG	ATT	TCT	TAT	ATC	920
Gly	Gln	Phe	Glu	Ser	Ser	Ala	Ser	Ser	Leu	Tyr	Lys	Ile	Ser	Tyr	Ile	
	275				280					285					290	
CCT	AAC	CTC	TTT	TCG	CTC	AAG	GAT	TAC	CAG	TCA	GCG	AGC	ATG	AAC	GGC	968
Pro	Asn	Leu	Phe	Ser	Leu	Lys	Asp	Tyr	Gln	Ser	Ala	Ser	Met	Asn	Gly	
				295					300					305		
TTT	GGG	GCT	AAG	ATG	GGC	TAT	AAA	CAA	TTT	TTC	ACC	CAT	AAG	AAA	AAT	1016
Phe	Gly	Ala	Lys	Met	Gly	Tyr	Lys	Gln	Phe	Phe	Thr	His	Lys	Lys	Asn	
			310					315					320			
GTT	GGC	TTA	AGG	TAT	TAC	GGG	TTT	TTG	GAT	TAT	GGC	TAT	GCG	AAC	TTT	1064
Val	Gly	Leu	Arg	Tyr	Tyr	Gly	Phe	Leu	Asp	Tyr	Gly	Tyr	Ala	Asn	Phe	
		325					330					335				

GGC GAT ACG AAT TTA AAA GTG GGG GCG AAT CTT GTT ACT TAT GGG GTA	1112
Gly Asp Thr Asn Leu Lys Val Gly Ala Asn Leu Val Thr Tyr Gly Val	
340 345 350	
GGA ACG GAT TTT TTA TAC AAT GTG TAT GAA CGC TCT AGA AGG AGG GAA	1160
Gly Thr Asp Phe Leu Tyr Asn Val Tyr Glu Arg Ser Arg Arg Arg Glu	
355 360 365 370	
AGG ACT ACG ATC GGT CTT TTC TTT GGC GCT CAA ATT GCA GGG CAA ACT	1208
Arg Thr Thr Ile Gly Leu Phe Phe Gly Ala Gln Ile Ala Gly Gln Thr	
375 380 385	
TGG AGC ACT AAT GTA ACG AAC TTA TTG AGC GGG CAA AGG CCT GAT GTC	1256
Trp Ser Thr Asn Val Thr Asn Leu Leu Ser Gly Gln Arg Pro Asp Val	
390 395 400	
AAG TCC AGT TCG TTC CAA TTC TTG TTT GAT TTG GGC GTG CGC ACC AAC	1304
Lys Ser Ser Ser Phe Gln Phe Leu Phe Asp Leu Gly Val Arg Thr Asn	
405 410 415	
TTT GCA AAA ACC AAT TTC AAT AAG CAC AGG CTA GAC CAA GGG ATA GAA	1352
Phe Ala Lys Thr Asn Phe Asn Lys His Arg Leu Asp Gln Gly Ile Glu	
420 425 430	
TTT GGG GTG AAA ATC CCT GTT ATC GCT CAT AAA TAT TTT GCA ACC CAA	1400
Phe Gly Val Lys Ile Pro Val Ile Ala His Lys Tyr Phe Ala Thr Gln	
435 440 445 450	
GGC TCA AGC GCG AGC TAT ATG AGG AAT TTT AGC TTC TAT GTG GGC TAT	1448
Gly Ser Ser Ala Ser Tyr Met Arg Asn Phe Ser Phe Tyr Val Gly Tyr	
455 460 465	
TCA GTC GGT TTT TAAGGAAGGC TCTTGATGAA AAATACCAAT ACAAAGAGA TAAAG	1505
Ser Val Gly Phe	
470	
AATACAAG	1513

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Met	Ser	Leu	Cys	Arg	Ala	Glu	Glu	Asp	Gly	Ala	Phe	Phe	Val	Ile	Asp
1			5						10					15	
Tyr	Gln	Thr	Ser	Leu	Ala	Arg	Gln	Glu	Leu	Lys	Asn	Pro	Gly	Phe	Thr
			20					25					30		
Gln	Ala	Gln	Glu	Leu	Arg	Gln	Leu	Ile	Arg	Asp	Gly	Ala	Val	Arg	Leu
		35					40					45			
Gln	Thr	Ser	Ala	Ile	Pro	Leu	Ser	Tyr	Tyr	Leu	Asp	Ile	Leu	Gly	Asn

50		55		60
Lys Thr Ala Thr Leu Leu Arg Glu Ser Leu Lys Asn Asn Ala Gln Pro				
65		70		80
Ser Gln Pro Asn Ala Gln Pro Pro Gln Gln Asn Gly Pro Ser Asn Gln				
	85		90	95
Ala Leu Ala Asn Leu Glu Gln Ser Leu Gly Ile Leu Gly Lys Leu Leu				
	100		105	110
Asp Leu Ser Gln Gln Tyr Ala Ser Gln Gly Val Ile Lys Pro Leu Val				
	115		120	125
Val Asp Val Gly Lys Glu Gln Ile Gly Ile Thr Asp Ser Met Leu Leu				
	130		135	140
Val Ala Gln Asn Ile Val Leu Ala Leu Gly Gln Val Asp Leu Ser Lys				
145		150		160
Ile Gln Gln Asn Asn Asn Glu Gln Leu Tyr Glu Asn Ile Met Lys Val				
	165		170	175
Met Leu Leu Gly Ala Gly Gly Thr Asn Gly Ala Tyr Asn Gly Val Ser				
	180		185	190
Val Gly Asp Ile Ala Thr Gly Met Gln Asn Phe Ser Ser Gln Thr Gly				
	195		200	205
Leu Ile Gly Ala Asn Ser Thr Val Ser Glu Leu Asn Ala Leu Ile Lys				
	210		215	220
Ser Gly Ile Ser Leu Asp Arg Glu Thr Leu Gly Leu Gly Ser Phe Ile				
225		230		240
Glu Lys Asn Ile Cys Ser Gly Ala Ser Ser Cys Phe Ser Gly Asn Gln				
	245		250	255
Leu Ile Tyr Lys Lys Gly Leu Asp Arg Thr Ile Asn Ile Ile Asn Thr				
	260		265	270
Val Leu Gly Gln Phe Glu Ser Ser Ala Ser Ser Leu Tyr Lys Ile Ser				
	275		280	285
Tyr Ile Pro Asn Leu Phe Ser Leu Lys Asp Tyr Gln Ser Ala Ser Met				
	290		295	300
Asn Gly Phe Gly Ala Lys Met Gly Tyr Lys Gln Phe Phe Thr His Lys				
305		310		320
Lys Asn Val Gly Leu Arg Tyr Tyr Gly Phe Leu Asp Tyr Gly Tyr Ala				
	325		330	335
Asn Phe Gly Asp Thr Asn Leu Lys Val Gly Ala Asn Leu Val Thr Tyr				
	340		345	350
Gly Val Gly Thr Asp Phe Leu Tyr Asn Val Tyr Glu Arg Ser Arg Arg				
	355		360	365
Arg Glu Arg Thr Thr Ile Gly Leu Phe Phe Gly Ala Gln Ile Ala Gly				
	370		375	380
Gln Thr Trp Ser Thr Asn Val Thr Asn Leu Leu Ser Gly Gln Arg Pro				
385		390		400
Asp Val Lys Ser Ser Ser Phe Gln Phe Leu Phe Asp Leu Gly Val Arg				
	405		410	415
Thr Asn Phe Ala Lys Thr Asn Phe Asn Lys His Arg Leu Asp Gln Gly				
	420		425	430
Ile Glu Phe Gly Val Lys Ile Pro Val Ile Ala His Lys Tyr Phe Ala				
	435		440	445
Thr Gln Gly Ser Ser Ala Ser Tyr Met Arg Asn Phe Ser Phe Tyr Val				
	450		455	460
Gly Tyr Ser Val Gly Phe				
465		470		

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 505 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...452
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

AAGACCCTAA ATACACACAA AATAAAACAA AATAAATCCA ATCAAATCCC	ATG TGC	56
	Met Cys	
	1	
CAA ATC CAA TGC TTG CTT ATT TTA CTT TCT ATC AAT ATA GTT AGC GCG		104
Gln Ile Gln Cys Leu Leu Ile Leu Leu Ser Ile Asn Ile Val Ser Ala		
5 10 15		
ATC ATC GTT TAT TTT TTC CAA GCA TTT CAA GGG GTT TTG AAT TTT GAA		152
Ile Ile Val Tyr Phe Phe Gln Ala Phe Gln Gly Val Leu Asn Phe Glu		
20 25 30		
GGG GGT TTT TTA GGG TTT TTT ATC GTG GCG TTG TCT TCG TAT TAC GGC		200
Gly Gly Phe Leu Gly Phe Phe Ile Val Ala Leu Ser Ser Tyr Tyr Gly		
35 40 45 50		
GTT AAA AAG CGT TTG GAT TTA AGG AAA CAA AAT TCA ATA GAA AAA GAA		248
Val Lys Lys Arg Leu Asp Leu Arg Lys Gln Asn Ser Ile Glu Lys Glu		
55 60 65		
GAA AAG CAA AAA TTC CAA AAA TTC GCC CTG GGC TTG GAA ATG TCT TTC		296
Glu Lys Gln Lys Phe Gln Lys Phe Ala Leu Gly Leu Glu Met Ser Phe		
70 75 80		
AAT GTG TGG CGT TTA GGA GGG TAT GGG GTT TTA CTA GGC ATT TTA GGA		344
Asn Val Trp Arg Leu Gly Gly Tyr Gly Val Leu Leu Gly Ile Leu Gly		
85 90 95		
ACG CTT TTA TTC TTG CAT CTT TTT AAC GGG TTA ATC TTT CTT ATT GGC		392
Thr Leu Leu Phe Leu His Leu Phe Asn Gly Leu Ile Phe Leu Ile Gly		
100 105 110		
GTG TTT GTG AGC TCG CTC TCT AGC GCG TTA TTA CGA TTT TTG AAT AAT		440
Val Phe Val Ser Ser Leu Ser Ser Ala Leu Leu Arg Phe Leu Asn Asn		
115 120 125 130		
AAT GGT AAG TTT TGACACAAAC TCACATGGAT TTTAACCCCT TTAATCCTCT TTTAA		497
Asn Gly Lys Phe		
TTTTTAAT		505

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

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Met Cys Gln Ile Gln Cys Leu Leu Ile Leu Leu Ser Ile Asn Ile Val
 1          5          10          15
Ser Ala Ile Ile Val Tyr Phe Phe Gln Ala Phe Gln Gly Val Leu Asn
          20          25          30
Phe Glu Gly Gly Phe Leu Gly Phe Phe Ile Val Ala Leu Ser Ser Tyr
          35          40          45
Tyr Gly Val Lys Lys Arg Leu Asp Leu Arg Lys Gln Asn Ser Ile Glu
          50          55          60
Lys Glu Glu Lys Gln Lys Phe Gln Lys Phe Ala Leu Gly Leu Glu Met
65          70          75          80
Ser Phe Asn Val Trp Arg Leu Gly Gly Tyr Gly Val Leu Leu Gly Ile
          85          90          95
Leu Gly Thr Leu Leu Phe Leu His Leu Phe Asn Gly Leu Ile Phe Leu
          100          105          110
Ile Gly Val Phe Val Ser Ser Leu Ser Ser Ala Leu Leu Arg Phe Leu
          115          120          125
Asn Asn Asn Gly Lys Phe
130

```

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...458
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

```

TTTTTGCACT ATCGTTGTTT GCGCTGTGGT GTTTGGCACG CTTGAAAAAA ATG CTC      56
                                     Met Leu
                                     1

AAG AGT ACC ATC AAA GAA GAT TAT TTG ATG CTG ATG TCT AGA GAA GTG      104
Lys Ser Thr Ile Lys Glu Asp Tyr Leu Met Leu Met Ser Arg Glu Val
 5          10          15

```

AGT GCT TTT GTG GGG ACT CTT TTC TTC ATT GGC TTG AGT TGC TAT GCG	152
Ser Ala Phe Val Gly Thr Leu Phe Phe Ile Gly Leu Ser Cys Tyr Ala	
20 25 30	
ATC TAT CAT GGC AAC ATG CCC GAT TAT TTG AGA CCG GCT TTG ATA GAC	200
Ile Tyr His Gly Asn Met Pro Asp Tyr Leu Arg Pro Ala Leu Ile Asp	
35 40 45 50	
ACT ATT AAG GCA GCG AGT GAT TCC ATC TAT TCC AGC TGC GAC TAC ATG	248
Thr Ile Lys Ala Ala Ser Asp Ser Ile Tyr Ser Ser Cys Asp Tyr Met	
55 60 65	
GAT TAT TTT TTG AAG GCT AGA AAG ATG TTA GAG GGG TTT GCT TGG TGG	296
Asp Tyr Phe Leu Lys Ala Arg Lys Met Leu Glu Gly Phe Ala Trp Trp	
70 75 80	
AGC ATG TTC AAA GCG GAG AGC ATG GGC TTA AAT AAG GGG TTT ATG GTT	344
Ser Met Phe Lys Ala Glu Ser Met Gly Leu Asn Lys Gly Phe Met Val	
85 90 95	
GCG GGC TGG GTA GCG TTT ATC ATC TAT AAC GCT CTT AGC GGG ATA GCC	392
Ala Gly Trp Val Ala Phe Ile Ile Tyr Asn Ala Leu Ser Gly Ile Ala	
100 105 110	
ATC AGC AGG CTG AGC GCT CAA ATC ATT TAT TGG TTA TCA AAA TAT TTT	440
Ile Ser Arg Leu Ser Ala Gln Ile Ile Tyr Trp Leu Ser Lys Tyr Phe	
115 120 125 130	
AGG AGT GAG TAT GGA AAA TGATGTTAAA GAAGATCTAG AGCAAGCAAG ACCAAAGT	496
Arg Ser Glu Tyr Gly Lys	
135	
TAGAGCCAGA AAAGC	511

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Met Leu Lys Ser Thr Ile Lys Glu Asp Tyr Leu Met Leu Met Ser Arg	
1 5 10 15	
Glu Val Ser Ala Phe Val Gly Thr Leu Phe Phe Ile Gly Leu Ser Cys	
20 25 30	
Tyr Ala Ile Tyr His Gly Asn Met Pro Asp Tyr Leu Arg Pro Ala Leu	
35 40 45	
Ile Asp Thr Ile Lys Ala Ala Ser Asp Ser Ile Tyr Ser Ser Cys Asp	
50 55 60	
Tyr Met Asp Tyr Phe Leu Lys Ala Arg Lys Met Leu Glu Gly Phe Ala	
65 70 75 80	
Trp Trp Ser Met Phe Lys Ala Glu Ser Met Gly Leu Asn Lys Gly Phe	

				85						90						95			
Met	Val	Ala	Gly	Trp	Val	Ala	Phe	Ile	Ile	Tyr	Asn	Ala	Leu	Ser	Gly				
			100						105				110						
Ile	Ala	Ile	Ser	Arg	Leu	Ser	Ala	Gln	Ile	Ile	Tyr	Trp	Leu	Ser	Lys				
		115					120					125							
Tyr	Phe	Arg	Ser	Glu	Tyr	Gly	Lys												
	130					135													

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2203 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...2150
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GAGTTACACA	CTCTTTGAGA	ACAAAACGCC	AAACCATTTA	GGAAATTACC	ATG CTA	56
					Met Leu	
					1	
AGA TTC GTT AGT AAA ACG ATT TGC TTG TCT TTA ATC GGC TTG TTC AAC	104					
Arg Phe Val Ser Lys Thr Ile Cys Leu Ser Leu Ile Gly Leu Phe Asn						
	5		10		15	
CCT TTA GAA GCC TTT CAA AAA CAC CAA AAA GAC GGC TTT TTT ATA GAA	152					
Pro Leu Glu Ala Phe Gln Lys His Gln Lys Asp Gly Phe Phe Ile Glu						
	20		25		30	
GCT GGG TTT GAA ACT GGG TTA TTA GAA GGA ACG CAA ACT AAA GAA GAA	200					
Ala Gly Phe Glu Thr Gly Leu Leu Glu Gly Thr Gln Thr Lys Glu Glu						
	35		40		45	50
GTC ATA ACC ACC CAA AAA ATC TAT GAA AAC CCC CTA ACC CAC CCA CAA	248					
Val Ile Thr Thr Gln Lys Ile Tyr Glu Asn Pro Leu Thr His Pro Gln						
	55		60		65	
ACT AAA GAA CAG CCT AAA GAA CAA AAT AAA AGC GAT ACG GCC ACC CCA	296					
Thr Lys Glu Gln Pro Lys Glu Gln Asn Lys Ser Asp Thr Ala Thr Pro						
	70		75		80	
CAA AGC GCT TAC GGA AAA TAC TAC ATA CCC CAA AGC ACC ATT TTA AAA	344					
Gln Ser Ala Tyr Gly Lys Tyr Tyr Ile Pro Gln Ser Thr Ile Leu Lys						
	85		90		95	
AAT GCA ACG GCT TTA TTC ACC ACG GAC AAG ATA GAA AAT GGC TTA ACT	392					
Asn Ala Thr Ala Leu Phe Thr Thr Asp Lys Ile Glu Asn Gly Leu Thr						
	100		105		110	

TTT TAT TCT CAA AAC CCT GTG TAT GCG AAT ATG GTT AAT GGG AGC GTA	440
Phe Tyr Ser Gln Asn Pro Val Tyr Ala Asn Met Val Asn Gly Ser Val	
115 120 125 130	
ACC ATA CAA AAC TTT CTG CCT TAT AAT TTA AAC AAT GTT GAA CTG AGT	488
Thr Ile Gln Asn Phe Leu Pro Tyr Asn Leu Asn Asn Val Glu Leu Ser	
135 140 145	
TTT AAA GAC GCT CAA GGC AAG GTG GTC AAT TTA GGC GTG ATA GAG ACC	536
Phe Lys Asp Ala Gln Gly Lys Val Val Asn Leu Gly Val Ile Glu Thr	
150 155 160	
ATC CCT AAA CAA TCT CAA ATT ACC TTG CCT GCA AGC TTG TTT AAT GAT	584
Ile Pro Lys Gln Ser Gln Ile Thr Leu Pro Ala Ser Leu Phe Asn Asp	
165 170 175	
TCA GAA TTT GAA CAA GCT GAT AGC TTT AAT TAC CAA CAA CTT CAA GCC	632
Ser Glu Phe Glu Gln Ala Asp Ser Phe Asn Tyr Gln Gln Leu Gln Ala	
180 185 190	
ACT GCC ACA CAA TTT TCT GAC GCT AAC ACG CAA AGT TTG TTT CAA AAG	680
Thr Ala Thr Gln Phe Ser Asp Ala Asn Thr Gln Ser Leu Phe Gln Lys	
195 200 205 210	
CTC AGC AAG ATC ACA ACC AAT GTA ACA ATG AGT TAT GAA AAC GCC GAT	728
Leu Ser Lys Ile Thr Asn Val Thr Met Ser Tyr Glu Asn Ala Asp	
215 220 225	
ACC AAC AAT TTT AAA GGT AAT TGC CAT GAT TGT GTG TCA GAT TTC ACC	776
Thr Asn Asn Phe Lys Gly Asn Cys His Asp Cys Val Ser Asp Phe Thr	
230 235 240	
CCA CAA ACC GCA GAA GAA TTG ACC AAT TTA ATG CTA GAT ATG ATT GCG	824
Pro Gln Thr Ala Glu Glu Leu Thr Asn Leu Met Leu Asp Met Ile Ala	
245 250 255	
GTG TTT GAC TCT AAA TCG TGG GAA GAA GCC GTT TTA AAC GCT CCT TTC	872
Val Phe Asp Ser Lys Ser Trp Glu Glu Ala Val Leu Asn Ala Pro Phe	
260 265 270	
CAA TTT TCT AAC AGC TCA TCA GAG TGC GGC TCT GAC TTT CCT AAG TGC	920
Gln Phe Ser Asn Ser Ser Ser Glu Cys Gly Ser Asp Phe Pro Lys Cys	
275 280 285 290	
GTG AAT CCT TTC AAT AAC GGG CGT GTC GCT CCC ATC TAT GAA AAA TAC	968
Val Asn Pro Phe Asn Asn Gly Arg Val Ala Pro Ile Tyr Glu Lys Tyr	
295 300 305	
GTG CTA ACC CCA CAA TCC GTT ATA GAT GCG TTT AGA AGA ACG ATC AAT	1016
Val Leu Thr Pro Gln Ser Val Ile Asp Ala Phe Arg Arg Thr Ile Asn	
310 315 320	
CTT GAA GTG AAT ATC CTA AAA TCA GGG TTT GTA GGG CTA GGG TAT GAA	1064
Leu Glu Val Asn Ile Leu Lys Ser Gly Phe Val Gly Leu Gly Tyr Glu	
325 330 335	
CTT GAT GAT AAT GAT GGT AAT CTG GGG ATA GAA GCT TCT GCC TTA AAT	1112
Leu Asp Asp Asn Asp Gly Asn Leu Gly Ile Glu Ala Ser Ala Leu Asn	

340	345	350	
CCT GAA AAA TTG TTT GGT AAA ACT TTG AAC AAA GTT GAT ATT GTG GAA	1160		
Pro Glu Lys Leu Phe Gly Lys Thr Leu Asn Lys Val Asp Ile Val Glu			
355 360 365 370			
TTA AGA GAC ATT ATC CAT GAA TTT AGC CAC ACT AAA GGC TAT ACG CAT	1208		
Leu Arg Asp Ile Ile His Glu Phe Ser His Thr Lys Gly Tyr Thr His			
375 380 385			
AAT GGG AAC ATG ACT TAT CAA AGA GTG CGC TTG TGT CAA GAA AAC GGC	1256		
Asn Gly Asn Met Thr Tyr Gln Arg Val Arg Leu Cys Gln Glu Asn Gly			
390 395 400			
GGA GCC ATA CAA GAA TGT GAG GGT GGG AAA GAA GAG TTA GTC AAT GGA	1304		
Gly Ala Ile Gln Glu Cys Glu Gly Gly Lys Glu Glu Leu Val Asn Gly			
405 410 415			
AAA GAA GAA CTA AAA TTT ACA AAT GGG AAA GAA GTG AAA GAT CAG GAT	1352		
Lys Glu Glu Leu Lys Phe Thr Asn Gly Lys Glu Val Lys Asp Gln Asp			
420 425 430			
GGT TAC ACC TAT GAT GTA TGT TCT TTT TAT AAG GAC AAC CAC CAA GTC	1400		
Gly Tyr Thr Tyr Asp Val Cys Ser Phe Tyr Lys Asp Asn His Gln Val			
435 440 445 450			
TAT ACA GCG AGC AAT TAC CCC AAT TCC ATT TAT ACG AAT TGC GCT CAA	1448		
Tyr Thr Ala Ser Asn Tyr Pro Asn Ser Ile Tyr Thr Asn Cys Ala Gln			
455 460 465			
GTC CCT GCT GGG CTT ATA GGG GTT ACC ACC GCT GTC TGG CAA CAG CTC	1496		
Val Pro Ala Gly Leu Ile Gly Val Thr Thr Ala Val Trp Gln Gln Leu			
470 475 480			
ATC AAT CAA AAC GCT CTG CCC ATT AAT TTC GCT AAT CTA AAT AGC CCA	1544		
Ile Asn Gln Asn Ala Leu Pro Ile Asn Phe Ala Asn Leu Asn Ser Pro			
485 490 495			
ACC AAC CAC TTA AAC GCC GGG TTG AAC GCA CAA AAT TTT GCA ACC TCT	1592		
Thr Asn His Leu Asn Ala Gly Leu Asn Ala Gln Asn Phe Ala Thr Ser			
500 505 510			
ATA GTC AGC GCG ATC GCG CAA AAT TTT TCC ACC ACT TCC ACC ACC ACT	1640		
Ile Val Ser Ala Ile Ala Gln Asn Phe Ser Thr Thr Ser Thr Thr			
515 520 525 530			
TAC CGC TCT TCA AGT AAG AAT TTT AGA AGC CCT ATT TTA GGG GTT AAT	1688		
Tyr Arg Ser Ser Ser Lys Asn Phe Arg Ser Pro Ile Leu Gly Val Asn			
535 540 545			
GTT AAA ATA GGC TAC CAA CAT TAT TTC AAT GAC TAC ATA GGG TTA GCC	1736		
Val Lys Ile Gly Tyr Gln His Tyr Phe Asn Asp Tyr Ile Gly Leu Ala			
550 555 560			
TAT TAC GGC ATT ATC AAA TAC AAT TAC GCC AAA ACT AAC GAT GAA AAA	1784		
Tyr Tyr Gly Ile Ile Lys Tyr Asn Tyr Ala Lys Thr Asn Asp Glu Lys			
565 570 575			

ATC	CAG	CAA	TTA	AGC	TAT	GGT	GGG	GGA	ATG	GAT	GTG	TTG	TTT	GAT	TTC	1832
Ile	Gln	Gln	Leu	Ser	Tyr	Gly	Gly	Gly	Met	Asp	Val	Leu	Phe	Asp	Phe	
580						585					590					
ATC	ACC	ACT	TAC	GCT	AAC	AAA	AAG	CAA	GAC	AAC	CCA	ACT	AAA	AAA	GTT	1880
Ile	Thr	Thr	Tyr	Ala	Asn	Lys	Lys	Gln	Asp	Asn	Pro	Thr	Lys	Lys	Val	
595					600					605					610	
TTT	GCT	TCC	TCT	TTT	GGG	GTG	TTT	GGG	GGG	TTA	AGG	GGC	TTA	TAC	AAT	1928
Phe	Ala	Ser	Ser	Phe	Gly	Val	Phe	Gly	Gly	Leu	Arg	Gly	Leu	Tyr	Asn	
				615					620					625		
AGC	TAT	TAT	GTC	TTC	AAC	CAA	GTC	AAA	GGA	AGC	GGT	AAT	TTA	GAT	ATA	1976
Ser	Tyr	Tyr	Val	Phe	Asn	Gln	Val	Lys	Gly	Ser	Gly	Asn	Leu	Asp	Ile	
			630					635					640			
GTT	ACT	GGG	TTT	AAT	TAC	CGC	TAC	AAG	CAT	TCT	AAA	TAT	TCT	GTA	GGC	2024
Val	Thr	Gly	Phe	Asn	Tyr	Arg	Tyr	Lys	His	Ser	Lys	Tyr	Ser	Val	Gly	
		645					650					655				
ATT	AGC	GTT	CCT	TTA	ATC	CAA	AGC	GGT	ATT	AAA	ATC	GCT	TCT	AAT	AAT	2072
Ile	Ser	Val	Pro	Leu	Ile	Gln	Ser	Gly	Ile	Lys	Ile	Ala	Ser	Asn	Asn	
		660				665				670						
GGC	ATC	TAT	GCG	AAC	TCC	GTT	GTT	TTG	AAT	GAA	GGG	GGC	AGT	CAT	TTT	2120
Gly	Ile	Tyr	Ala	Asn	Ser	Val	Val	Leu	Asn	Glu	Gly	Gly	Ser	His	Phe	
675					680					685					690	
AAA	GTG	TTT	TTT	AAT	TAC	GGG	TGG	ATT	TTT	TAGGATT	TAA	AATCCCCA	AAT	AAC		2173
Lys	Val	Phe	Phe	Asn	Tyr	Gly	Trp	Ile	Phe							
				695				700								
CCCCTAAACT	TGTGCGATAC	TCGCTACAAA														2203

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Met	Leu	Arg	Phe	Val	Ser	Lys	Thr	Ile	Cys	Leu	Ser	Leu	Ile	Gly	Leu	
1				5					10					15		
Phe	Asn	Pro	Leu	Glu	Ala	Phe	Gln	Lys	His	Gln	Lys	Asp	Gly	Phe	Phe	
			20					25					30			
Ile	Glu	Ala	Gly	Phe	Glu	Thr	Gly	Leu	Leu	Glu	Gly	Thr	Gln	Thr	Lys	
		35					40					45				
Glu	Glu	Val	Ile	Thr	Thr	Gln	Lys	Ile	Tyr	Glu	Asn	Pro	Leu	Thr	His	
		50				55					60					
Pro	Gln	Thr	Lys	Glu	Gln	Pro	Lys	Glu	Gln	Asn	Lys	Ser	Asp	Thr	Ala	
65					70					75					80	
Thr	Pro	Gln	Ser	Ala	Tyr	Gly	Lys	Tyr	Tyr	Ile	Pro	Gln	Ser	Thr	Ile	

				85					90					95			
Leu	Lys	Asn	Ala	Thr	Ala	Leu	Phe	Thr	Thr	Asp	Lys	Ile	Glu	Asn	Gly		
			100						105					110			
Leu	Thr	Phe	Tyr	Ser	Gln	Asn	Pro	Val	Tyr	Ala	Asn	Met	Val	Asn	Gly		
		115						120				125					
Ser	Val	Thr	Ile	Gln	Asn	Phe	Leu	Pro	Tyr	Asn	Leu	Asn	Asn	Val	Glu		
	130					135					140						
Leu	Ser	Phe	Lys	Asp	Ala	Gln	Gly	Lys	Val	Val	Asn	Leu	Gly	Val	Ile		
145					150					155					160		
Glu	Thr	Ile	Pro	Lys	Gln	Ser	Gln	Ile	Thr	Leu	Pro	Ala	Ser	Leu	Phe		
				165					170					175			
Asn	Asp	Ser	Glu	Phe	Glu	Gln	Ala	Asp	Ser	Phe	Asn	Tyr	Gln	Gln	Leu		
			180					185					190				
Gln	Ala	Thr	Ala	Thr	Gln	Phe	Ser	Asp	Ala	Asn	Thr	Gln	Ser	Leu	Phe		
		195					200					205					
Gln	Lys	Leu	Ser	Lys	Ile	Thr	Thr	Asn	Val	Thr	Met	Ser	Tyr	Glu	Asn		
	210					215					220						
Ala	Asp	Thr	Asn	Asn	Phe	Lys	Gly	Asn	Cys	His	Asp	Cys	Val	Ser	Asp		
225					230				235						240		
Phe	Thr	Pro	Gln	Thr	Ala	Glu	Glu	Leu	Thr	Asn	Leu	Met	Leu	Asp	Met		
				245					250					255			
Ile	Ala	Val	Phe	Asp	Ser	Lys	Ser	Trp	Glu	Glu	Ala	Val	Leu	Asn	Ala		
			260					265					270				
Pro	Phe	Gln	Phe	Ser	Asn	Ser	Ser	Ser	Glu	Cys	Gly	Ser	Asp	Phe	Pro		
		275					280					285					
Lys	Cys	Val	Asn	Pro	Phe	Asn	Asn	Gly	Arg	Val	Ala	Pro	Ile	Tyr	Glu		
	290					295					300						
Lys	Tyr	Val	Leu	Thr	Pro	Gln	Ser	Val	Ile	Asp	Ala	Phe	Arg	Arg	Thr		
305					310				315						320		
Ile	Asn	Leu	Glu	Val	Asn	Ile	Leu	Lys	Ser	Gly	Phe	Val	Gly	Leu	Gly		
				325					330					335			
Tyr	Glu	Leu	Asp	Asp	Asn	Asp	Gly	Asn	Leu	Gly	Ile	Glu	Ala	Ser	Ala		
			340					345					350				
Leu	Asn	Pro	Glu	Lys	Leu	Phe	Gly	Lys	Thr	Leu	Asn	Lys	Val	Asp	Ile		
		355					360					365					
Val	Glu	Leu	Arg	Asp	Ile	Ile	His	Glu	Phe	Ser	His	Thr	Lys	Gly	Tyr		
	370					375					380						
Thr	His	Asn	Gly	Asn	Met	Thr	Tyr	Gln	Arg	Val	Arg	Leu	Cys	Gln	Glu		
385					390				395						400		
Asn	Gly	Gly	Ala	Ile	Gln	Glu	Cys	Glu	Gly	Gly	Lys	Glu	Glu	Leu	Val		
				405					410					415			
Asn	Gly	Lys	Glu	Glu	Leu	Lys	Phe	Thr	Asn	Gly	Lys	Glu	Val	Lys	Asp		
			420					425					430				
Gln	Asp	Gly	Tyr	Thr	Tyr	Asp	Val	Cys	Ser	Phe	Tyr	Lys	Asp	Asn	His		
		435					440					445					
Gln	Val	Tyr	Thr	Ala	Ser	Asn	Tyr	Pro	Asn	Ser	Ile	Tyr	Thr	Asn	Cys		
	450					455					460						
Ala	Gln	Val	Pro	Ala	Gly	Leu	Ile	Gly	Val	Thr	Thr	Ala	Val	Trp	Gln		
465					470					475					480		
Gln	Leu	Ile	Asn	Gln	Asn	Ala	Leu	Pro	Ile	Asn	Phe	Ala	Asn	Leu	Asn		
				485					490					495			
Ser	Pro	Thr	Asn	His	Leu	Asn	Ala	Gly	Leu	Asn	Ala	Gln	Asn	Phe	Ala		
			500					505					510				
Thr	Ser	Ile	Val	Ser	Ala	Ile	Ala	Gln	Asn	Phe	Ser	Thr	Thr	Ser	Thr		
		515					520					525					
Thr	Thr	Tyr	Arg	Ser	Ser	Ser	Lys	Asn	Phe	Arg	Ser	Pro	Ile	Leu	Gly		
	530					535					540						
Val	Asn	Val	Lys	Ile	Gly	Tyr	Gln	His	Tyr	Phe	Asn	Asp	Tyr	Ile	Gly		

545		550		555		560									
Leu	Ala	Tyr	Tyr	Gly	Ile	Ile	Lys	Tyr	Asn	Tyr	Ala	Lys	Thr	Asn	Asp
				565					570					575	
Glu	Lys	Ile	Gln	Gln	Leu	Ser	Tyr	Gly	Gly	Gly	Met	Asp	Val	Leu	Phe
			580					585					590		
Asp	Phe	Ile	Thr	Thr	Tyr	Ala	Asn	Lys	Lys	Gln	Asp	Asn	Pro	Thr	Lys
		595					600					605			
Lys	Val	Phe	Ala	Ser	Ser	Phe	Gly	Val	Phe	Gly	Gly	Leu	Arg	Gly	Leu
	610					615				620					
Tyr	Asn	Ser	Tyr	Tyr	Val	Phe	Asn	Gln	Val	Lys	Gly	Ser	Gly	Asn	Leu
625					630					635				640	
Asp	Ile	Val	Thr	Gly	Phe	Asn	Tyr	Arg	Tyr	Lys	His	Ser	Lys	Tyr	Ser
			645						650					655	
Val	Gly	Ile	Ser	Val	Pro	Leu	Ile	Gln	Ser	Gly	Ile	Lys	Ile	Ala	Ser
			660					665					670		
Asn	Asn	Gly	Ile	Tyr	Ala	Asn	Ser	Val	Val	Leu	Asn	Glu	Gly	Gly	Ser
		675					680					685			
His	Phe	Lys	Val	Phe	Phe	Asn	Tyr	Gly	Trp	Ile	Phe				
	690					695					700				

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...344
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCGTTT	TGGA	AAA	GATATA	GCCCAT	GCGC	GTTTCA	AAGGG	TAATGAA	AGC	ATG	GTG				56	
										Met	Val					
										1						
TAT	GAA	GAA	AAT	TTT	GTG	CAT	GCC	GGG	TTT	GTG	CTT	ATT	GCG	TGC	AAT	104
Tyr	Glu	Glu	Asn	Phe	Val	His	Ala	Gly	Phe	Val	Leu	Ile	Ala	Cys	Asn	
		5					10					15				
TAT	GCG	GCC	TTG	TGC	GCG	TTG	AAT	AAA	AGA	CAC	AGC	GTG	GTG	GTT	TCT	152
Tyr	Ala	Ala	Leu	Cys	Ala	Leu	Asn	Lys	Arg	His	Ser	Val	Val	Val	Ser	
	20					25				30						
AAT	AAC	ATC	AAT	TTT	TAT	GCC	CCC	CTA	GAA	TTG	AAT	CAA	GAA	GCA	CTC	200
Asn	Asn	Ile	Asn	Phe	Tyr	Ala	Pro	Leu	Glu	Leu	Asn	Gln	Glu	Ala	Leu	
35					40				45				50			
ATT	AAA	GCG	CAA	GTG	ATT	CAA	GAT	GGC	GTG	AAA	AAA	GCT	GAA	ATA	AAA	248
Ile	Lys	Ala	Gln	Val	Ile	Gln	Asp	Gly	Val	Lys	Lys	Ala	Glu	Ile	Lys	
			55						60					65		

ATA GAG GCG TTT GTG TTA GAC ATT CAG GTT TTA GAG GGA ATG ATA GAA 296
 Ile Glu Ala Phe Val Leu Asp Ile Gln Val Leu Glu Gly Met Ile Glu
 70 75 80

ATT GTG GTG TTT GAT AAA AAG CCT TTT AAA TTC AAT TTT AAA GAA GAG T 345
 Ile Val Val Phe Asp Lys Lys Pro Phe Lys Phe Asn Phe Lys Glu Glu
 85 90 95

AGTTAAATGG TTATTGTTTT AGTCGTGGAT AGTTTTTAAAG ACACCAGTAA TG 397

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Met Val Tyr Glu Glu Asn Phe Val His Ala Gly Phe Val Leu Ile Ala
 1 5 10 15
 Cys Asn Tyr Ala Ala Leu Cys Ala Leu Asn Lys Arg His Ser Val Val
 20 25 30
 Val Ser Asn Asn Ile Asn Phe Tyr Ala Pro Leu Glu Leu Asn Gln Glu
 35 40 45
 Ala Leu Ile Lys Ala Gln Val Ile Gln Asp Gly Val Lys Lys Ala Glu
 50 55 60
 Ile Lys Ile Glu Ala Phe Val Leu Asp Ile Gln Val Leu Glu Gly Met
 65 70 75 80
 Ile Glu Ile Val Val Phe Asp Lys Lys Pro Phe Lys Phe Asn Phe Lys
 85 90 95
 Glu Glu

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1208
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

ATGATAGTAA GGAAATAAGA GTGGAATGCA AGAATCACCC TATTGAAAAG ATG GCA 56

Met Ala

1

GAA	AAA	TTA	GAG	GAA	ACT	AAT	CCT	GAA	TGG	TTT	GAA	AAA	TGG	AGG	GAA	104
Glu	Lys	Leu	Glu	Glu	Thr	Asn	Pro	Glu	Trp	Phe	Glu	Lys	Trp	Arg	Glu	
		5					10					15				
AAA	CAA	TAC	ACC	CAA	ACT	GGC	GAA	TCT	AAG	CCA	TCA	AAA	CGA	ATC	AAA	152
Lys	Gln	Tyr	Thr	Gln	Thr	Gly	Glu	Ser	Lys	Pro	Ser	Lys	Arg	Ile	Lys	
	20					25					30					
GTT	TTT	AAA	AAC	TTT	ACG	GCA	TTT	GAT	GAC	AGA	TTG	TAT	ACA	ATT	GAA	200
Val	Phe	Lys	Asn	Phe	Thr	Ala	Phe	Asp	Asp	Arg	Leu	Tyr	Thr	Ile	Glu	
35					40					45					50	
TGT	AAT	TTA	AAA	AAT	CTG	GAT	ACC	CAT	CAA	AAA	AAG	TTT	GAA	ATT	TGT	248
Cys	Asn	Leu	Lys	Asn	Leu	Asp	Thr	His	Gln	Lys	Lys	Phe	Glu	Ile	Cys	
				55					60					65		
GGG	GCT	CTG	TAT	GAC	ATT	TAT	GAA	CAA	ATT	TTT	GAT	GAA	ACA	CCA	AGC	296
Gly	Ala	Leu	Tyr	Asp	Ile	Tyr	Glu	Gln	Ile	Phe	Asp	Glu	Thr	Pro	Ser	
			70					75					80			
TTG	AAA	GGG	CGC	GAT	TTA	GAA	ACA	TAC	AAA	GCA	CAA	GAT	TTG	TCA	AAG	344
Leu	Lys	Gly	Arg	Asp	Leu	Glu	Thr	Tyr	Lys	Ala	Gln	Asp	Leu	Ser	Lys	
		85					90					95				
AAA	TTC	ATG	CAT	TTA	GGT	TTT	GAA	CAG	ATC	TCA	AAA	GAT	TTA	AAC	GAC	392
Lys	Phe	Met	His	Leu	Gly	Phe	Glu	Gln	Ile	Ser	Lys	Asp	Leu	Asn	Asp	
	100					105					110					
TCT	AGA	TTG	AAC	GCT	TTA	TTG	TGC	TAT	GAG	GAA	AAA	GTC	ATG	CAA	GCT	440
Ser	Arg	Leu	Asn	Ala	Leu	Leu	Cys	Tyr	Glu	Glu	Lys	Val	Met	Gln	Ala	
115					120					125					130	
TTG	GCT	AAA	AAA	TAC	CCT	AGT	TTT	TTA	CAA	GAT	TTG	CAT	GAT	ATA	AAA	488
Leu	Ala	Lys	Lys	Tyr	Pro	Ser	Phe	Leu	Gln	Asp	Leu	His	Asp	Ile	Lys	
				135					140					145		
AAA	TAC	AGG	AAT	AAA	GAT	AAA	CAC	GGC	GAG	AAA	CCA	CAA	GAT	GGG	TCT	536
Lys	Tyr	Arg	Asn	Lys	Asp	Lys	His	Gly	Glu	Lys	Pro	Gln	Asp	Gly	Ser	
			150					155					160			
TCT	TTA	ACG	AGA	GTG	GAA	TTA	GAA	AGA	TAC	AGA	GAT	GGA	ATT	TAT	TTT	584
Ser	Leu	Thr	Arg	Val	Glu	Leu	Glu	Arg	Tyr	Arg	Asp	Gly	Ile	Tyr	Phe	
		165					170					175				
CTA	GTA	GAA	AAT	CTT	TTA	AAA	AAC	CCC	TTG	ATT	AAA	GAG	AGA	GAA	AAT	632
Leu	Val	Glu	Asn	Leu	Leu	Lys	Asn	Pro	Leu	Ile	Lys	Glu	Arg	Glu	Asn	
	180					185					190					
GCT	CAA	GAA	GAA	AAA	CAT	TAT	AAG	AAA	AAT	GCA	GAG	ATT	GAC	GAC	CGA	680
Ala	Gln	Glu	Glu	Lys	His	Tyr	Lys	Lys	Asn	Ala	Glu	Ile	Asp	Asp	Arg	
195					200					205					210	
TCC	CAG	CTA	TCA	AAC	TTA	AAC	GCA	CCC	AAA	CCC	TTA	TTT	GAA	TGT	TTT	728
Ser	Gln	Leu	Ser	Asn	Leu	Asn	Ala	Pro	Lys	Pro	Leu	Phe	Glu	Cys	Phe	
				215					220					225		

GTA GGA GTT AAT CTG GCC AAA GCC AAA TAT TAT TCT AAA AAA GAA GAA	776
Val Gly Val Asn Leu Ala Lys Ala Lys Tyr Tyr Ser Lys Lys Glu Glu	
230 235 240	
AGA GAA AAA GAA AAG ATG ATC TTG AAT TTT TGT AAG ATA TTT GAA ATT	824
Arg Glu Lys Glu Lys Met Ile Leu Asn Phe Cys Lys Ile Phe Glu Ile	
245 250 255	
ATT CTT TTT GAA GCT ATC CAA AAA CAA CCA AAG CCT GAT TTT AAA AAT	872
Ile Leu Phe Glu Ala Ile Gln Lys Gln Pro Lys Pro Asp Phe Lys Asn	
260 265 270	
AAA GAC GAG CTT TTA GGG GAT TAT CCT AAT CTT AAA AAT TTA GAT TCT	920
Lys Asp Glu Leu Leu Gly Asp Tyr Pro Asn Leu Lys Asn Leu Asp Ser	
275 280 285 290	
TTA AGA GAA GTG AGG GAA GAC TTT TTG AAA AGA GCG TTT AAG AAT GAT	968
Leu Arg Glu Val Arg Glu Asp Phe Leu Lys Arg Ala Phe Lys Asn Asp	
295 300 305	
GAA GCG AGT TTG GGA GCG TAT GTG TTA GTG TTG CTT AGC TGT AAG TAT	1016
Glu Ala Ser Leu Gly Ala Tyr Val Leu Val Leu Leu Ser Cys Lys Tyr	
310 315 320	
TTT GAG AGC GTG TTT GAA AAA GTT CAA GAA TGG CTA GAT TTT ATC GCT	1064
Phe Glu Ser Val Phe Glu Lys Val Gln Glu Trp Leu Asp Phe Ile Ala	
325 330 335	
AGG CTT ATT GCT TTG AGA GGC CAT GTG CAC AAG ATA ACT AAA GAA CTT	1112
Arg Leu Ile Ala Leu Arg Gly His Val His Lys Ile Thr Lys Glu Leu	
340 345 350	
GAA AGA TTA GAA GAA GAG GAT TTA GAA AAA TTG GAA AAA CAA GCA CTA	1160
Glu Arg Leu Glu Glu Glu Asp Leu Glu Lys Leu Glu Lys Gln Ala Leu	
355 360 365 370	
GAA TAT TTT AAT AAA ATA GCA AAT AAA ATA TAT CTA AAG GAG AAA CGA T	1209
Glu Tyr Phe Asn Lys Ile Ala Asn Lys Ile Tyr Leu Lys Glu Lys Arg	
375 380 385	
GAGCGGGAAT GAAGAATTGG AGCTAAGAGC CAGAGAAACT GAGTTGGATA AA	1261

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Met	Ala	Glu	Lys	Leu	Glu	Glu	Thr	Asn	Pro	Glu	Trp	Phe	Glu	Lys	Trp
1				5					10					15	
Arg	Glu	Lys	Gln	Tyr	Thr	Gln	Thr	Gly	Glu	Ser	Lys	Pro	Ser	Lys	Arg

Ile	Lys	Val	Phe	Lys	Asn	Phe	Thr	Ala	Phe	Asp	Asp	Arg	Leu	Tyr	Thr
		35					40					45			
Ile	Glu	Cys	Asn	Leu	Lys	Asn	Leu	Asp	Thr	His	Gln	Lys	Lys	Phe	Glu
	50					55					60				
Ile	Cys	Gly	Ala	Leu	Tyr	Asp	Ile	Tyr	Glu	Gln	Ile	Phe	Asp	Glu	Thr
65					70					75					80
Pro	Ser	Leu	Lys	Gly	Arg	Asp	Leu	Glu	Thr	Tyr	Lys	Ala	Gln	Asp	Leu
			85						90					95	
Ser	Lys	Lys	Phe	Met	His	Leu	Gly	Phe	Glu	Gln	Ile	Ser	Lys	Asp	Leu
			100					105					110		
Asn	Asp	Ser	Arg	Leu	Asn	Ala	Leu	Leu	Cys	Tyr	Glu	Glu	Lys	Val	Met
		115					120					125			
Gln	Ala	Leu	Ala	Lys	Lys	Tyr	Pro	Ser	Phe	Leu	Gln	Asp	Leu	His	Asp
	130					135					140				
Ile	Lys	Lys	Tyr	Arg	Asn	Lys	Asp	Lys	His	Gly	Glu	Lys	Pro	Gln	Asp
145					150					155					160
Gly	Ser	Ser	Leu	Thr	Arg	Val	Glu	Leu	Glu	Arg	Tyr	Arg	Asp	Gly	Ile
			165						170					175	
Tyr	Phe	Leu	Val	Glu	Asn	Leu	Leu	Lys	Asn	Pro	Leu	Ile	Lys	Glu	Arg
			180					185					190		
Glu	Asn	Ala	Gln	Glu	Glu	Lys	His	Tyr	Lys	Lys	Asn	Ala	Glu	Ile	Asp
	195						200					205			
Asp	Arg	Ser	Gln	Leu	Ser	Asn	Leu	Asn	Ala	Pro	Lys	Pro	Leu	Phe	Glu
	210					215					220				
Cys	Phe	Val	Gly	Val	Asn	Leu	Ala	Lys	Ala	Lys	Tyr	Tyr	Ser	Lys	Lys
225					230					235					240
Glu	Glu	Arg	Glu	Lys	Glu	Lys	Met	Ile	Leu	Asn	Phe	Cys	Lys	Ile	Phe
			245					250						255	
Glu	Ile	Ile	Leu	Phe	Glu	Ala	Ile	Gln	Lys	Gln	Pro	Lys	Pro	Asp	Phe
			260					265					270		
Lys	Asn	Lys	Asp	Glu	Leu	Leu	Gly	Asp	Tyr	Pro	Asn	Leu	Lys	Asn	Leu
	275						280					285			
Asp	Ser	Leu	Arg	Glu	Val	Arg	Glu	Asp	Phe	Leu	Lys	Arg	Ala	Phe	Lys
	290					295					300				
Asn	Asp	Glu	Ala	Ser	Leu	Gly	Ala	Tyr	Val	Leu	Val	Leu	Leu	Ser	Cys
305					310					315					320
Lys	Tyr	Phe	Glu	Ser	Val	Phe	Glu	Lys	Val	Gln	Glu	Trp	Leu	Asp	Phe
			325						330					335	
Ile	Ala	Arg	Leu	Ile	Ala	Leu	Arg	Gly	His	Val	His	Lys	Ile	Thr	Lys
			340					345					350		
Glu	Leu	Glu	Arg	Leu	Glu	Glu	Glu	Asp	Leu	Glu	Lys	Leu	Glu	Lys	Gln
	355						360					365			
Ala	Leu	Glu	Tyr	Phe	Asn	Lys	Ile	Ala	Asn	Lys	Ile	Tyr	Leu	Lys	Glu
	370					375					380				
Lys	Arg														
385															

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...359
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

CATTTAATGC TAAGTCTAAT AAGATTGCCC TAGATAGACA TTACGCCAAA ATG TTT	56
Met Phe	
1	
TTG CAA GTT GTA GCA AGA ACT CTA AGA AAG AAT GTC AAT ATA TTA GAA	104
Leu Gln Val Val Ala Arg Thr Leu Arg Lys Asn Val Asn Ile Leu Glu	
5 10 15	
GAG CAA GGT TTT ATT GAA GTC ATT AAA GGA AAA CAA AGA TAC TTG TAT	152
Glu Gln Gly Phe Ile Glu Val Ile Lys Gly Lys Gln Arg Tyr Leu Tyr	
20 25 30	
GTG TAT CTT AAA GAT TAC AGA GAA TTA GAG GGC TAT AAC TCC GTA GGA	200
Val Tyr Leu Lys Asp Tyr Arg Glu Leu Glu Gly Tyr Asn Ser Val Gly	
35 40 45 50	
GCT AAT CAA AAG AAC AAT ATC CCA TCG CCT TTT TTC TTA CAG ATT ATG	248
Ala Asn Gln Lys Asn Asn Ile Pro Ser Pro Phe Phe Leu Gln Ile Met	
55 60 65	
CGT TTC TTA GAA AAG TTT GCC AAA GAA ATT GAG AGA GTA AAA ATA ACA	296
Arg Phe Leu Glu Lys Phe Ala Lys Glu Ile Glu Arg Val Lys Ile Thr	
70 75 80	
ACA AAG AAT GTG TTA TGC ATA TTC CTA GCC AAG AGC TTA TGC AAA GAG	344
Thr Lys Asn Val Leu Cys Ile Phe Leu Ala Lys Ser Leu Cys Lys Glu	
85 90 95	
TTA ATA ATG TTG TTT TAA AATTCAC GCCTATTTCT AATCCTAATA CCACTTACAC T	400
Leu Ile Met Leu Phe	
100	
TTATCCTACA AG	412

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Met Phe Leu Gln Val Val Ala Arg Thr Leu Arg Lys Asn Val Asn Ile
1 5 10 15
Leu Glu Glu Gln Gly Phe Ile Glu Val Ile Lys Gly Lys Gln Arg Tyr

	20		25		30
Leu Tyr Val Tyr Leu Lys Asp Tyr Arg Glu Leu Glu Gly Tyr Asn Ser					
	35		40		45
Val Gly Ala Asn Gln Lys Asn Asn Ile Pro Ser Pro Phe Phe Leu Gln					
	50		55		60
Ile Met Arg Phe Leu Glu Lys Phe Ala Lys Glu Ile Glu Arg Val Lys					
65		70		75	80
Ile Thr Thr Lys Asn Val Leu Cys Ile Phe Leu Ala Lys Ser Leu Cys					
	85		90		95
Lys Glu Leu Ile Met Leu Phe					
	100				

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1151
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

TTCTATTAAA ATTAGTGTAT GATTGAGATT ATTTTGTATT AGGATCAACC ATG CAA	56
Met Gln	
1	
AAA GCC TTA TTA CAT TCA TCA TTC TTT TTA CCT TTA TTT TTA TCT TTT	104
Lys Ala Leu Leu His Ser Ser Phe Phe Leu Pro Leu Phe Leu Ser Phe	
5 10 15	
TGT ATC GCT GAA GAA AAT GGG GCG TAT GCG AGC GTG GGT TTT GAA TAT	152
Cys Ile Ala Glu Glu Asn Gly Ala Tyr Ala Ser Val Gly Phe Glu Tyr	
20 25 30	
TCC ATT AGT CAT GCC GTT GAA CAC AAT AAC CCC TTT TTA AAT CAA GAA	200
Ser Ile Ser His Ala Val Glu His Asn Asn Pro Phe Leu Asn Gln Glu	
35 40 45 50	
CGC ATC CAA ATC ATT TCT AAC GCT CAA AAT AAA ATC TAT AAA CTC CAT	248
Arg Ile Gln Ile Ile Ser Asn Ala Gln Asn Lys Ile Tyr Lys Leu His	
55 60 65	
CAA GTT AAA AAT GAA ATC ACA AGC ATG CCT AAA ACC TTT GCA TAT ATC	296
Gln Val Lys Asn Glu Ile Thr Ser Met Pro Lys Thr Phe Ala Tyr Ile	
70 75 80	
AAC AAC GCT TTA AAA AAC AAC TCC AAA TTA ACC CCC ACT GAA ATG CAA	344
Asn Asn Ala Leu Lys Asn Asn Ser Lys Leu Thr Pro Thr Glu Met Gln	
85 90 95	

GCC GAA CAA TAC TAC CTC CAA TCC ACC TTT CAA AAC ATT GAA AAA ATA Ala Glu Gln Tyr Tyr Leu Gln Ser Thr Phe Gln Asn Ile Glu Lys Ile 100 105 110	392
GTA ATG CTT AGC GGT GGC GTT TCA TCT AAC CCA CAA TTA GTC CAA GCG Val Met Leu Ser Gly Gly Val Ser Ser Asn Pro Gln Leu Val Gln Ala 115 120 125 130	440
TTG GAA AAA ATG CAA GAA CCC ATT ACT AAC CCT TTA GAA TTT GAA GAA Leu Glu Lys Met Gln Glu Pro Ile Thr Asn Pro Leu Glu Phe Glu Glu 135 140 145	488
AAC TTA AGA AAT TTA GAA GTG CAA TTT GCT CAA TCT CAA AAC CGC ATG Asn Leu Arg Asn Leu Glu Val Gln Phe Ala Gln Ser Gln Asn Arg Met 150 155 160	536
CTT TCT TCT TTA TCT TCT CAA ATC GCT GCC ATT TCA AAT TCC TTA AAC Leu Ser Ser Leu Ser Ser Gln Ile Ala Ala Ile Ser Asn Ser Leu Asn 165 170 175	584
GCG CTT GAT CCT AAC TCT TAT TCT AAA AAC ATT TCA AGC ATG TAT GGG Ala Leu Asp Pro Asn Ser Tyr Ser Lys Asn Ile Ser Ser Met Tyr Gly 180 185 190	632
GTG AGT TTG AGC GTA GGT TAT AAG CAT TTC TTT ACC AAG AAA AAA AAT Val Ser Leu Ser Val Gly Tyr Lys His Phe Phe Thr Lys Lys Lys Asn 195 200 205 210	680
CAA GGG TTG CGC TAT TAC TTG TTT TAT GAC TAT GGT TAC ACT AAT TTT Gln Gly Leu Arg Tyr Tyr Leu Phe Tyr Asp Tyr Gly Tyr Thr Asn Phe 215 220 225	728
GGT TTT GTG GGC AAT GGC TTT GAT GGT TTA GGC AAA ATG AAT AAC CAT Gly Phe Val Gly Asn Gly Phe Asp Gly Leu Gly Lys Met Asn Asn His 230 235 240	776
CTC TAT GGG CTT GGG ATA GAC TAT CTT TAT AAT TTC ATT GAT AAT GCA Leu Tyr Gly Leu Gly Ile Asp Tyr Leu Tyr Asn Phe Ile Asp Asn Ala 245 250 255	824
AAA AAA CAC TCT AGC GTA GGT TTT TAT CTG GGT TTT GCT TTA GCG GGG Lys Lys His Ser Ser Val Gly Phe Tyr Leu Gly Phe Ala Leu Ala Gly 260 265 270	872
AGT TCG TGG GTA GGG AGT GGT TTG AGC ATG TGG GTG AGC CAA ACG GAT Ser Ser Trp Val Gly Ser Gly Leu Ser Met Trp Val Ser Gln Thr Asp 275 280 285 290	920
TTT ATC AAC AAT TAC TTG ACG GGC TAT CAA GCT AAA ATG CAC ACG AGT Phe Ile Asn Asn Tyr Leu Thr Gly Tyr Gln Ala Lys Met His Thr Ser 295 300 305	968
TTT TTC CAG ATC CCT TTG AAT TTT GGG GTT CGT GTG AAT GTC AAT AGG Phe Phe Gln Ile Pro Leu Asn Phe Gly Val Arg Val Asn Val Asn Arg 310 315 320	1016
CAT AAT GGC TTT GAA ATG GGC TTG AAA ATC CCT TTA GCG ATG AAT TCC His Asn Gly Phe Glu Met Gly Leu Lys Ile Pro Leu Ala Met Asn Ser	1064

	260		265		270
Ala Gly Ser Ser Trp Val Gly Ser Gly Leu Ser Met Trp Val Ser Gln					
	275		280		285
Thr Asp Phe Ile Asn Asn Tyr Leu Thr Gly Tyr Gln Ala Lys Met His					
	290		295		300
Thr Ser Phe Phe Gln Ile Pro Leu Asn Phe Gly Val Arg Val Asn Val					
305			310		315
Asn Arg His Asn Gly Phe Glu Met Gly Leu Lys Ile Pro Leu Ala Met					
	325		330		335
Asn Ser Phe Tyr Glu Thr His Gly Lys Gly Leu Asn Thr Ser Leu Phe					
	340		345		350
Phe Lys Arg Leu Val Met Phe Asn Val Ser Tyr Val Tyr Ser Phe					
355			360		365

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1687 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1634
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TTATTTTAC AGAGTAATTT ATCTATTCTC AGGTAAAGTA AGGAAGAGGA ATG AAA	56
Met Lys	
1	
TTA AAG AAA CGA AAA GTT GCG GCT GCA TTG CTA AAG CGT TTT ACC TTG	104
Leu Lys Lys Arg Lys Val Ala Ala Ala Leu Leu Lys Arg Phe Thr Leu	
5 10 15	
CCA CTA TTG TTC ACT ACG GGT TCA TTA GGG GCG GTT ACT TAT GAA GTG	152
Pro Leu Leu Phe Thr Thr Gly Ser Leu Gly Ala Val Thr Tyr Glu Val	
20 25 30	
CAT GGA GAT TTT ATC AAT TTT GCT AAA GTG GGT TTT AAC CAT TCG CCC	200
His Gly Asp Phe Ile Asn Phe Ala Lys Val Gly Phe Asn His Ser Pro	
35 40 45 50	
ATT AAT CCT GTT AAA GGT ATC TAT CCC ACA GAA ACT TTT GTT AAC CTT	248
Ile Asn Pro Val Lys Gly Ile Tyr Pro Thr Glu Thr Phe Val Asn Leu	
55 60 65	
ACG GGT AAG CTA GAG GGG TCT GTG CAT TTA GGT AGG GGA TGG ACC GTG	296
Thr Gly Lys Leu Glu Gly Ser Val His Leu Gly Arg Gly Trp Thr Val	
70 75 80	
AAT TTA GGC GGT GTT TTG GGC GGA CAG GCT TAT GAT GGC ACT AAG TAT	344

Asn	Leu	Gly	Gly	Val	Leu	Gly	Gly	Gln	Ala	Tyr	Asp	Gly	Thr	Lys	Tyr	
	85						90					95				
GAT	AGG	TGG	GCG	AAG	GAT	TTT	ACC	CCC	CCA	AGC	TAT	TGG	GAT	AAA	ACT	392
Asp	Arg	Trp	Ala	Lys	Asp	Phe	Thr	Pro	Pro	Ser	Tyr	Trp	Asp	Lys	Thr	
	100					105					110					
TCT	TGC	GGT	ACT	GAT	TCT	ATG	AGT	CTT	TGT	ATG	AAT	GCC	ACT	AAA	ATG	440
Ser	Cys	Gly	Thr	Asp	Ser	Met	Ser	Leu	Cys	Met	Asn	Ala	Thr	Lys	Met	
	115				120					125					130	
TGG	CAG	CAA	TCA	GGG	CCA	GGT	GGC	GTC	ATT	AAC	CCT	AGA	GGT	ATT	GGT	488
Trp	Gln	Gln	Ser	Gly	Pro	Gly	Gly	Val	Ile	Asn	Pro	Arg	Gly	Ile	Gly	
				135					140					145		
TGG	GAA	TAC	ATG	GGT	GAG	TGG	AAC	GGC	TTG	TTC	CCT	AAC	TAC	TAT	CCG	536
Trp	Glu	Tyr	Met	Gly	Glu	Trp	Asn	Gly	Leu	Phe	Pro	Asn	Tyr	Tyr	Pro	
			150					155					160			
GCT	AAC	GCC	TAC	TTG	CCT	GGT	GGC	TCA	AGG	CGC	TAT	CAA	GTC	TAT	AAA	584
Ala	Asn	Ala	Tyr	Leu	Pro	Gly	Gly	Ser	Arg	Arg	Tyr	Gln	Val	Tyr	Lys	
		165					170					175				
GCA	AAT	TTG	ACC	TAT	GAT	AGC	GAC	AGG	GTC	CAT	ATG	GTA	ATG	GGG	CGT	632
Ala	Asn	Leu	Thr	Tyr	Asp	Ser	Asp	Arg	Val	His	Met	Val	Met	Gly	Arg	
	180					185					190					
TTT	GAC	ATT	ACC	GAG	CAG	GAG	CAA	ATG	GAT	TGG	ATT	TAC	CAA	TTG	TTC	680
Phe	Asp	Ile	Thr	Glu	Gln	Glu	Gln	Met	Asp	Trp	Ile	Tyr	Gln	Leu	Phe	
	195				200					205					210	
CAA	GGG	TTT	TAT	GGG	ACT	TTC	AAG	CTC	ACT	AAG	AAT	ATG	AAA	TTC	TTG	728
Gln	Gly	Phe	Tyr	Gly	Thr	Phe	Lys	Leu	Thr	Lys	Asn	Met	Lys	Phe	Leu	
				215					220					225		
CTC	TTT	AGT	GGT	TGG	GGT	CGT	GGT	ATC	GCT	GAT	GGT	CAG	TGG	TTG	TTC	776
Leu	Phe	Ser	Gly	Trp	Gly	Arg	Gly	Ile	Ala	Asp	Gly	Gln	Trp	Leu	Phe	
			230					235					240			
CCT	ATC	TAT	CGT	GAA	AAG	CCT	TGG	GGG	GTT	CAT	AAA	GCG	GGT	ATT	ATT	824
Pro	Ile	Tyr	Arg	Glu	Lys	Pro	Trp	Gly	Val	His	Lys	Ala	Gly	Ile	Ile	
		245					250					255				
TAT	CGC	CCT	ACA	AAG	AAT	TTG	ATG	ATC	CAC	CCT	TAT	GTG	TAT	CTT	ATC	872
Tyr	Arg	Pro	Thr	Lys	Asn	Leu	Met	Ile	His	Pro	Tyr	Val	Tyr	Leu	Ile	
	260					265					270					
CCA	ATG	GTA	GGC	ACA	TTG	CCT	GGT	GCT	AAA	ATA	GAA	TAC	GAT	ACC	AAT	920
Pro	Met	Val	Gly	Thr	Leu	Pro	Gly	Ala	Lys	Ile	Glu	Tyr	Asp	Thr	Asn	
	275				280					285					290	
CCT	GAA	TTT	AGC	GGT	AGG	GGC	ATT	AGG	AAC	AGA	ACG	ACT	TTC	TAT	GCG	968
Pro	Glu	Phe	Ser	Gly	Arg	Gly	Ile	Arg	Asn	Arg	Thr	Thr	Phe	Tyr	Ala	
				295					300					305		
TTG	TAT	GAC	TAT	CGT	TGG	AAT	AAC	GCT	GAA	TAC	GGT	CGT	TAC	GCG	CCC	1016
Leu	Tyr	Asp	Tyr	Arg	Trp	Asn	Asn	Ala	Glu	Tyr	Gly	Arg	Tyr	Ala	Pro	
			310					315					320			

GCT CGT TAT AAC ACT TGG GAT CCG TTC TTG GAT AAT GGT AAG TGG CGT	1064
Ala Arg Tyr Asn Thr Trp Asp Pro Phe Leu Asp Asn Gly Lys Trp Arg	
325 330 335	
GGC TTG CAA GGT CCT GGT GGT GCG ACG CTC CTT TTA CGC CAC CAT ATA	1112
Gly Leu Gln Gly Pro Gly Gly Ala Thr Leu Leu Leu Arg His His Ile	
340 345 350	
GAT ATT AAC AAC TAC TTT GTG GTT GGT GGT GCT TAT CTC AAC ATT GGT	1160
Asp Ile Asn Asn Tyr Phe Val Val Gly Gly Ala Tyr Leu Asn Ile Gly	
355 360 365 370	
AAC CCT AAC ATG AAC TTA GGT ACT TGG GGT AAC CCT GTG GCT GTT GAT	1208
Asn Pro Asn Met Asn Leu Gly Thr Trp Gly Asn Pro Val Ala Val Asp	
375 380 385	
GGT ATC GAA CAA TGG GTC GGT AGT ATC TAT AGC TTA GGG TTT GCG GGG	1256
Gly Ile Glu Gln Trp Val Gly Ser Ile Tyr Ser Leu Gly Phe Ala Gly	
390 395 400	
ATT GAC AAC ATT ACC GAT GCT GAC GCG TTC ACC GAG TAT GTT AAA GGT	1304
Ile Asp Asn Ile Thr Asp Ala Asp Ala Phe Thr Glu Tyr Val Lys Gly	
405 410 415	
GGA GGC AAG CAT GGT AAG TTT AGT TGG AGC GTT TAT CAG CGC TTC ACT	1352
Gly Gly Lys His Gly Lys Phe Ser Trp Ser Val Tyr Gln Arg Phe Thr	
420 425 430	
ACC GCT CCA AGG GCT TTG GAA TAT GGT ATC GGT ATG TAT CTA GAC TAT	1400
Thr Ala Pro Arg Ala Leu Glu Tyr Gly Ile Gly Met Tyr Leu Asp Tyr	
435 440 445 450	
CAG TTC AGC AAG CAT GTT AAA GCG GGT CTC AAA CTC GTA TGG TTA GAG	1448
Gln Phe Ser Lys His Val Lys Ala Gly Leu Lys Leu Val Trp Leu Glu	
455 460 465	
TTC CAA ATT CGT GCG GGT TAC AAC CCT GGA ACC GGT TTC CTT GGG CCA	1496
Phe Gln Ile Arg Ala Gly Tyr Asn Pro Gly Thr Gly Phe Leu Gly Pro	
470 475 480	
AAC GGT CAG CCG CTT AAC TTG AAT ACT GGT TTG TTT GAG TCT TCA GCG	1544
Asn Gly Gln Pro Leu Asn Leu Asn Thr Gly Leu Phe Glu Ser Ser Ala	
485 490 495	
TTC GCT CAA GGC CCT CAA AAC ATG GGC GGT ATC GCA AAA AGC ATC ACT	1592
Phe Ala Gln Gly Pro Gln Asn Met Gly Gly Ile Ala Lys Ser Ile Thr	
500 505 510	
CAA GAC AGA AGC CAT TTG ATG ACA CAC ATT AGT TAT AGT TTC TAAGAGAGT	1643
Gln Asp Arg Ser His Leu Met Thr His Ile Ser Tyr Ser Phe	
515 520 525	
TCTCCCCCTA TCTCTTAGAT ATGCCTTTTT GTATTTTTAT TTTA	1687

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 528 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Met	Lys	Leu	Lys	Lys	Arg	Lys	Val	Ala	Ala	Ala	Leu	Leu	Lys	Arg	Phe
1				5					10					15	
Thr	Leu	Pro	Leu	Leu	Phe	Thr	Thr	Gly	Ser	Leu	Gly	Ala	Val	Thr	Tyr
			20					25					30		
Glu	Val	His	Gly	Asp	Phe	Ile	Asn	Phe	Ala	Lys	Val	Gly	Phe	Asn	His
		35				40						45			
Ser	Pro	Ile	Asn	Pro	Val	Lys	Gly	Ile	Tyr	Pro	Thr	Glu	Thr	Phe	Val
	50					55					60				
Asn	Leu	Thr	Gly	Lys	Leu	Glu	Gly	Ser	Val	His	Leu	Gly	Arg	Gly	Trp
65					70					75					80
Thr	Val	Asn	Leu	Gly	Gly	Val	Leu	Gly	Gly	Gln	Ala	Tyr	Asp	Gly	Thr
			85						90					95	
Lys	Tyr	Asp	Arg	Trp	Ala	Lys	Asp	Phe	Thr	Pro	Pro	Ser	Tyr	Trp	Asp
			100					105					110		
Lys	Thr	Ser	Cys	Gly	Thr	Asp	Ser	Met	Ser	Leu	Cys	Met	Asn	Ala	Thr
		115					120					125			
Lys	Met	Trp	Gln	Gln	Ser	Gly	Pro	Gly	Gly	Val	Ile	Asn	Pro	Arg	Gly
	130					135					140				
Ile	Gly	Trp	Glu	Tyr	Met	Gly	Glu	Trp	Asn	Gly	Leu	Phe	Pro	Asn	Tyr
145					150					155					160
Tyr	Pro	Ala	Asn	Ala	Tyr	Leu	Pro	Gly	Gly	Ser	Arg	Arg	Tyr	Gln	Val
			165						170					175	
Tyr	Lys	Ala	Asn	Leu	Thr	Tyr	Asp	Ser	Asp	Arg	Val	His	Met	Val	Met
			180					185					190		
Gly	Arg	Phe	Asp	Ile	Thr	Glu	Gln	Glu	Gln	Met	Asp	Trp	Ile	Tyr	Gln
		195					200					205			
Leu	Phe	Gln	Gly	Phe	Tyr	Gly	Thr	Phe	Lys	Leu	Thr	Lys	Asn	Met	Lys
	210					215					220				
Phe	Leu	Leu	Phe	Ser	Gly	Trp	Gly	Arg	Gly	Ile	Ala	Asp	Gly	Gln	Trp
225					230					235					240
Leu	Phe	Pro	Ile	Tyr	Arg	Glu	Lys	Pro	Trp	Gly	Val	His	Lys	Ala	Gly
			245						250					255	
Ile	Ile	Tyr	Arg	Pro	Thr	Lys	Asn	Leu	Met	Ile	His	Pro	Tyr	Val	Tyr
		260						265					270		
Leu	Ile	Pro	Met	Val	Gly	Thr	Leu	Pro	Gly	Ala	Lys	Ile	Glu	Tyr	Asp
	275						280					285			
Thr	Asn	Pro	Glu	Phe	Ser	Gly	Arg	Gly	Ile	Arg	Asn	Arg	Thr	Thr	Phe
	290					295					300				
Tyr	Ala	Leu	Tyr	Asp	Tyr	Arg	Trp	Asn	Asn	Ala	Glu	Tyr	Gly	Arg	Tyr
305					310					315					320
Ala	Pro	Ala	Arg	Tyr	Asn	Thr	Trp	Asp	Pro	Phe	Leu	Asp	Asn	Gly	Lys
			325						330					335	
Trp	Arg	Gly	Leu	Gln	Gly	Pro	Gly	Gly	Ala	Thr	Leu	Leu	Leu	Arg	His
		340					345						350		
His	Ile	Asp	Ile	Asn	Asn	Tyr	Phe	Val	Val	Gly	Gly	Ala	Tyr	Leu	Asn
	355						360					365			
Ile	Gly	Asn	Pro	Asn	Met	Asn	Leu	Gly	Thr	Trp	Gly	Asn	Pro	Val	Ala
	370					375					380				
Val	Asp	Gly	Ile	Glu	Gln	Trp	Val	Gly	Ser	Ile	Tyr	Ser	Leu	Gly	Phe

385		390		395		400
Ala Gly Ile Asp Asn Ile Thr Asp Ala Asp Ala Phe Thr Glu Tyr Val						
		405		410		415
Lys Gly Gly Gly Lys His Gly Lys Phe Ser Trp Ser Val Tyr Gln Arg						
		420		425		430
Phe Thr Thr Ala Pro Arg Ala Leu Glu Tyr Gly Ile Gly Met Tyr Leu						
		435		440		445
Asp Tyr Gln Phe Ser Lys His Val Lys Ala Gly Leu Lys Leu Val Trp						
		450		455		460
Leu Glu Phe Gln Ile Arg Ala Gly Tyr Asn Pro Gly Thr Gly Phe Leu						
		465		470		475
Gly Pro Asn Gly Gln Pro Leu Asn Leu Asn Thr Gly Leu Phe Glu Ser						
		485		490		495
Ser Ala Phe Ala Gln Gly Pro Gln Asn Met Gly Gly Ile Ala Lys Ser						
		500		505		510
Ile Thr Gln Asp Arg Ser His Leu Met Thr His Ile Ser Tyr Ser Phe						
		515		520		525

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...359
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

TTTTGTCTGA TTTGTTGCTA CCAAAACCAT TACCAACCAA AGCAGATCCC	ATG TTT	56
	Met Phe	
	1	
TTG ATA CTA TCG AAT CCA TTC TTC AAC ACT TCT GCC ATA AAA TTC TTG		104
Leu Ile Leu Ser Asn Pro Phe Phe Asn Thr Ser Ala Ile Lys Phe Leu		
5 10 15		
ATA TTG TCC ATA GGC AAG TTG AAT TTT TTC CCT AAT ATT TCA TTA AGT		152
Ile Leu Ser Ile Gly Lys Leu Asn Phe Phe Pro Asn Ile Ser Leu Ser		
20 25 30		
CCC ATC ATT AAC ATC AGG AAG AAC AAA AAA TTT AAT ATC ATA GAA AAC		200
Pro Ile Ile Asn Ile Arg Lys Asn Lys Lys Phe Asn Ile Ile Glu Asn		
35 40 45 50		
AAA TCA CTG GAT AAA CCT GTA AAA AGA TTT GTT CCG CCA CCC AAC AAA		248
Lys Ser Leu Asp Lys Pro Val Lys Arg Phe Val Pro Pro Pro Asn Lys		
55 60 65		
GAA GCT AAA ATT TTT CCC ATG ATC AGT CCT TTT ATT TTT GGT TGT GTA		296
Glu Ala Lys Ile Phe Pro Met Ile Ser Pro Phe Ile Phe Gly Cys Val		
70 75 80		

AGT TCT TGC TTG TTC GGA TCT CTA ATG CGT GTT TTA GTA GGA AGC ATT 344
 Ser Ser Cys Leu Phe Gly Ser Leu Met Arg Val Leu Val Gly Ser Ile
 85 90 95

TCA CAA TGG CAT ACC TAAAGCTACT AAGAAAATTC TTGAATCTAT TGGTAAGATT A 400
 Ser Gln Trp His Thr
 100

CTCATGAAAT CA 412

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Met Phe Leu Ile Leu Ser Asn Pro Phe Phe Asn Thr Ser Ala Ile Lys
 1 5 10 15
 Phe Leu Ile Leu Ser Ile Gly Lys Leu Asn Phe Phe Pro Asn Ile Ser
 20 25 30
 Leu Ser Pro Ile Ile Asn Ile Arg Lys Asn Lys Lys Phe Asn Ile Ile
 35 40 45
 Glu Asn Lys Ser Leu Asp Lys Pro Val Lys Arg Phe Val Pro Pro Pro
 50 55 60
 Asn Lys Glu Ala Lys Ile Phe Pro Met Ile Ser Pro Phe Ile Phe Gly
 65 70 75 80
 Cys Val Ser Ser Cys Leu Phe Gly Ser Leu Met Arg Val Leu Val Gly
 85 90 95
 Ser Ile Ser Gln Trp His Thr
 100

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 67...405
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

TCCAATCCGT CTAATATCTC TTTATTTTCG CTCAATTCTT TAACCATAAC GGGTTTTTTA 60
 GCGCTT GTG GGG GTT ACT GGG CTA AAG TTT GGA GCG TTT TGC ACT TCT 108

Val	Gly	Val	Thr	Gly	Leu	Lys	Phe	Gly	Ala	Phe	Cys	Thr	Ser			
1				5					10							
TTT	TCT	TCT	TTT	TTT	AGA	TTT	TCC	TTT	ATC	ATT	TCT	TCT	ATC	CTT	CCT	156
Phe	Ser	Ser	Phe	Phe	Arg	Phe	Ser	Phe	Ile	Ile	Ser	Ser	Ile	Leu	Pro	
15					20					25					30	
TCT	ATC	ATT	TCT	TCT	TGC	GTG	TTT	TCT	TGT	GGG	TTT	TCT	TCT	TTT	TTA	204
Ser	Ile	Ile	Ser	Ser	Cys	Val	Phe	Ser	Cys	Gly	Phe	Ser	Ser	Phe	Leu	
				35					40					45		
GGG	TGG	TTG	GGG	GTT	TTT	TGG	TTT	TCT	GTT	TTG	TTG	TCA	TTT	TCT	ATT	252
Gly	Trp	Leu	Gly	Val	Phe	Trp	Phe	Ser	Val	Leu	Leu	Ser	Phe	Ser	Ile	
			50					55					60			
ATG	GGT	GCA	AGT	GTG	GGC	ATG	ATA	GGT	TTG	GGC	GTG	GTG	GGC	GTA	AGA	300
Met	Gly	Ala	Ser	Val	Gly	Met	Ile	Gly	Leu	Gly	Val	Val	Gly	Val	Arg	
		65					70						75			
GTT	TCT	TTT	GTA	GGC	GTG	GGT	TCT	CTT	TCT	TTA	GTT	TCT	TGT	TTA	ATT	348
Val	Ser	Phe	Val	Gly	Val	Gly	Ser	Leu	Ser	Leu	Val	Ser	Cys	Leu	Ile	
	80					85					90					
TCT	TTT	AAA	GGG	GGG	TTA	GTG	GGG	TTA	GTC	AAA	TCA	TCA	AAT	CGG	TTT	396
Ser	Phe	Lys	Gly	Gly	Leu	Val	Gly	Leu	Val	Lys	Ser	Ser	Asn	Arg	Phe	
95					100					105					110	
CTT	TTA	GGG	TAAAT	GGTGTAAATGG	GTAGGGGGGT	GGGAGGAAAT	TTGGACT									447
Leu	Leu	Gly														

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Val	Gly	Val	Thr	Gly	Leu	Lys	Phe	Gly	Ala	Phe	Cys	Thr	Ser	Phe	Ser	
1				5					10					15		
Ser	Phe	Phe	Arg	Phe	Ser	Phe	Ile	Ile	Ser	Ser	Ile	Leu	Pro	Ser	Ile	
			20					25					30			
Ile	Ser	Ser	Cys	Val	Phe	Ser	Cys	Gly	Phe	Ser	Ser	Phe	Leu	Gly	Trp	
		35					40					45				
Leu	Gly	Val	Phe	Trp	Phe	Ser	Val	Leu	Leu	Ser	Phe	Ser	Ile	Met	Gly	
	50					55					60					
Ala	Ser	Val	Gly	Met	Ile	Gly	Leu	Gly	Val	Val	Gly	Val	Arg	Val	Ser	
65					70					75					80	
Phe	Val	Gly	Val	Gly	Ser	Leu	Ser	Leu	Val	Ser	Cys	Leu	Ile	Ser	Phe	
			85					90					95			
Lys	Gly	Gly	Leu	Val	Gly	Leu	Val	Lys	Ser	Ser	Asn	Arg	Phe	Leu	Leu	
			100					105					110			

Gly

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1127
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CCAAGAAAGA GTATAATAGC GCATAAGAAT TTAAGTATG AAGAGGTTTA	ATG CTA	56
	Met Leu	
	1	
GAA AAT AGA GTT AAG ACC AAG CAA ATT TTT ATC GGT GGC GTG GCC ATA		104
Glu Asn Arg Val Lys Thr Lys Gln Ile Phe Ile Gly Gly Val Ala Ile		
5 10 15		
GGG GGT GAT GCT CCC ATA AGC ACG CAA AGC ATG ACC TTT AGC AAA ACC		152
Gly Gly Asp Ala Pro Ile Ser Thr Gln Ser Met Thr Phe Ser Lys Thr		
20 25 30		
GCT GAT ATT GAA AGC ACT AAA AAT CAA ATT GAC AGA CTC AAA CTC GCC		200
Ala Asp Ile Glu Ser Thr Lys Asn Gln Ile Asp Arg Leu Lys Leu Ala		
35 40 45 50		
GGG GCC GAT TTA GTG AGG GTG GCG GTG AGT AAT GAA AAG GAC GCT CTA		248
Gly Ala Asp Leu Val Arg Val Ala Val Ser Asn Glu Lys Asp Ala Leu		
55 60 65		
GCC TTA AAA GAA TTG AAA AAA GTG TCC CCT TTG CCT TTA ATC GCT GAT		296
Ala Leu Lys Glu Leu Lys Lys Val Ser Pro Leu Pro Leu Ile Ala Asp		
70 75 80		
ATT CAT TTC CAT TAT AAA TTC GCT CTC ATT GCC GCT CAA AGC GTG GAT		344
Ile His Phe His Tyr Lys Phe Ala Leu Ile Ala Ala Gln Ser Val Asp		
85 90 95		
GCG ATC AGG ATT AAC CCC GGA AAC ATC GGC TCT AAA GAG AAG ATC AAA		392
Ala Ile Arg Ile Asn Pro Gly Asn Ile Gly Ser Lys Glu Lys Ile Lys		
100 105 110		
GCG GTG GTT GAT GCT TGT AAA GAA AAA AAC ATT CCT ATA AGA ATT GGC		440
Ala Val Val Asp Ala Cys Lys Glu Lys Asn Ile Pro Ile Arg Ile Gly		
115 120 125 130		
GTG AAT GCT GGG AGT TTA GAA AAG CAG TTT GAT CAA AAA TAC GGA CCC		488
Val Asn Ala Gly Ser Leu Glu Lys Gln Phe Asp Gln Lys Tyr Gly Pro		

135										140					145					
ACC	CCA	AAA	GGC	ATG	GTA	GAA	AGC	GCT	TTG	TAT	AAC	GCC	AAA	CTT	TTA	536				
Thr	Pro	Lys	Gly	Met	Val	Glu	Ser	Ala	Leu	Tyr	Asn	Ala	Lys	Leu	Leu					
			150					155					160							
GAA	GAT	TTG	GAT	TTT	ACC	AAT	TTT	AAG	ATT	TCT	TTA	AAA	GCG	AGC	GAT	584				
Glu	Asp	Leu	Asp	Phe	Thr	Asn	Phe	Lys	Ile	Ser	Leu	Lys	Ala	Ser	Asp					
		165					170					175								
GTG	ATT	CGC	ACC	ATA	GAA	GCT	TAC	AGG	ATG	CTT	CGC	CCT	CTT	GTG	ATC	632				
Val	Ile	Arg	Thr	Ile	Glu	Ala	Tyr	Arg	Met	Leu	Arg	Pro	Leu	Val	Ile					
	180					185					190									
TAT	CCT	TTC	CAT	TTG	GGG	GTT	ACG	GAG	GCG	GGG	AAT	CTT	TTT	AGC	TCC	680				
Tyr	Pro	Phe	His	Leu	Gly	Val	Thr	Glu	Ala	Gly	Asn	Leu	Phe	Ser	Ser					
195				200				205							210					
AGT	ATC	AAA	TCC	GCT	ATG	GCT	TTA	GGG	GGG	CTT	TTA	ATG	GAG	GGC	ATT	728				
Ser	Ile	Lys	Ser	Ala	Met	Ala	Leu	Gly	Gly	Leu	Leu	Met	Glu	Gly	Ile					
			215					220					225							
GGG	GAT	ACG	ATG	CGC	GTA	TCC	ATC	ACA	GGG	GAA	TTA	GAA	AAT	GAA	ATC	776				
Gly	Asp	Thr	Met	Arg	Val	Ser	Ile	Thr	Gly	Glu	Leu	Glu	Asn	Glu	Ile					
			230					235					240							
AAA	GTG	GCC	AGA	GCA	ATT	TTA	CGC	CAT	AGC	GGG	CGG	TTG	AAA	GAA	GGG	824				
Lys	Val	Ala	Arg	Ala	Ile	Leu	Arg	His	Ser	Gly	Arg	Leu	Lys	Glu	Gly					
		245					250					255								
ATT	AAT	TGG	ATT	TCT	TGC	CCC	ACT	TGC	GGG	CGC	ATT	GAA	GCC	AAT	TTA	872				
Ile	Asn	Trp	Ile	Ser	Cys	Pro	Thr	Cys	Gly	Arg	Ile	Glu	Ala	Asn	Leu					
	260					265					270									
GTG	GAT	ATG	GCG	ATC	AAG	GTA	GAA	AAA	CGC	TTA	AGC	CAC	ATC	AAA	ACC	920				
Val	Asp	Met	Ala	Ile	Lys	Val	Glu	Lys	Arg	Leu	Ser	His	Ile	Lys	Thr					
	275				280				285						290					
CCT	TTA	GAC	ATT	AGC	GTG	ATG	GGT	TGC	GTG	GTG	AAT	GCT	TTG	GGT	GAA	968				
Pro	Leu	Asp	Ile	Ser	Val	Met	Gly	Cys	Val	Val	Asn	Ala	Leu	Gly	Glu					
				295				300						305						
GCC	AAG	CAT	GCA	GAC	ATG	GCG	ATC	GCT	TTT	GGG	AAT	CGC	AGC	GGT	TTG	1016				
Ala	Lys	His	Ala	Asp	Met	Ala	Ile	Ala	Phe	Gly	Asn	Arg	Ser	Gly	Leu					
			310					315					320							
ATC	ATT	AAA	GAG	GGT	AAA	GTC	ATT	CAC	AAA	CTG	GCT	GAA	AAG	GAT	TTA	1064				
Ile	Ile	Lys	Glu	Gly	Lys	Val	Ile	His	Lys	Leu	Ala	Glu	Lys	Asp	Leu					
		325					330					335								
TTT	GAA	ACT	TTT	GTG	ATA	GAA	GTG	GAA	AAT	TTA	GCT	AAA	GAA	AGA	GAA	1112				
Phe	Glu	Thr	Phe	Val	Ile	Glu	Val	Glu	Asn	Leu	Ala	Lys	Glu	Arg	Glu					
	340					345					350									
AAA	AGT	TTA	AAG	GAT	TAGGCATGAT CAATAAGTTT AAAAATTTTG TGAGCAACTA C										1168					
Lys	Ser	Leu	Lys	Asp																
															355					

CAGCAATCTA AC

1180

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Met	Leu	Glu	Asn	Arg	Val	Lys	Thr	Lys	Gln	Ile	Phe	Ile	Gly	Gly	Val	1	5	10	15
Ala	Ile	Gly	Gly	Asp	Ala	Pro	Ile	Ser	Thr	Gln	Ser	Met	Thr	Phe	Ser	20	25	30	
Lys	Thr	Ala	Asp	Ile	Glu	Ser	Thr	Lys	Asn	Gln	Ile	Asp	Arg	Leu	Lys	35	40	45	
Leu	Ala	Gly	Ala	Asp	Leu	Val	Arg	Val	Ala	Val	Ser	Asn	Glu	Lys	Asp	50	55	60	
Ala	Leu	Ala	Leu	Lys	Glu	Leu	Lys	Lys	Val	Ser	Pro	Leu	Pro	Leu	Ile	65	70	75	80
Ala	Asp	Ile	His	Phe	His	Tyr	Lys	Phe	Ala	Leu	Ile	Ala	Ala	Gln	Ser	85	90	95	
Val	Asp	Ala	Ile	Arg	Ile	Asn	Pro	Gly	Asn	Ile	Gly	Ser	Lys	Glu	Lys	100	105	110	
Ile	Lys	Ala	Val	Val	Asp	Ala	Cys	Lys	Glu	Lys	Asn	Ile	Pro	Ile	Arg	115	120	125	
Ile	Gly	Val	Asn	Ala	Gly	Ser	Leu	Glu	Lys	Gln	Phe	Asp	Gln	Lys	Tyr	130	135	140	
Gly	Pro	Thr	Pro	Lys	Gly	Met	Val	Glu	Ser	Ala	Leu	Tyr	Asn	Ala	Lys	145	150	155	160
Leu	Leu	Glu	Asp	Leu	Asp	Phe	Thr	Asn	Phe	Lys	Ile	Ser	Leu	Lys	Ala	165	170	175	
Ser	Asp	Val	Ile	Arg	Thr	Ile	Glu	Ala	Tyr	Arg	Met	Leu	Arg	Pro	Leu	180	185	190	
Val	Ile	Tyr	Pro	Phe	His	Leu	Gly	Val	Thr	Glu	Ala	Gly	Asn	Leu	Phe	195	200	205	
Ser	Ser	Ser	Ile	Lys	Ser	Ala	Met	Ala	Leu	Gly	Gly	Leu	Leu	Met	Glu	210	215	220	
Gly	Ile	Gly	Asp	Thr	Met	Arg	Val	Ser	Ile	Thr	Gly	Glu	Leu	Glu	Asn	225	230	235	240
Glu	Ile	Lys	Val	Ala	Arg	Ala	Ile	Leu	Arg	His	Ser	Gly	Arg	Leu	Lys	245	250	255	
Glu	Gly	Ile	Asn	Trp	Ile	Ser	Cys	Pro	Thr	Cys	Gly	Arg	Ile	Glu	Ala	260	265	270	
Asn	Leu	Val	Asp	Met	Ala	Ile	Lys	Val	Glu	Lys	Arg	Leu	Ser	His	Ile	275	280	285	
Lys	Thr	Pro	Leu	Asp	Ile	Ser	Val	Met	Gly	Cys	Val	Val	Asn	Ala	Leu	290	295	300	
Gly	Glu	Ala	Lys	His	Ala	Asp	Met	Ala	Ile	Ala	Phe	Gly	Asn	Arg	Ser	305	310	315	320
Gly	Leu	Ile	Ile	Lys	Glu	Gly	Lys	Val	Ile	His	Lys	Leu	Ala	Glu	Lys	325	330	335	
Asp	Leu	Phe	Glu	Thr	Phe	Val	Ile	Glu	Val	Glu	Asn	Leu	Ala	Lys	Glu				

340
Arg Glu Lys Ser Leu Lys Asp
355

345

350

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1346
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GCCTATGAAA TCTTAAAGCG TTATCCGGCT AAAGCAAAGG TATAAATAAC ATG AAA	56
Met Lys	
1	
AAA TTT TTA ATC ACT TTA TTA TTA GGA GTT TTT ATG GGG TTA CAA GCG	104
Lys Phe Leu Ile Thr Leu Leu Leu Gly Val Phe Met Gly Leu Gln Ala	
5 10 15	
AGC GCT TTG ACA CAC CAA GAA ATC AAT CAA GCT AAA GTC CCT GTG ATT	152
Ser Ala Leu Thr His Gln Glu Ile Asn Gln Ala Lys Val Pro Val Ile	
20 25 30	
TAT GAA GAA AAC CAT TTG TTG CCT ATG GGG TTT ATC CAT TTA GCC TTT	200
Tyr Glu Glu Asn His Leu Leu Pro Met Gly Phe Ile His Leu Ala Phe	
35 40 45 50	
AGG GGG GGT GGG AGC TTA AGC GAT AAA AAC CAG TTG GGT TTG GCG AAA	248
Arg Gly Gly Gly Ser Leu Ser Asp Lys Asn Gln Leu Gly Leu Ala Lys	
55 60 65	
TTA TTC GCG CAA GTT TTA AAC GAA GGC ACT AAA GAG CTT GGT GCG GTG	296
Leu Phe Ala Gln Val Leu Asn Glu Gly Thr Lys Glu Leu Gly Ala Val	
70 75 80	
GGG TTT GCG CAA CTT TTA GAG CAA AAA GCG ATC AGT TTG AAT GTG GAT	344
Gly Phe Ala Gln Leu Leu Glu Gln Lys Ala Ile Ser Leu Asn Val Asp	
85 90 95	
ACC AGC ACA GAA GAT TTG CAA ATC ACT TTA GAA TTT TTA AAA GAA TAC	392
Thr Ser Thr Glu Asp Leu Gln Ile Thr Leu Glu Phe Leu Lys Glu Tyr	
100 105 110	
GAA GAT GAA GCC ATT ACG CGC TTA AAA GAG CTT TTA AAA TCC CCT AAT	440
Glu Asp Glu Ala Ile Thr Arg Leu Lys Glu Leu Leu Lys Ser Pro Asn	

115	120	125	130	
TTC ACG CAA AAC GCT TTA GAA AAA GTC AAA ACC CAA ATG TTA GCC GCA				488
Phe Thr Gln Asn Ala Leu Glu Lys Val Lys Thr Gln Met Leu Ala Ala	135	140	145	
CTT TTA CAA AAA GAA AGC GAT TTT GAC TAT TTG GCT AAA TTG ACT TTA				536
Leu Leu Gln Lys Glu Ser Asp Phe Asp Tyr Leu Ala Lys Leu Thr Leu	150	155	160	
AAG CAA GAG CTT TTT GCT AAC ACC CCT TTA GCT AAC GCA GCC TTA GGC				584
Lys Gln Glu Leu Phe Ala Asn Thr Pro Leu Ala Asn Ala Ala Leu Gly	165	170	175	
ACT AAA GAG AGC ATT CAA AAA ATC AAG CTA GAC GAT TTG AAA CAG CAA				632
Thr Lys Glu Ser Ile Gln Lys Ile Lys Leu Asp Asp Leu Lys Gln Gln	180	185	190	
TTT GCT AAG GTC TTT GAA CTC AAT AAG CTC GTG GTG GTG CTT GGG GGC				680
Phe Ala Lys Val Phe Glu Leu Asn Lys Leu Val Val Val Leu Gly Gly	195	200	205	210
GAT TTG AAA ATC GAT CAA ACC CTT AAG CGT TTG AAT AAC GCC CTT AAT				728
Asp Leu Lys Ile Asp Gln Thr Leu Lys Arg Leu Asn Asn Ala Leu Asn	215	220	225	
TTC TTG CCA CAA GGT AAA GCG TAT GAA GAG CCT TAT TTT GAA ACG AGC				776
Phe Leu Pro Gln Gly Lys Ala Tyr Glu Glu Pro Tyr Phe Glu Thr Ser	230	235	240	
GAT AAA AAA AGC GAA AAA GTC CTC TAT AAA GAC ACT GAG CAG GCT TTC				824
Asp Lys Lys Ser Glu Lys Val Leu Tyr Lys Asp Thr Glu Gln Ala Phe	245	250	255	
GTG TAT TTT GGT GCG CCC TTT AAA ATC AAG GAT TTA AAA CAG GAT TTA				872
Val Tyr Phe Gly Ala Pro Phe Lys Ile Lys Asp Leu Lys Gln Asp Leu	260	265	270	
GCG AAA TCT AAA GTC ATG ATG TTT GTG CTT GGT GGG GGG TTT GGC TCT				920
Ala Lys Ser Lys Val Met Met Phe Val Leu Gly Gly Gly Phe Gly Ser	275	280	285	290
CGT TTA ATG GAA AAA ATC AGG GTT CAA GAG GGA TTA GCT TAT AGC GTG				968
Arg Leu Met Glu Lys Ile Arg Val Gln Glu Gly Leu Ala Tyr Ser Val	295	300	305	
TAT ATC CGC TCC AAT TTT TCT AAA GTG GCG CAT TTT GCG AGC GGG TAT				1016
Tyr Ile Arg Ser Asn Phe Ser Lys Val Ala His Phe Ala Ser Gly Tyr	310	315	320	
TTG CAA ACC AAG CTC AGC ACT CAA ACT AAA AGC GTT GCC TTA GTT AAA				1064
Leu Gln Thr Lys Leu Ser Thr Gln Thr Lys Ser Val Ala Leu Val Lys	325	330	335	
AAA ATC GTT AAG GAA TTT ATA GAA AAA GGC ATG ACG CAA CAA GAA TTA				1112
Lys Ile Val Lys Glu Phe Ile Glu Lys Gly Met Thr Gln Gln Glu Leu	340	345	350	

GAC GAC GCT AAA AAG TTT TTA CTA GGC TCT GAG CCT TTA AGG AAT GAA	1160
Asp Asp Ala Lys Lys Phe Leu Leu Gly Ser Glu Pro Leu Arg Asn Glu	
355 360 365 370	
ACG ATC TCT AGC CGC TTG AAC ACC ACT TAC AAT TAT TTT TAT TTA GGT	1208
Thr Ile Ser Ser Arg Leu Asn Thr Thr Tyr Asn Tyr Phe Tyr Leu Gly	
375 380 385	
TTG CCT TTA AAT TTT AAC CAA ACG CTG CTC AAT CAA ATC CAA AAA ATG	1256
Leu Pro Leu Asn Phe Asn Gln Thr Leu Leu Asn Gln Ile Gln Lys Met	
390 395 400	
AGT TTG AAA GAA ATC AAT GAT TTC ATT AAA GCC CAC ACC GAA ATC AAC	1304
Ser Leu Lys Glu Ile Asn Asp Phe Ile Lys Ala His Thr Glu Ile Asn	
405 410 415	
GAC TTG ACT TTT GCT ATT GTG AGC AAT AAA AAG AAG GAC AAA TGATGCCAT	1355
Asp Leu Thr Phe Ala Ile Val Ser Asn Lys Lys Lys Asp Lys	
420 425 430	
TTGAAGCTGT AATCGGGCTA GAAGTCCATG TCCAAC TCAA CACC	1399

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Met Lys Lys Phe Leu Ile Thr Leu Leu Leu Gly Val Phe Met Gly Leu	
1 5 10 15	
Gln Ala Ser Ala Leu Thr His Gln Glu Ile Asn Gln Ala Lys Val Pro	
20 25 30	
Val Ile Tyr Glu Glu Asn His Leu Leu Pro Met Gly Phe Ile His Leu	
35 40 45	
Ala Phe Arg Gly Gly Gly Ser Leu Ser Asp Lys Asn Gln Leu Gly Leu	
50 55 60	
Ala Lys Leu Phe Ala Gln Val Leu Asn Glu Gly Thr Lys Glu Leu Gly	
65 70 75 80	
Ala Val Gly Phe Ala Gln Leu Leu Glu Gln Lys Ala Ile Ser Leu Asn	
85 90 95	
Val Asp Thr Ser Thr Glu Asp Leu Gln Ile Thr Leu Glu Phe Leu Lys	
100 105 110	
Glu Tyr Glu Asp Glu Ala Ile Thr Arg Leu Lys Glu Leu Leu Lys Ser	
115 120 125	
Pro Asn Phe Thr Gln Asn Ala Leu Glu Lys Val Lys Thr Gln Met Leu	
130 135 140	
Ala Ala Leu Leu Gln Lys Glu Ser Asp Phe Asp Tyr Leu Ala Lys Leu	
145 150 155 160	
Thr Leu Lys Gln Glu Leu Phe Ala Asn Thr Pro Leu Ala Asn Ala Ala	
165 170 175	
Leu Gly Thr Lys Glu Ser Ile Gln Lys Ile Lys Leu Asp Asp Leu Lys	



269

CAA GCT CTC AGC CCC CTA GAA GAT CAA GAA TTT TTA ATT TCG TAC CGC	152
Gln Ala Leu Ser Pro Leu Glu Asp Gln Glu Phe Leu Ile Ser Tyr Arg	
20 25 30	
TTG AAA ATC GTT GAT TCT AGA GTG ATG GGC GAA GAG TAT TCT GTC TCT	200
Leu Lys Ile Val Asp Ser Arg Val Met Gly Glu Glu Tyr Ser Val Ser	
35 40 45 50	
AAA CCT ATC GTT AGC CGC ATT AAA ACA GCC CCC TAT GTT TTA GAC TAT	248
Lys Pro Ile Val Ser Arg Ile Lys Thr Ala Pro Tyr Val Leu Asp Tyr	
55 60 65	
CAT TGC TCC ATC ATC ACT CGT AAC TTA CCC AAT TTG AAA AAC CCC TTG	296
His Cys Ser Ile Ile Thr Arg Asn Leu Pro Asn Leu Lys Asn Pro Leu	
70 75 80	
CTC CCA ATA AAG TTA GAA CGC TTC CTT TTA GAA ATC GCG TTA AAA AAA	344
Leu Pro Ile Lys Leu Glu Arg Phe Leu Leu Glu Ile Ala Leu Lys Lys	
85 90 95	
GAA AAA GAG CGG GTC ATA GAC TGC ATT TTA AAA AGC CAG GTC GCT ATC	392
Glu Lys Glu Arg Val Ile Asp Cys Ile Leu Lys Ser Gln Val Ala Ile	
100 105 110	
ACG CAT TAT GAT CAT AGC TAT AAA AAC GGC ACC ACT ACC ACA AGC ATT	440
Thr His Tyr Asp His Ser Tyr Lys Asn Gly Thr Thr Thr Thr Ser Ile	
115 120 125 130	
CTT GCC CTC AAA GCC TTA AGC GTT AGA GCG AGT TTA GTG GGA GAT GCG	488
Leu Ala Leu Lys Ala Leu Ser Val Arg Ala Ser Leu Val Gly Asp Ala	
135 140 145	
CTG TTT TTA GAT ATT TTT AGA AAG GAA GAA GAA TGAAAATCGC CATTGTAGAA	541
Leu Phe Leu Asp Ile Phe Arg Lys Glu Glu Glu	
150 155	
GATGATATTA ACATGCGTAA AAGCCTGGAG CTT	574

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Met Arg Phe Phe Ser Phe Phe Tyr Phe Leu Phe Tyr Phe Leu Gly Val	
1 5 10 15	
Ser Leu Gln Ala Leu Ser Pro Leu Glu Asp Gln Glu Phe Leu Ile Ser	
20 25 30	
Tyr Arg Leu Lys Ile Val Asp Ser Arg Val Met Gly Glu Glu Tyr Ser	
35 40 45	
Val Ser Lys Pro Ile Val Ser Arg Ile Lys Thr Ala Pro Tyr Val Leu	

50	55	60
Asp Tyr His Cys Ser Ile	Ile Thr Arg Asn Leu	Pro Asn Leu Lys Asn
65	70	75
Pro Leu Leu Pro Ile	Lys Leu Glu Arg Phe	Leu Leu Glu Ile Ala Leu
	85	90
Lys Lys Glu Lys Glu Arg Val Ile	Asp Cys Ile Leu Lys Ser Gln Val	
	100	105
Ala Ile Thr His Tyr Asp His Ser Tyr Lys Asn Gly Thr Thr Thr Thr		110
	115	120
Ser Ile Leu Ala Leu Lys Ala Leu Ser Val Arg Ala Ser Leu Val Gly		125
	130	135
Asp Ala Leu Phe Leu Asp Ile Phe Arg Lys Glu Glu Glu		140
145	150	155

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...950
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

ATCATGAGAA AACGCTTCAC TCCACTTTTG TTATTCAGGA AATAATACAG ATG AGA	56
Met Arg	
1	
AAA ACG ATT TCA GCG TTG TTT TTA TCA GCG TGC ATA GGG TTA TCG TCT	104
Lys Thr Ile Ser Ala Leu Phe Leu Ser Ala Cys Ile Gly Leu Ser Ser	
5 10 15	
GTT TAT GCA GAT AAC GCT TTG ATT TTG CAA ACC GAT TTT AGT CTA AAA	152
Val Tyr Ala Asp Asn Ala Leu Ile Leu Gln Thr Asp Phe Ser Leu Lys	
20 25 30	
GAT GGG GCC GTC TCG GCG ATG AAA GGC GTC GCT TTC AGC GTT GAT TCC	200
Asp Gly Ala Val Ser Ala Met Lys Gly Val Ala Phe Ser Val Asp Ser	
35 40 45 50	
CAT CTT AAA ATC TTT GAT TTA ACG CAC GAA ATC CCC CCG TAT AAC ATC	248
His Leu Lys Ile Phe Asp Leu Thr His Glu Ile Pro Pro Tyr Asn Ile	
55 60 65	
TGG GAA GGC GCT TAC CGC TTG TAT CAG ACC GCC AGT TAT TGG CCA AAA	296
Trp Glu Gly Ala Tyr Arg Leu Tyr Gln Thr Ala Ser Tyr Trp Pro Lys	
70 75 80	
GGT TCG GTA TTT GTG AGC GTA GTT GAT CCG GGC GTA GGC ACT AAG CGT	344

Gly	Ser	Val	Phe	Val	Ser	Val	Val	Asp	Pro	Gly	Val	Gly	Thr	Lys	Arg	
		85					90						95			
AAA	TCG	GTG	GTA	CTA	AAA	ACT	AAA	AAC	GGC	CAG	TAT	TTC	GTC	TCG	CCG	392
Lys	Ser	Val	Val	Leu	Lys	Thr	Lys	Asn	Gly	Gln	Tyr	Phe	Val	Ser	Pro	
	100					105					110					
GAT	AAC	GGC	ACG	CTG	ACT	TTG	GTG	GCA	CAA	ACT	TTG	GGG	ATT	GAT	AGC	440
Asp	Asn	Gly	Thr	Leu	Thr	Leu	Val	Ala	Gln	Thr	Leu	Gly	Ile	Asp	Ser	
	115				120				125						130	
GTG	CGT	GAA	ATT	GAT	GAA	AAA	GCT	AAC	CGC	TTG	AAA	GGT	TCT	GAA	AAA	488
Val	Arg	Glu	Ile	Asp	Glu	Lys	Ala	Asn	Arg	Leu	Lys	Gly	Ser	Glu	Lys	
				135					140					145		
TCC	TAT	ACT	TTC	CAT	GGT	CGT	GAT	GTG	TAT	GCT	TAC	ACC	GGT	GCA	CGC	536
Ser	Tyr	Thr	Phe	His	Gly	Arg	Asp	Val	Tyr	Ala	Tyr	Thr	Gly	Ala	Arg	
			150					155					160			
TTG	GCT	TCT	GGG	GCG	ATC	ACA	TTC	GAG	CAG	GTC	GGG	CCA	GAG	CTT	CCC	584
Leu	Ala	Ser	Gly	Ala	Ile	Thr	Phe	Glu	Gln	Val	Gly	Pro	Glu	Leu	Pro	
	165						170					175				
CCA	AAA	GTC	GTT	GAA	ATT	CCT	TAC	CAA	AAA	GCG	AAA	GCC	ACA	AAA	GGG	632
Pro	Lys	Val	Val	Glu	Ile	Pro	Tyr	Gln	Lys	Ala	Lys	Ala	Thr	Lys	Gly	
	180					185					190					
GAA	GTG	AAA	GGT	AAT	ATC	CCG	ATT	TTG	GAT	ATT	CAA	TAT	GGC	AAT	GTT	680
Glu	Val	Lys	Gly	Asn	Ile	Pro	Ile	Leu	Asp	Ile	Gln	Tyr	Gly	Asn	Val	
	195				200					205					210	
TGG	AGC	AAC	ATC	AGC	GAT	AAA	TTA	CTC	AAT	CAA	GCA	AAA	ATC	AAA	CTC	728
Trp	Ser	Asn	Ile	Ser	Asp	Lys	Leu	Leu	Asn	Gln	Ala	Lys	Ile	Lys	Leu	
				215					220					225		
AAT	GAC	ACG	CTG	TGT	GTA	ACG	ATT	TTT	AAA	GGT	TCT	AAG	AAA	CAA	TAC	776
Asn	Asp	Thr	Leu	Cys	Val	Thr	Ile	Phe	Lys	Gly	Ser	Lys	Lys	Gln	Tyr	
			230					235					240			
GAA	GGG	AAA	ATG	CCG	TAT	GTC	GCA	AGC	TTT	GGC	GAT	GTG	CCA	GAA	GGC	824
Glu	Gly	Lys	Met	Pro	Tyr	Val	Ala	Ser	Phe	Gly	Asp	Val	Pro	Glu	Gly	
		245					250				255					
CAG	CCG	TTA	GTT	TAT	TTA	AAC	AGC	TTG	TTA	AAT	GTT	TCC	GTG	GCG	CTG	872
Gln	Pro	Leu	Val	Tyr	Leu	Asn	Ser	Leu	Leu	Asn	Val	Ser	Val	Ala	Leu	
	260					265					270					
AAT	AGG	GAT	AAT	TTC	GCG	CAA	AAA	TAT	CAA	ATC	AAA	TCC	GGT	GCT	GAC	920
Asn	Arg	Asp	Asn	Phe	Ala	Gln	Lys	Tyr	Gln	Ile	Lys	Ser	Gly	Ala	Asp	
	275				280					285					290	
TGG	AAT	ATT	GAT	ATA	AAG	AAG	TGC	GCT	AAG	TAAAGCGCTG	TTTAGAAAAT	TAA				973
Trp	Asn	Ile	Asp	Ile	Lys	Lys	Cys	Ala	Lys							
				295					300							
GGGGCGTGAA	ACGCCCTAAC	CGCTAAAGAT														1003

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Met	Arg	Lys	Thr	Ile	Ser	Ala	Leu	Phe	Leu	Ser	Ala	Cys	Ile	Gly	Leu	1	5	10	15
Ser	Ser	Val	Tyr	Ala	Asp	Asn	Ala	Leu	Ile	Leu	Gln	Thr	Asp	Phe	Ser	20	25	30	
Leu	Lys	Asp	Gly	Ala	Val	Ser	Ala	Met	Lys	Gly	Val	Ala	Phe	Ser	Val	35	40	45	
Asp	Ser	His	Leu	Lys	Ile	Phe	Asp	Leu	Thr	His	Glu	Ile	Pro	Pro	Tyr	50	55	60	
Asn	Ile	Trp	Glu	Gly	Ala	Tyr	Arg	Leu	Tyr	Gln	Thr	Ala	Ser	Tyr	Trp	65	70	75	80
Pro	Lys	Gly	Ser	Val	Phe	Val	Ser	Val	Val	Asp	Pro	Gly	Val	Gly	Thr	85	90	95	
Lys	Arg	Lys	Ser	Val	Val	Leu	Lys	Thr	Lys	Asn	Gly	Gln	Tyr	Phe	Val	100	105	110	
Ser	Pro	Asp	Asn	Gly	Thr	Leu	Thr	Leu	Val	Ala	Gln	Thr	Leu	Gly	Ile	115	120	125	
Asp	Ser	Val	Arg	Glu	Ile	Asp	Glu	Lys	Ala	Asn	Arg	Leu	Lys	Gly	Ser	130	135	140	
Glu	Lys	Ser	Tyr	Thr	Phe	His	Gly	Arg	Asp	Val	Tyr	Ala	Tyr	Thr	Gly	145	150	155	160
Ala	Arg	Leu	Ala	Ser	Gly	Ala	Ile	Thr	Phe	Glu	Gln	Val	Gly	Pro	Glu	165	170	175	
Leu	Pro	Pro	Lys	Val	Val	Glu	Ile	Pro	Tyr	Gln	Lys	Ala	Lys	Ala	Thr	180	185	190	
Lys	Gly	Glu	Val	Lys	Gly	Asn	Ile	Pro	Ile	Leu	Asp	Ile	Gln	Tyr	Gly	195	200	205	
Asn	Val	Trp	Ser	Asn	Ile	Ser	Asp	Lys	Leu	Leu	Asn	Gln	Ala	Lys	Ile	210	215	220	
Lys	Leu	Asn	Asp	Thr	Leu	Cys	Val	Thr	Ile	Phe	Lys	Gly	Ser	Lys	Lys	225	230	235	240
Gln	Tyr	Glu	Gly	Lys	Met	Pro	Tyr	Val	Ala	Ser	Phe	Gly	Asp	Val	Pro	245	250	255	
Glu	Gly	Gln	Pro	Leu	Val	Tyr	Leu	Asn	Ser	Leu	Leu	Asn	Val	Ser	Val	260	265	270	
Ala	Leu	Asn	Arg	Asp	Asn	Phe	Ala	Gln	Lys	Tyr	Gln	Ile	Lys	Ser	Gly	275	280	285	
Ala	Asp	Trp	Asn	Ile	Asp	Ile	Lys	Lys	Cys	Ala	Lys					290	295	300	

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 51...1160

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

ATTATTTT	TA	ATCTTGCATG	AAATCTTAAA	TATAGAATTA	GTCCCTTTGG	ATG	GGA	56
						Met	Gly	
						1		
TTT	TCN	CTC	GCG	CTA	GGC	TAT	TTG	104
Phe	Xaa	Leu	Ala	Leu	Gly	Tyr	Leu	
	5					10		
								15
GCT	TCT	TTA	ATC	TCT	GAA	AAA	GCC	152
Ala	Ser	Leu	Ile	Ser	Glu	Lys	Ala	
	20					25		
								30
GCT	AAA	GAT	AAA	ATC	ACC	TCT	TTA	200
Ala	Lys	Asp	Lys	Ile	Thr	Ser	Leu	
	35					40		
								45
								50
ACC	GGA	AGC	TTT	GGG	AAA	ACC	AGC	248
Thr	Gly	Ser	Phe	Gly	Lys	Thr	Ser	
				55				60
								65
TTA	CAA	ACC	ACA	TTC	AAC	GCG	CAT	296
Leu	Gln	Thr	Thr	Phe	Asn	Ala	His	
				70				75
								80
CTT	TTA	GGG	CTT	GCG	AAT	GAT	ATT	344
Leu	Leu	Gly	Leu	Ala	Asn	Asp	Ile	
	85							90
								95
GAA	ATC	TAT	ATC	GCT	GAA	GCC	GGG	392
Glu	Ile	Tyr	Ile	Ala	Glu	Ala	Gly	
	100					105		
								110
GAA	ATC	ACC	TGT	CTC	ATT	GAA	CCG	440
Glu	Ile	Thr	Cys	Leu	Ile	Glu	Pro	
	115					120		
								125
								130
GGC	GAA	CAG	CAT	TTA	GAA	TAC	TTT	488
Gly	Glu	Gln	His	Leu	Glu	Tyr	Phe	
				135				140
								145
ACT	AAA	GCG	GAA	TTA	TTG	GAT	TCC	536
Thr	Lys	Ala	Glu	Leu	Leu	Asp	Ser	
				150				155
								160
TAC	TCG	GTG	GAA	AAG	ATC	AAG	CCC	584
Tyr	Ser	Val	Glu	Lys	Ile	Lys	Pro	
			165					170
								175

ATA GAC TAT TCT AGC CTG GTT AAA AAC ATC CAA TCC ACT TTA AAA GGC	632
Ile Asp Tyr Ser Ser Leu Val Lys Asn Ile Gln Ser Thr Leu Lys Gly	
180 185 190	
ACT TCT TTT GAA ATG CTT ATA GGT AGC GTT TGG GAA AGA TTT GAA ACA	680
Thr Ser Phe Glu Met Leu Ile Gly Ser Val Trp Glu Arg Phe Glu Thr	
195 200 205 210	
AAG GTT CTA GGG GAG TTT AGC GCT TAT AAT ATC GCT TCA GCC ATT TTA	728
Lys Val Leu Gly Glu Phe Ser Ala Tyr Asn Ile Ala Ser Ala Ile Leu	
215 220 225	
ATC GCT AAG CAT TTA GGC TTA GAG ACC GAA AGG ATC AAA CGG CTT GTT	776
Ile Ala Lys His Leu Gly Leu Glu Thr Glu Arg Ile Lys Arg Leu Val	
230 235 240	
TTA GAA CTC AAC CCT ATT GCT CAT CGT TTG CAA CTT TTG GAA GTG AAT	824
Leu Glu Leu Asn Pro Ile Ala His Arg Leu Gln Leu Leu Glu Val Asn	
245 250 255	
CAA AAA ATC ATC ATA GAC GAT AGC TTT AAT GGG AAT TTA AAG GGC ATG	872
Gln Lys Ile Ile Ile Asp Asp Ser Phe Asn Gly Asn Leu Lys Gly Met	
260 265 270	
TTA GAG GGC ATT CGT TTA GCG AGT TTG CAC AAA GGG CGT AAA GTC ATT	920
Leu Glu Gly Ile Arg Leu Ala Ser Leu His Lys Gly Arg Lys Val Ile	
275 280 285 290	
GTA ACA CCG GGC TTA GTG GAA AGC AAT ACA GAA AGT AAT GAG GCT TTA	968
Val Thr Pro Gly Leu Val Glu Ser Asn Thr Glu Ser Asn Glu Ala Leu	
295 300 305	
GCG CAA AAA ATA GAC GGG GTT TTT GAT GTC GCT ATC ATC ACA GGG GAG	1016
Ala Gln Lys Ile Asp Gly Val Phe Asp Val Ala Ile Ile Thr Gly Glu	
310 315 320	
TTG AAT TCC AAA ACG ATT GCT TCA CAA TTG AAA ACC CCC CAA AAA ATC	1064
Leu Asn Ser Lys Thr Ile Ala Ser Gln Leu Lys Thr Pro Gln Lys Ile	
325 330 335	
TTA CTC AAG GAT AAG GCG CAA TTG GAA AAT ATC TTA CAA GCC ACC ACG	1112
Leu Leu Lys Asp Lys Ala Gln Leu Glu Asn Ile Leu Gln Ala Thr Thr	
340 345 350	
ATT CAA GGC GAT TTG ATT TTA TTC GCT AAT GAC GCC CCT AAT TAC ATT T	1161
Ile Gln Gly Asp Leu Ile Leu Phe Ala Asn Asp Ala Pro Asn Tyr Ile	
355 360 365 370	
AGGAAATGAA CATGCAACAT TTATACGCTC CTTGGCGCGA AAGTTATTTG AA	1213

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Met	Gly	Phe	Xaa	Leu	Ala	Leu	Gly	Tyr	Leu	Cys	Leu	Phe	Ile	Phe	Val	1	5	10	15
Leu	Ser	Ala	Ser	Leu	Ile	Ser	Glu	Lys	Ala	Leu	Ser	Lys	Gln	Tyr	Leu	20	25	30	
Gln	Thr	Ala	Lys	Asp	Lys	Ile	Thr	Ser	Leu	Lys	Asn	Leu	Lys	Val	Ile	35	40	45	
Ala	Ile	Thr	Gly	Ser	Phe	Gly	Lys	Thr	Ser	Thr	Lys	Asn	Phe	Leu	Leu	50	55	60	
Gln	Ile	Leu	Gln	Thr	Thr	Phe	Asn	Ala	His	Ala	Ser	Pro	Lys	Ser	Val	65	70	75	
Asn	Thr	Leu	Leu	Gly	Leu	Ala	Asn	Asp	Ile	Asn	Gln	Asn	Leu	Asp	Asp	85	90	95	
Arg	Ser	Glu	Ile	Tyr	Ile	Ala	Glu	Ala	Gly	Ala	Arg	Asn	Lys	Gly	Asp	100	105	110	
Ile	Lys	Glu	Ile	Thr	Cys	Leu	Ile	Glu	Pro	His	Leu	Val	Val	Val	Ala	115	120	125	
Glu	Val	Gly	Glu	Gln	His	Leu	Glu	Tyr	Phe	Lys	Thr	Leu	Glu	Asn	Ile	130	135	140	
Cys	Glu	Thr	Lys	Ala	Glu	Leu	Leu	Asp	Ser	Lys	Arg	Leu	Glu	Lys	Ala	145	150	155	
Phe	Cys	Tyr	Ser	Val	Glu	Lys	Ile	Lys	Pro	Tyr	Ala	Pro	Lys	Asp	Ser	165	170	175	
Pro	Leu	Ile	Asp	Tyr	Ser	Ser	Leu	Val	Lys	Asn	Ile	Gln	Ser	Thr	Leu	180	185	190	
Lys	Gly	Thr	Ser	Phe	Glu	Met	Leu	Ile	Gly	Ser	Val	Trp	Glu	Arg	Phe	195	200	205	
Glu	Thr	Lys	Val	Leu	Gly	Glu	Phe	Ser	Ala	Tyr	Asn	Ile	Ala	Ser	Ala	210	215	220	
Ile	Leu	Ile	Ala	Lys	His	Leu	Gly	Leu	Glu	Thr	Glu	Arg	Ile	Lys	Arg	225	230	235	
Leu	Val	Leu	Glu	Leu	Asn	Pro	Ile	Ala	His	Arg	Leu	Gln	Leu	Leu	Glu	245	250	255	
Val	Asn	Gln	Lys	Ile	Ile	Ile	Asp	Asp	Ser	Phe	Asn	Gly	Asn	Leu	Lys	260	265	270	
Gly	Met	Leu	Glu	Gly	Ile	Arg	Leu	Ala	Ser	Leu	His	Lys	Gly	Arg	Lys	275	280	285	
Val	Ile	Val	Thr	Pro	Gly	Leu	Val	Glu	Ser	Asn	Thr	Glu	Ser	Asn	Glu	290	295	300	
Ala	Leu	Ala	Gln	Lys	Ile	Asp	Gly	Val	Phe	Asp	Val	Ala	Ile	Ile	Thr	305	310	315	
Gly	Glu	Leu	Asn	Ser	Lys	Thr	Ile	Ala	Ser	Gln	Leu	Lys	Thr	Pro	Gln	325	330	335	
Lys	Ile	Leu	Leu	Lys	Asp	Lys	Ala	Gln	Leu	Glu	Asn	Ile	Leu	Gln	Ala	340	345	350	
Thr	Thr	Ile	Gln	Gly	Asp	Leu	Ile	Leu	Phe	Ala	Asn	Asp	Ala	Pro	Asn	355	360	365	
Tyr	Ile															370			

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1303 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...1250
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

CCTTGTGGTC TCATTGTTT CTGTTTACT TGTAGCTTGG AGGACTAGGC ATG TAT	56
Met Tyr	
1	
AAA TTA GGG GTG TTT TTG TTA GCC ACC TTA CTA TCA GCT AAC ACG CAA	104
Lys Leu Gly Val Phe Leu Leu Ala Thr Leu Leu Ser Ala Asn Thr Gln	
5 10 15	
AAA GTG AGC GAT ATT GCT AAA GAT ATC CAA CAT AAA GAA ACC CTT TTG	152
Lys Val Ser Asp Ile Ala Lys Asp Ile Gln His Lys Glu Thr Leu Leu	
20 25 30	
AAA AAA ACC CAT GAA GAA AAA AAC CAA CTA AAC AGC CGT TTG AGT TCT	200
Lys Lys Thr His Glu Glu Lys Asn Gln Leu Asn Ser Arg Leu Ser Ser	
35 40 45 50	
TTA GGC GAA GCG ATC CGC TCT AAA GAG CTT CAA AAG GCT GAG ATG GAG	248
Leu Gly Glu Ala Ile Arg Ser Lys Glu Leu Gln Lys Ala Glu Met Glu	
55 60 65	
CGC CAA ATG ATC GCT TTA AAA AAG AGT CTT GAA AAA AAT CGT AAC GAA	296
Arg Gln Met Ile Ala Leu Lys Lys Ser Leu Glu Lys Asn Arg Asn Glu	
70 75 80	
AGT TTG GCG CAA GAA AAA GTC CTA ACC AAC TAC CGC AAG TCT TTA GAT	344
Ser Leu Ala Gln Glu Lys Val Leu Thr Asn Tyr Arg Lys Ser Leu Asp	
85 90 95	
CAT TTG CAA AAA AAG CGA TCA TTT TTA CAA AAG AGG GTG TTT GAT ACG	392
His Leu Gln Lys Lys Arg Ser Phe Leu Gln Lys Arg Val Phe Asp Thr	
100 105 110	
CTT TTA CAG GAT TTC CTT TTT TCA CAA GCC CTA AAG GGG CAG AAT TTA	440
Leu Leu Gln Asp Phe Leu Phe Ser Gln Ala Leu Lys Gly Gln Asn Leu	
115 120 125 130	
GCC TCT TCT AAT GAT GTT GTT TTG CAA GTG GCG TTT GAA AAC TTG CAC	488
Ala Ser Ser Asn Asp Val Val Leu Gln Val Ala Phe Glu Asn Leu His	
135 140 145	
CAA AGC ACT CTG TCT AAA ATG TCG CAA CTG AGC CAA GAA GAA AAG GAA	536
Gln Ser Thr Leu Ser Lys Met Ser Gln Leu Ser Gln Glu Glu Lys Glu	
150 155 160	

CTC AAT ACG CAA GCT TTA AAA GTC AAA AAC AGC ATT CAA AAA ATC TCA Leu Asn Thr Gln Ala Leu Lys Val Lys Asn Ser Ile Gln Lys Ile Ser 165 170 175	584
TCC ATC ATA GAT GAG CAA AAA ACT CGT GAA GTA ACC TTA AAA TCC TTG Ser Ile Ile Asp Glu Gln Lys Thr Arg Glu Val Thr Leu Lys Ser Leu 180 185 190	632
AAA ACC GAA CAA GAT AAG CTC ATT TTG AGC ATG CAA AAA GAT TAT GCG Lys Thr Glu Gln Asp Lys Leu Ile Leu Ser Met Gln Lys Asp Tyr Ala 195 200 205 210	680
ATC TAC AAC CAA CGC CTA ACC CTT TTA GAA AAA GAG CGC CAG AAT TTA Ile Tyr Asn Gln Arg Leu Thr Leu Leu Glu Lys Glu Arg Gln Asn Leu 215 220 225	728
AAC GCT CTT TTA AAA CGC TTG AAT ATC ATC AAA CAA AAC AGA GAA AAT Asn Ala Leu Leu Lys Arg Leu Asn Ile Ile Lys Gln Asn Arg Glu Asn 230 235 240	776
GAA GAA AAA GTC AGT TTG AAA AAA TCT TCT CAA GCC TTA GAA GTC AAA Glu Glu Lys Val Ser Leu Lys Lys Ser Ser Gln Ala Leu Glu Val Lys 245 250 255	824
CAA GTG GCT AGC TCT TAT CAA AAT ATC AAC ACC ACG AGC TAT AAC GGA Gln Val Ala Ser Ser Tyr Gln Asn Ile Asn Thr Thr Ser Tyr Asn Gly 260 265 270	872
CCA AAA ACG ATC GCT CCC TTG AAC GAT TAT GAA GTG GTG CAA AAA TTT Pro Lys Thr Ile Ala Pro Leu Asn Asp Tyr Glu Val Val Gln Lys Phe 275 280 285 290	920
GGC CCC TAT ATT GAC CCG GTT TAT AAT TTA AAA ATT TTT AGC GAG TCT Gly Pro Tyr Ile Asp Pro Val Tyr Asn Leu Lys Ile Phe Ser Glu Ser 295 300 305	968
ATT ACG CTC GTG TCA AAA ACC CCA AAC GCT TTG GTG CGT AAT GTT TTA Ile Thr Leu Val Ser Lys Thr Pro Asn Ala Leu Val Arg Asn Val Leu 310 315 320	1016
GAC GGG AAA ATC GTG TTC GCT AAA GAA ATC AAC ATG CTT AAA AAA GTC Asp Gly Lys Ile Val Phe Ala Lys Glu Ile Asn Met Leu Lys Lys Val 325 330 335	1064
GTT ATC ATT GAG CAT AAA AAT GGG ATC CGC ACG ATT TAT TCT CAA TTG Val Ile Ile Glu His Lys Asn Gly Ile Arg Thr Ile Tyr Ser Gln Leu 340 345 350	1112
GAT AAA ATC GCT CCC ACC ATT AAA AGC GGC ATG CGG ATC CAA AAA GGC Asp Lys Ile Ala Pro Thr Ile Lys Ser Gly Met Arg Ile Gln Lys Gly 355 360 365 370	1160
TAT GTT TTA GGG CGC ATT GAT CAA CGC TTG GGC TTT GAA GTT ACC ATG Tyr Val Leu Gly Arg Ile Asp Gln Arg Leu Gly Phe Glu Val Thr Met 375 380 385	1208
AGA GAA AAA CAC ATC AAC CCC TTA GAA CTC ATC GCA CGC AAT TAAACAAAT Arg Glu Lys His Ile Asn Pro Leu Glu Leu Ile Ala Arg Asn	1259

390

395

400

CGTTTTTATT GCCGATATTG GCTAAAGAAT TTATGCAAAC AAAT

1303

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Met	Tyr	Lys	Leu	Gly	Val	Phe	Leu	Leu	Ala	Thr	Leu	Leu	Ser	Ala	Asn	1	5	10	15
Thr	Gln	Lys	Val	Ser	Asp	Ile	Ala	Lys	Asp	Ile	Gln	His	Lys	Glu	Thr	20	25	30	
Leu	Leu	Lys	Lys	Thr	His	Glu	Glu	Lys	Asn	Gln	Leu	Asn	Ser	Arg	Leu	35	40	45	
Ser	Ser	Leu	Gly	Glu	Ala	Ile	Arg	Ser	Lys	Glu	Leu	Gln	Lys	Ala	Glu	50	55	60	
Met	Glu	Arg	Gln	Met	Ile	Ala	Leu	Lys	Lys	Ser	Leu	Glu	Lys	Asn	Arg	65	70	75	80
Asn	Glu	Ser	Leu	Ala	Gln	Glu	Lys	Val	Leu	Thr	Asn	Tyr	Arg	Lys	Ser	85	90	95	
Leu	Asp	His	Leu	Gln	Lys	Lys	Arg	Ser	Phe	Leu	Gln	Lys	Arg	Val	Phe	100	105	110	
Asp	Thr	Leu	Leu	Gln	Asp	Phe	Leu	Phe	Ser	Gln	Ala	Leu	Lys	Gly	Gln	115	120	125	
Asn	Leu	Ala	Ser	Ser	Asn	Asp	Val	Val	Leu	Gln	Val	Ala	Phe	Glu	Asn	130	135	140	
Leu	His	Gln	Ser	Thr	Leu	Ser	Lys	Met	Ser	Gln	Leu	Ser	Gln	Glu	Glu	145	150	155	160
Lys	Glu	Leu	Asn	Thr	Gln	Ala	Leu	Lys	Val	Lys	Asn	Ser	Ile	Gln	Lys	165	170	175	
Ile	Ser	Ser	Ile	Ile	Asp	Glu	Gln	Lys	Thr	Arg	Glu	Val	Thr	Leu	Lys	180	185	190	
Ser	Leu	Lys	Thr	Glu	Gln	Asp	Lys	Leu	Ile	Leu	Ser	Met	Gln	Lys	Asp	195	200	205	
Tyr	Ala	Ile	Tyr	Asn	Gln	Arg	Leu	Thr	Leu	Leu	Glu	Lys	Glu	Arg	Gln	210	215	220	
Asn	Leu	Asn	Ala	Leu	Leu	Lys	Arg	Leu	Asn	Ile	Ile	Lys	Gln	Asn	Arg	225	230	235	240
Glu	Asn	Glu	Glu	Lys	Val	Ser	Leu	Lys	Lys	Ser	Ser	Gln	Ala	Leu	Glu	245	250	255	
Val	Lys	Gln	Val	Ala	Ser	Ser	Tyr	Gln	Asn	Ile	Asn	Thr	Thr	Ser	Tyr	260	265	270	
Asn	Gly	Pro	Lys	Thr	Ile	Ala	Pro	Leu	Asn	Asp	Tyr	Glu	Val	Val	Gln	275	280	285	
Lys	Phe	Gly	Pro	Tyr	Ile	Asp	Pro	Val	Tyr	Asn	Leu	Lys	Ile	Phe	Ser	290	295	300	
Glu	Ser	Ile	Thr	Leu	Val	Ser	Lys	Thr	Pro	Asn	Ala	Leu	Val	Arg	Asn	305	310	315	320
Val	Leu	Asp	Gly	Lys	Ile	Val	Phe	Ala	Lys	Glu	Ile	Asn	Met	Leu	Lys				

				325						330					335				
Lys	Val	Val	Ile	Ile	Glu	His	Lys	Asn	Gly	Ile	Arg	Thr	Ile	Tyr	Ser				
			340					345					350						
Gln	Leu	Asp	Lys	Ile	Ala	Pro	Thr	Ile	Lys	Ser	Gly	Met	Arg	Ile	Gln				
		355					360				365								
Lys	Gly	Tyr	Val	Leu	Gly	Arg	Ile	Asp	Gln	Arg	Leu	Gly	Phe	Glu	Val				
	370					375				380									
Thr	Met	Arg	Glu	Lys	His	Ile	Asn	Pro	Leu	Glu	Leu	Ile	Ala	Arg	Asn				
385					390				395						400				

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...308
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

AGGATTTAAG ATTGCGTTTG AAGTTAGCTA GCGTATGCTT GGGCGTTTTG ATG AGT	56
Met Ser	
1	
GGT TGT GCG TCT TCT TCG CCA ACT GGC ACT CTT ATC ACT ATG GTA ACG	104
Gly Cys Ala Ser Ser Ser Pro Thr Gly Thr Leu Ile Thr Met Val Thr	
5 10 15	
ATG CCA GTT TCT GGG AAT GAT GCA CAA TAC TCC AAA GAA GGG CGT GCG	152
Met Pro Val Ser Gly Asn Asp Ala Gln Tyr Ser Lys Glu Gly Arg Ala	
20 25 30	
AGT TGT TGG AGT GTT TTT AGT CTT GTG GCT GCC GGT AAT TGT TCG GTA	200
Ser Cys Trp Ser Val Phe Ser Leu Val Ala Ala Gly Asn Cys Ser Val	
35 40 45 50	
GAA AAA GCG GCT AAA AGT GGC GGT GTT ACC AAG ATT AAA ATG GTG AGC	248
Glu Lys Ala Ala Lys Ser Gly Gly Val Thr Lys Ile Lys Met Val Ser	
55 60 65	
CGT GAG ACA AAC AAC TTT TTA GGT ATT GTT GGC AAA TAC ACC ACG ATC	296
Arg Glu Thr Asn Asn Phe Leu Gly Ile Val Gly Lys Tyr Thr Thr Ile	
70 75 80	
GTT CAA GGC GAC TAGTTTAAAT ATTTAGAGAG CGTAGTTGAA TCGTCTTTCG TTCCA	353
Val Gln Gly Asp	
85	
CTCTAGGC	361

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Met	Ser	Gly	Cys	Ala	Ser	Ser	Ser	Pro	Thr	Gly	Thr	Leu	Ile	Thr	Met
1				5					10					15	
Val	Thr	Met	Pro	Val	Ser	Gly	Asn	Asp	Ala	Gln	Tyr	Ser	Lys	Glu	Gly
			20					25					30		
Arg	Ala	Ser	Cys	Trp	Ser	Val	Phe	Ser	Leu	Val	Ala	Ala	Gly	Asn	Cys
		35					40					45			
Ser	Val	Glu	Lys	Ala	Ala	Lys	Ser	Gly	Gly	Val	Thr	Lys	Ile	Lys	Met
	50					55				60					
Val	Ser	Arg	Glu	Thr	Asn	Asn	Phe	Leu	Gly	Ile	Val	Gly	Lys	Tyr	Thr
65					70				75					80	
Thr	Ile	Val	Gln	Gly	Asp										
				85											

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1511
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

TTTAAACCTG	AATTTTCATAT	TTTTGATTTT	TTAAAGGGAT	TAGAGTTCTT	ATG ATT	56
					Met Ile	
					1	
GAA TGG ATG CAA AAT CAT AGA AAA TAT TTA GTG GTT ACA ATA TGG ATA						104
Glu Trp Met Gln Asn His Arg Lys Tyr Leu Val Val Thr Ile Trp Ile						
	5		10		15	
AGC ACG ATC GCT TTT ATT GCC GCT GGG ATG ATA GGC TGG GGG CAA TAC						152
Ser Thr Ile Ala Phe Ile Ala Ala Gly Met Ile Gly Trp Gly Gln Tyr						
	20		25		30	
AGC TTT TCT TTA GAT AGC GAT AGC GCT GCC AAA GTG GGA CAG ATT AAG						200
Ser Phe Ser Leu Asp Ser Asp Ser Ala Ala Lys Val Gly Gln Ile Lys						

35	40					45					50					
ATT TCT CAA GAA GAA TTA GCC CAA GAA TAC CGC CGC CTT AAA GAC GCA	Ile Ser Gln Glu Glu Leu Ala Gln Glu Tyr Arg Arg Leu Lys Asp Ala					55 60 65					248					
TAT GCT GAG TCT ATC CCT GAT TTT AAA GAA CTC ACC AAA GAT CAA ATC	Tyr Ala Glu Ser Ile Pro Asp Phe Lys Glu Leu Thr Lys Asp Gln Ile					70 75 80					296					
AAA GCC ATG CAT TTA GAA AAA AGC GCT TTA GAT TCG CTC ATC AAT CAA	Lys Ala Met His Leu Glu Lys Ser Ala Leu Asp Ser Leu Ile Asn Gln					85 90 95					344					
GCC TTA TTG AGA AAT CTC GCT TTA GAT TTA GGG CTT GGC GCT ACA AAG	Ala Leu Leu Arg Asn Leu Ala Leu Asp Leu Gly Leu Gly Ala Thr Lys					100 105 110					392					
CAA GAA GTG GCG AAA GAG ATC AGA AAA ACG AGC GTT TTC CAA AAA GAT	Gln Glu Val Ala Lys Glu Ile Arg Lys Thr Ser Val Phe Gln Lys Asp					115 120 125 130					440					
GGC GTT TTT GAT GAA GAA TTG TAT AAA AAT ATC TTA AAG CAA AGC CAT	Gly Val Phe Asp Glu Glu Leu Tyr Lys Asn Ile Leu Lys Gln Ser His					135 140 145					488					
TAC CGC CCC AAA CAT TTT GAA GAA AGC GTT GAA AGG CTT TTA ATC CTT	Tyr Arg Pro Lys His Phe Glu Glu Ser Val Glu Arg Leu Leu Ile Leu					150 155 160					536					
CAA AAA ATC AGC ACT CTA TTC CCC AAA ACC ACT ACC CCT TTG GAG CAA	Gln Lys Ile Ser Thr Leu Phe Pro Lys Thr Thr Thr Pro Leu Glu Gln					165 170 175					584					
TCC AGC CTA TCG CTT TGG GCA AAA TTG CAA GAC AAA TTA GAC ATT CTT	Ser Ser Leu Ser Leu Trp Ala Lys Leu Gln Asp Lys Leu Asp Ile Leu					180 185 190					632					
ATC CTA AAC CCT AGT GAT GTT AAA ATC TCT CTT AAT GAA GAA GAG ATG	Ile Leu Asn Pro Ser Asp Val Lys Ile Ser Leu Asn Glu Glu Glu Met					195 200 205 210					680					
AAA AAA TAT TAC GAG TCC CAT AAA AAG GAT TTT AAA AAG CCC ACG AGC	Lys Lys Tyr Tyr Glu Ser His Lys Lys Asp Phe Lys Lys Pro Thr Ser					215 220 225					728					
TTT AAA ACA CGC TCT TTA TAT TTT GAC GCT AGT TTG GAA AAA CCT GAT	Phe Lys Thr Arg Ser Leu Tyr Phe Asp Ala Ser Leu Glu Lys Pro Asp					230 235 240					776					
TTG AAG GAG TTG GAG GAA TAC TAC CAT AAA AAC AAG GTG TCT TAT TTG	Leu Lys Glu Leu Glu Glu Tyr Tyr His Lys Asn Lys Val Ser Tyr Leu					245 250 255					824					
GAC AAA GAG GGG AAA TTG CAG GAT TTT AAA AGC GTT CAA GAG CAA GTC	Asp Lys Glu Gly Lys Leu Gln Asp Phe Lys Ser Val Gln Glu Gln Val					260 265 270					872					

AAG CAT GAT TTA AGC ATG CAA AAA GCG AAT GAA AAA GCC TTA AGG AGC	920
Lys His Asp Leu Ser Met Gln Lys Ala Asn Glu Lys Ala Leu Arg Ser	
275 280 285 290	
TAT ATC GCT CTA AAA AAA GCG AAC GCG CAA AAC TAC ACC ACA CAA GAT	968
Tyr Ile Ala Leu Lys Lys Ala Asn Ala Gln Asn Tyr Thr Thr Gln Asp	
295 300 305	
TTT GAA GAG AAC AAC TCC CCC TAT ACT GCT GAA ATC ACG CAA AAA CTC	1016
Phe Glu Glu Asn Asn Ser Pro Tyr Thr Ala Glu Ile Thr Gln Lys Leu	
310 315 320	
ACC GCT CTC AAA CCC CTT GAA ATC CTA AAG CCA GAG CCT TTT AAA GAT	1064
Thr Ala Leu Lys Pro Leu Glu Ile Leu Lys Pro Glu Pro Phe Lys Asp	
325 330 335	
GGT TTT ATT GTG GTG CAA CTC ATC TCT CAA ATT AAA GAC GAA TTG CAA	1112
Gly Phe Ile Val Val Gln Leu Ile Ser Gln Ile Lys Asp Glu Leu Gln	
340 345 350	
AAT TTT AAT GAA GCT AAA AGC GCT CTT AAA ACC CGC CTA ACT CAA GAA	1160
Asn Phe Asn Glu Ala Lys Ser Ala Leu Lys Thr Arg Leu Thr Gln Glu	
355 360 365 370	
AAA ACC CTT ATG GCG TTG CAA ACT TTA GCC AAA GAA AAG CTT AAG GAT	1208
Lys Thr Leu Met Ala Leu Gln Thr Leu Ala Lys Glu Lys Leu Lys Asp	
375 380 385	
TTT AAG GGC AAA AGC GTG GGC TAT GTA AGC CCT AAT TTT GGA GGC ACT	1256
Phe Lys Gly Lys Ser Val Gly Tyr Val Ser Pro Asn Phe Gly Gly Thr	
390 395 400	
ATT AGT GAG CTT AAC CAA GAA GAA AGT GCT AAG TTT ATC AAC GCT CTT	1304
Ile Ser Glu Leu Asn Gln Glu Glu Ser Ala Lys Phe Ile Asn Ala Leu	
405 410 415	
TTT AAC CGC CAG GAA AAA AAG GGG TTT ATC GCT ATT AAT AAT AAA GTG	1352
Phe Asn Arg Gln Glu Lys Lys Gly Phe Ile Ala Ile Asn Asn Lys Val	
420 425 430	
GTG CTC TAT CAA ATC ACA GAA CAA AAT TTC AAC CAC TCA TTT AGT GCA	1400
Val Leu Tyr Gln Ile Thr Glu Gln Asn Phe Asn His Ser Phe Ser Ala	
435 440 445 450	
GAA GAA AGC CAG TAT ATG CAG CGT TTA GTC AAT AAC ACT AAA ACG GAT	1448
Glu Glu Ser Gln Tyr Met Gln Arg Leu Val Asn Asn Thr Lys Thr Asp	
455 460 465	
TTT TTT GAT AAA GCG TTG ATA GAA GAA TTG AAA AAA CGC TAT AAG ATA	1496
Phe Phe Asp Lys Ala Leu Ile Glu Glu Leu Lys Lys Arg Tyr Lys Ile	
470 475 480	
GTC AAA TAC ATT CAA TAAATGCAAG GGGAAATCAT GGAACATAAA GAAATCGTTA T	1552
Val Lys Tyr Ile Gln	
485	
AGGGGTTGAT CT	1564

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Met	Ile	Glu	Trp	Met	Gln	Asn	His	Arg	Lys	Tyr	Leu	Val	Val	Thr	Ile
1				5					10					15	
Trp	Ile	Ser	Thr	Ile	Ala	Phe	Ile	Ala	Gly	Met	Ile	Gly	Trp	Gly	
			20					25				30			
Gln	Tyr	Ser	Phe	Ser	Leu	Asp	Ser	Asp	Ser	Ala	Ala	Lys	Val	Gly	Gln
		35				40						45			
Ile	Lys	Ile	Ser	Gln	Glu	Glu	Leu	Ala	Gln	Glu	Tyr	Arg	Arg	Leu	Lys
	50				55					60					
Asp	Ala	Tyr	Ala	Glu	Ser	Ile	Pro	Asp	Phe	Lys	Glu	Leu	Thr	Lys	Asp
65				70					75					80	
Gln	Ile	Lys	Ala	Met	His	Leu	Glu	Lys	Ser	Ala	Leu	Asp	Ser	Leu	Ile
			85					90					95		
Asn	Gln	Ala	Leu	Leu	Arg	Asn	Leu	Ala	Leu	Asp	Leu	Gly	Leu	Gly	Ala
			100					105					110		
Thr	Lys	Gln	Glu	Val	Ala	Lys	Glu	Ile	Arg	Lys	Thr	Ser	Val	Phe	Gln
		115					120					125			
Lys	Asp	Gly	Val	Phe	Asp	Glu	Glu	Leu	Tyr	Lys	Asn	Ile	Leu	Lys	Gln
	130					135				140					
Ser	His	Tyr	Arg	Pro	Lys	His	Phe	Glu	Glu	Ser	Val	Glu	Arg	Leu	Leu
145				150					155					160	
Ile	Leu	Gln	Lys	Ile	Ser	Thr	Leu	Phe	Pro	Lys	Thr	Thr	Thr	Pro	Leu
			165					170						175	
Glu	Gln	Ser	Ser	Leu	Ser	Leu	Trp	Ala	Lys	Leu	Gln	Asp	Lys	Leu	Asp
		180					185					190			
Ile	Leu	Ile	Leu	Asn	Pro	Ser	Asp	Val	Lys	Ile	Ser	Leu	Asn	Glu	Glu
	195						200				205				
Glu	Met	Lys	Lys	Tyr	Tyr	Glu	Ser	His	Lys	Lys	Asp	Phe	Lys	Lys	Pro
	210					215				220					
Thr	Ser	Phe	Lys	Thr	Arg	Ser	Leu	Tyr	Phe	Asp	Ala	Ser	Leu	Glu	Lys
225				230					235					240	
Pro	Asp	Leu	Lys	Glu	Leu	Glu	Glu	Tyr	Tyr	His	Lys	Asn	Lys	Val	Ser
			245					250					255		
Tyr	Leu	Asp	Lys	Glu	Gly	Lys	Leu	Gln	Asp	Phe	Lys	Ser	Val	Gln	Glu
		260					265					270			
Gln	Val	Lys	His	Asp	Leu	Ser	Met	Gln	Lys	Ala	Asn	Glu	Lys	Ala	Leu
	275						280				285				
Arg	Ser	Tyr	Ile	Ala	Leu	Lys	Lys	Ala	Asn	Ala	Gln	Asn	Tyr	Thr	Thr
	290					295				300					
Gln	Asp	Phe	Glu	Glu	Asn	Asn	Ser	Pro	Tyr	Thr	Ala	Glu	Ile	Thr	Gln
305				310					315					320	
Lys	Leu	Thr	Ala	Leu	Lys	Pro	Leu	Glu	Ile	Leu	Lys	Pro	Glu	Pro	Phe
			325					330				335			
Lys	Asp	Gly	Phe	Ile	Val	Val	Gln	Leu	Ile	Ser	Gln	Ile	Lys	Asp	Glu
		340					345				350				
Leu	Gln	Asn	Phe	Asn	Glu	Ala	Lys	Ser	Ala	Leu	Lys	Thr	Arg	Leu	Thr

355					360					365					
Gln	Glu	Lys	Thr	Leu	Met	Ala	Leu	Gln	Thr	Leu	Ala	Lys	Glu	Lys	Leu
370					375					380					
Lys	Asp	Phe	Lys	Gly	Lys	Ser	Val	Gly	Tyr	Val	Ser	Pro	Asn	Phe	Gly
385					390					395					
Gly	Thr	Ile	Ser	Glu	Leu	Asn	Gln	Glu	Glu	Ser	Ala	Lys	Phe	Ile	Asn
405					410					415					
Ala	Leu	Phe	Asn	Arg	Gln	Glu	Lys	Lys	Gly	Phe	Ile	Ala	Ile	Asn	Asn
420					425					430					
Lys	Val	Val	Leu	Tyr	Gln	Ile	Thr	Glu	Gln	Asn	Phe	Asn	His	Ser	Phe
435					440					445					
Ser	Ala	Glu	Glu	Ser	Gln	Tyr	Met	Gln	Arg	Leu	Val	Asn	Asn	Thr	Lys
450					455					460					
Thr	Asp	Phe	Phe	Asp	Lys	Ala	Leu	Ile	Glu	Glu	Leu	Lys	Lys	Arg	Tyr
465					470					475					
Lys	Ile	Val	Lys	Tyr	Ile	Gln									
485															

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1382
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

CAAAAAGATG	GATTTTTGAG	CGTCAAAGAG	GCTATAGGAG	CGGATTTAAG	ATG AAA	56
					Met Lys	
					1	
CAT TTT TCT GTT AAA AGA CTT TTA GGG CTT AGT TCT GTC TTG TTA GTC	104					
His Phe Ser Val Lys Arg Leu Leu Gly Leu Ser Ser Val Leu Leu Val						
5 10 15						
ACT TTA GGA GCG AGC ATG CAC GCA CAA TCT TAC TTA CCC AAA CAT GAG	152					
Thr Leu Gly Ala Ser Met His Ala Gln Ser Tyr Leu Pro Lys His Glu						
20 25 30						
AGC GTT ACC TTA AAA AAC GGG TTG CAA GTC GTG AGC GTC CCC CTA GAA	200					
Ser Val Thr Leu Lys Asn Gly Leu Gln Val Val Ser Val Pro Leu Glu						
35 40 45 50						
AAT AAA ACC GGG GTT ATA GAA GTG GAT GTG CTT TAT AAA GTC GGC TCT	248					
Asn Lys Thr Gly Val Ile Glu Val Asp Val Leu Tyr Lys Val Gly Ser						
55 60 65						
AGA AAC GAA ACC ATG GGA AAG AGC GGG ATC GCT CAC ATG TTA GAG CAT	296					

Arg	Asn	Glu	Thr	Met	Gly	Lys	Ser	Gly	Ile	Ala	His	Met	Leu	Glu	His	
70								75				80				
TTG	AAT	TTT	AAA	AGC	ACC	AAA	AAC	CTT	AAA	GCC	GGC	GAA	TTT	GAT	AAA	344
Leu	Asn	Phe	Lys	Ser	Thr	Lys	Asn	Leu	Lys	Ala	Gly	Glu	Phe	Asp	Lys	
85								90				95				
ATC	GTT	AAG	CGT	TTT	GGG	GGC	GTG	AGT	AAC	GCT	TCT	ACG	AGT	TTT	GAT	392
Ile	Val	Lys	Arg	Phe	Gly	Gly	Val	Ser	Asn	Ala	Ser	Thr	Ser	Phe	Asp	
100								105				110				
ATT	ACG	CGC	TAC	TTC	ATT	AAA	ACC	AGT	CAG	GCT	AAC	TTG	GAT	AAG	TCT	440
Ile	Thr	Arg	Tyr	Phe	Ile	Lys	Thr	Ser	Gln	Ala	Asn	Leu	Asp	Lys	Ser	
115				120				125				130				
TTA	GAA	TTG	TTC	GCT	GAA	ACC	ATG	GGT	TCA	TTG	AAT	TTA	AAA	GAA	GAT	488
Leu	Glu	Leu	Phe	Ala	Glu	Thr	Met	Gly	Ser	Leu	Asn	Leu	Lys	Glu	Asp	
135								140				145				
GAG	TTT	TTG	CCT	GAG	CGT	CAA	GTG	GTC	GCT	GAA	GAA	AGG	CGA	TGG	CGC	536
Glu	Phe	Leu	Pro	Glu	Arg	Gln	Val	Val	Ala	Glu	Glu	Arg	Arg	Trp	Arg	
150								155				160				
ACT	GAT	AAT	TCC	CCT	ATC	GGC	ATG	CTT	TAT	TTC	CGC	TTT	TTT	AAC	ACC	584
Thr	Asp	Asn	Ser	Pro	Ile	Gly	Met	Leu	Tyr	Phe	Arg	Phe	Phe	Asn	Thr	
165								170				175				
GCT	TAT	GTC	TAT	CAC	CCC	TAC	CAT	TGG	ACG	CCC	ATT	GGT	TTT	ATG	GAT	632
Ala	Tyr	Val	Tyr	His	Pro	Tyr	His	Trp	Thr	Pro	Ile	Gly	Phe	Met	Asp	
180				185				190								
GAT	ATT	CAA	AAT	TGG	ACT	TTA	AAA	GAC	ATT	AAA	AAA	TTC	CAT	TCG	CTC	680
Asp	Ile	Gln	Asn	Trp	Thr	Leu	Lys	Asp	Ile	Lys	Lys	Phe	His	Ser	Leu	
195				200				205				210				
TAT	TAT	CAG	CCT	AAA	AAC	GCT	ATC	GTT	TTG	GTG	GTA	GGC	GAT	GTC	AAT	728
Tyr	Tyr	Gln	Pro	Lys	Asn	Ala	Ile	Val	Leu	Val	Val	Gly	Asp	Val	Asn	
215								220				225				
TCC	CAA	AAG	GTT	TTT	GAA	TTG	AGT	AAA	AAG	CAT	TTT	GAA	TCC	TTA	AAA	776
Ser	Gln	Lys	Val	Phe	Glu	Leu	Ser	Lys	Lys	His	Phe	Glu	Ser	Leu	Lys	
230								235				240				
AAC	CTT	GAT	GAA	AAA	GCT	ATC	CCC	ACC	CCT	TAC	ATG	AAA	GAG	CCT	AAG	824
Asn	Leu	Asp	Glu	Lys	Ala	Ile	Pro	Thr	Pro	Tyr	Met	Lys	Glu	Pro	Lys	
245								250				255				
CAA	GAT	GGA	GCC	AGA	ACG	GCA	GTC	GTG	CAT	AAA	GAT	GGG	GTC	CAT	TTA	872
Gln	Asp	Gly	Ala	Arg	Thr	Ala	Val	Val	His	Lys	Asp	Gly	Val	His	Leu	
260				265				270								
GAA	TGG	GTG	GCC	CTT	GGG	TAT	AAA	GTG	CCT	GCT	TTC	AAG	CAT	AAA	GAT	920
Glu	Trp	Val	Ala	Leu	Gly	Tyr	Lys	Val	Pro	Ala	Phe	Lys	His	Lys	Asp	
275				280				285				290				
CAA	GTC	GCC	TTA	GAC	GCA	CTA	AGT	AGG	CTT	TTA	GGC	GAA	GGC	AAA	AGC	968
Gln	Val	Ala	Leu	Asp	Ala	Leu	Ser	Arg	Leu	Leu	Gly	Glu	Gly	Lys	Ser	
295								300				305				

TCG TGG TTG CAA AGC GAA TTA GTG GAT AAA AAA CGC TTG GCT TCT CAA	1016
Ser Trp Leu Gln Ser Glu Leu Val Asp Lys Lys Arg Leu Ala Ser Gln	
310 315 320	
GCT TTC TCG CAC AAC ATG CAA TTA CAA GAT GAA AGC GTG TTT TTA TTC	1064
Ala Phe Ser His Asn Met Gln Leu Gln Asp Glu Ser Val Phe Leu Phe	
325 330 335	
ATT GCG GGG GGT AAT CCT AAT GTC AAA GCC GAA GCC TTA CAA AAA GAA	1112
Ile Ala Gly Gly Asn Pro Asn Val Lys Ala Glu Ala Leu Gln Lys Glu	
340 345 350	
ATC GTA GCG CTT TTA GAA AAG CTG AAA AAA GGC GAA ATC ACT CAA GCG	1160
Ile Val Ala Leu Leu Glu Lys Leu Lys Lys Gly Glu Ile Thr Gln Ala	
355 360 365 370	
GAA TTA GAC AAG CTC AAA ATC AAT CAA AAA GCT GAC TTT ATT TCT AAT	1208
Glu Leu Asp Lys Leu Lys Ile Asn Gln Lys Ala Asp Phe Ile Ser Asn	
375 380 385	
TTA GAA AGT TCT AGC GAT GTT GCG GGG CTT TTT GCG GAC TAT TTA GTG	1256
Leu Glu Ser Ser Ser Asp Val Ala Gly Leu Phe Ala Asp Tyr Leu Val	
390 395 400	
CAA AAC GAT ATT CAA GGC TTG ACG GAT TAC CAG CGA CAA TTT TTG GAT	1304
Gln Asn Asp Ile Gln Gly Leu Thr Asp Tyr Gln Arg Gln Phe Leu Asp	
405 410 415	
TTA AAA GTG AGC GAT TTG GTG CGT GTG GCC AAT GAA TAT TTT AAA GAC	1352
Leu Lys Val Ser Asp Leu Val Arg Val Ala Asn Glu Tyr Phe Lys Asp	
420 425 430	
ACC CAA TCA ACC ACC GTG TTT TTG AAA CCT TAAAGAGCC TTATAACATG CAA	1405
Thr Gln Ser Thr Thr Val Phe Leu Lys Pro	
435 440	
TTTCATTCAT CTAGCGCGTT GATTACGCCT	1435

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Met Lys His Phe Ser Val Lys Arg Leu Leu Gly Leu Ser Ser Val Leu	
1 5 10 15	
Leu Val Thr Leu Gly Ala Ser Met His Ala Gln Ser Tyr Leu Pro Lys	
20 25 30	
His Glu Ser Val Thr Leu Lys Asn Gly Leu Gln Val Val Ser Val Pro	
35 40 45	
Leu Glu Asn Lys Thr Gly Val Ile Glu Val Asp Val Leu Tyr Lys Val	

50		55		60
Gly Ser Arg Asn Glu Thr Met Gly Lys Ser Gly Ile Ala His Met Leu				
65		70		80
Glu His Leu Asn Phe Lys Ser Thr Lys Asn Leu Lys Ala Gly Glu Phe				
	85		90	95
Asp Lys Ile Val Lys Arg Phe Gly Gly Val Ser Asn Ala Ser Thr Ser				
	100		105	110
Phe Asp Ile Thr Arg Tyr Phe Ile Lys Thr Ser Gln Ala Asn Leu Asp				
	115		120	125
Lys Ser Leu Glu Leu Phe Ala Glu Thr Met Gly Ser Leu Asn Leu Lys				
	130		135	140
Glu Asp Glu Phe Leu Pro Glu Arg Gln Val Val Ala Glu Glu Arg Arg				
145		150		160
Trp Arg Thr Asp Asn Ser Pro Ile Gly Met Leu Tyr Phe Arg Phe Phe				
	165		170	175
Asn Thr Ala Tyr Val Tyr His Pro Tyr His Trp Thr Pro Ile Gly Phe				
	180		185	190
Met Asp Asp Ile Gln Asn Trp Thr Leu Lys Asp Ile Lys Lys Phe His				
	195		200	205
Ser Leu Tyr Tyr Gln Pro Lys Asn Ala Ile Val Leu Val Val Gly Asp				
	210		215	220
Val Asn Ser Gln Lys Val Phe Glu Leu Ser Lys Lys His Phe Glu Ser				
225		230		240
Leu Lys Asn Leu Asp Glu Lys Ala Ile Pro Thr Pro Tyr Met Lys Glu				
	245		250	255
Pro Lys Gln Asp Gly Ala Arg Thr Ala Val Val His Lys Asp Gly Val				
	260		265	270
His Leu Glu Trp Val Ala Leu Gly Tyr Lys Val Pro Ala Phe Lys His				
	275		280	285
Lys Asp Gln Val Ala Leu Asp Ala Leu Ser Arg Leu Leu Gly Glu Gly				
	290		295	300
Lys Ser Ser Trp Leu Gln Ser Glu Leu Val Asp Lys Lys Arg Leu Ala				
305		310		320
Ser Gln Ala Phe Ser His Asn Met Gln Leu Gln Asp Glu Ser Val Phe				
	325		330	335
Leu Phe Ile Ala Gly Gly Asn Pro Asn Val Lys Ala Glu Ala Leu Gln				
	340		345	350
Lys Glu Ile Val Ala Leu Leu Glu Lys Leu Lys Lys Gly Glu Ile Thr				
	355		360	365
Gln Ala Glu Leu Asp Lys Leu Lys Ile Asn Gln Lys Ala Asp Phe Ile				
	370		375	380
Ser Asn Leu Glu Ser Ser Ser Asp Val Ala Gly Leu Phe Ala Asp Tyr				
385		390		400
Leu Val Gln Asn Asp Ile Gln Gly Leu Thr Asp Tyr Gln Arg Gln Phe				
	405		410	415
Leu Asp Leu Lys Val Ser Asp Leu Val Arg Val Ala Asn Glu Tyr Phe				
	420		425	430
Lys Asp Thr Gln Ser Thr Thr Val Phe Leu Lys Pro				
	435		440	

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...197
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ATATAATCTT TTCTTAATTT TGAAGTTTAG CAAATTTTAA GGAAGTAACC ATG ATG	56
Met Met	
1	
AAA AAA ACC CTT TTT ATC TCT TTG GCT TTA GCG TTA AGC TTG AAT GCG	104
Lys Lys Thr Leu Phe Ile Ser Leu Ala Leu Ala Leu Ser Leu Asn Ala	
5 10 15	
GGC AAT ATC CAA ATC CAG AGC ATG CCC AAA GTT AAA GAG CGA GTG AGT	152
Gly Asn Ile Gln Ile Gln Ser Met Pro Lys Val Lys Glu Arg Val Ser	
20 25 30	
GTC CCC TCT AAA GAC GAT ACG GAT CTA TTC TTA CCA CGA TTC TAT TAAGG	202
Val Pro Ser Lys Asp Asp Thr Asp Leu Phe Leu Pro Arg Phe Tyr	
35 40 45	
ACTCTATTAA GCGGGTGGTG AATATCTCCA CTGAAAAGAA GATTAAAA	250

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Met Met Lys Lys Thr Leu Phe Ile Ser Leu Ala Leu Ala Leu Ser Leu	
1 5 10 15	
Asn Ala Gly Asn Ile Gln Ile Gln Ser Met Pro Lys Val Lys Glu Arg	
20 25 30	
Val Ser Val Pro Ser Lys Asp Asp Thr Asp Leu Phe Leu Pro Arg Phe	
35 40 45	
Tyr	

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 328 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...275
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

TTAAGATTGC GGTTATACTG AAAAAACAA TATGAAATCA AGGAGCTTGT ATG CAA	56
Met Gln	
1	
CAG CGT CAT TTA GGC CCT TTA AAA GTG GGT GCA TTA GCT CTA GGG TGC	104
Gln Arg His Leu Gly Pro Leu Lys Val Gly Ala Leu Ala Leu Gly Cys	
5 10 15	
ATG GGC ATG ACT TAT GGG TAT GGG GAA GTC CAT GAT AAA AAG CAG ATG	152
Met Gly Met Thr Tyr Gly Tyr Gly Glu Val His Asp Lys Lys Gln Met	
20 25 30	
GTT AAA CTT ATC CAT AAG GCT TTG GAA TTG GGT ATT AAC TTT TTT GAC	200
Val Lys Leu Ile His Lys Ala Leu Glu Leu Gly Ile Asn Phe Phe Asp	
35 40 45 50	
ACT GCA GAG GCT TAT GGG GAA GAT AAT GAA AAG CTT TTA GGC GAA CGA	248
Thr Ala Glu Ala Tyr Gly Glu Asp Asn Glu Lys Leu Leu Gly Glu Arg	
55 60 65	
TCA AGC CTT TTA AAG ACA AGG TTG TGG TAGCGAGCAA GTTTGGGATT TACTACG	302
Ser Ser Leu Leu Lys Thr Arg Leu Trp	
70 75	
CAGATCCTAA TGACAAATAC GCAACC	328

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Met Gln Gln Arg His Leu Gly Pro Leu Lys Val Gly Ala Leu Ala Leu	
1 5 10 15	
Gly Cys Met Gly Met Thr Tyr Gly Tyr Gly Glu Val His Asp Lys Lys	
20 25 30	
Gln Met Val Lys Leu Ile His Lys Ala Leu Glu Leu Gly Ile Asn Phe	
35 40 45	
Phe Asp Thr Ala Glu Ala Tyr Gly Glu Asp Asn Glu Lys Leu Leu Gly	
50 55 60	

Glu Arg Ser Ser Leu Leu Lys Thr Arg Leu Trp
65 70 75

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 649 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...596
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

CGAATTGCTG TATAGTTAGC GTTTTAAATT CAAAATGAAG TGAGGAAACA ATG AAA	56
Met Lys	
1	
AAA GCG TTA ATA TCC ACC CTT TTT GGT GTT AGT TTG GCG TTT GCA AAA	104
Lys Ala Leu Ile Ser Thr Leu Phe Gly Val Ser Leu Ala Phe Ala Lys	
5 10 15	
CCT TAT ACG ATT GAT AAG GCA AAC TCT AGC GTG TGG TTT GAG GTC AAA	152
Pro Tyr Thr Ile Asp Lys Ala Asn Ser Ser Val Trp Phe Glu Val Lys	
20 25 30	
CAC TTC ACG TTC AAT GAA ACA AGA GGC GCG TTT GAT AAT TTT GAT GGC	200
His Phe Thr Phe Asn Glu Thr Arg Gly Ala Phe Asp Asn Phe Asp Gly	
35 40 45 50	
AAA ATT GAT CTA GAG CCC AAC ACT AAA ATG CTC AGC GTT TTT GAA GGC	248
Lys Ile Asp Leu Glu Pro Asn Thr Lys Met Leu Ser Val Phe Glu Gly	
55 60 65	
AAT ATT GAT GTG AAA AGC GTC AAT ACT AGG GAT AGA AAA AGA GAT AAC	296
Asn Ile Asp Val Lys Ser Val Asn Thr Arg Asp Arg Lys Arg Asp Asn	
70 75 80	
CAC TTG AAA ACA GCG GAC TTT TTT GAT GTG GTA AAA TAC CCC AAA GGG	344
His Leu Lys Thr Ala Asp Phe Phe Asp Val Val Lys Tyr Pro Lys Gly	
85 90 95	
AGC TTT AAA ATG ACC AAA TAC GAA GAT GGT AAA ATC TAT GGG GAT TTG	392
Ser Phe Lys Met Thr Lys Tyr Glu Asp Gly Lys Ile Tyr Gly Asp Leu	
100 105 110	
ACT CTT CGT GGC GTA ACC AAG CCT GTC GTA TTG GAA GCC AAA ATC CAA	440
Thr Leu Arg Gly Val Thr Lys Pro Val Val Leu Glu Ala Lys Ile Gln	
115 120 125 130	

GCC CCC TTA CAA AAC CCC ATG AAT AAA AAA GAA TTC ATG GTG TTA CAA 488
 Ala Pro Leu Gln Asn Pro Met Asn Lys Lys Glu Phe Met Val Leu Gln
 135 140 145

 GCT GAA GGC AAA ATC AAC CGC AAG GAT TTT GGT ATC GGT AAA ACC TTT 536
 Ala Glu Gly Lys Ile Asn Arg Lys Asp Phe Gly Ile Gly Lys Thr Phe
 150 155 160

 AGC GAT GCT GTC GTT GGA GAT GAG GTA AAG ATT GAG CTC AAA CTA GAA 584
 Ser Asp Ala Val Val Gly Asp Glu Val Lys Ile Glu Leu Lys Leu Glu
 165 170 175

 GCT TAC GCC CAA TAATCGTTTT GCAAGAGATA GATATCTTCT TCTCTTGCGT TTTTC 641
 Ala Tyr Ala Gln
 180

 TAACAGCA 649

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Met Lys Lys Ala Leu Ile Ser Thr Leu Phe Gly Val Ser Leu Ala Phe
 1 5 10 15
 Ala Lys Pro Tyr Thr Ile Asp Lys Ala Asn Ser Ser Val Trp Phe Glu
 20 25 30
 Val Lys His Phe Thr Phe Asn Glu Thr Arg Gly Ala Phe Asp Asn Phe
 35 40 45
 Asp Gly Lys Ile Asp Leu Glu Pro Asn Thr Lys Met Leu Ser Val Phe
 50 55 60
 Glu Gly Asn Ile Asp Val Lys Ser Val Asn Thr Arg Asp Arg Lys Arg
 65 70 75 80
 Asp Asn His Leu Lys Thr Ala Asp Phe Phe Asp Val Val Lys Tyr Pro
 85 90 95
 Lys Gly Ser Phe Lys Met Thr Lys Tyr Glu Asp Gly Lys Ile Tyr Gly
 100 105 110
 Asp Leu Thr Leu Arg Gly Val Thr Lys Pro Val Val Leu Glu Ala Lys
 115 120 125
 Ile Gln Ala Pro Leu Gln Asn Pro Met Asn Lys Lys Glu Phe Met Val
 130 135 140
 Leu Gln Ala Glu Gly Lys Ile Asn Arg Lys Asp Phe Gly Ile Gly Lys
 145 150 155 160
 Thr Phe Ser Asp Ala Val Val Gly Asp Glu Val Lys Ile Glu Leu Lys
 165 170 175
 Leu Glu Ala Tyr Ala Gln
 180

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...425
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TCCGTTTCGCA ACAAGAATTT TCTTGTTATC TTAATGTAAA GGTCAAAACG ATG AAA	56
Met Lys	
1	
AAG TTA GCC GCT TTA TTT TTA GTA AGC GTG TTG GGG GTT ATG GGT TTA	104
Lys Leu Ala Ala Leu Phe Leu Val Ser Val Leu Gly Val Met Gly Leu	
5 10 15	
AAC GCA TGG GAG CAA ACC CTA AAA GCT AAT GAC TTG GAA GTG AAA ATC	152
Asn Ala Trp Glu Gln Thr Leu Lys Ala Asn Asp Leu Glu Val Lys Ile	
20 25 30	
AAA TCC GTG GGT AAC CCC ATT AAA GGC GAT AAC ACT TTC ATT CTC AGC	200
Lys Ser Val Gly Asn Pro Ile Lys Gly Asp Asn Thr Phe Ile Leu Ser	
35 40 45 50	
CCC ACT TTA AAA GGT AAG GCT TTA GAA AAA GCT ATC GTT AGG GTG CAG	248
Pro Thr Leu Lys Gly Lys Ala Leu Glu Lys Ala Ile Val Arg Val Gln	
55 60 65	
TTT ATG ATG CCT GAA ATG CCC GGC ATG CCA GCG ATG AAA GAA ATG GCG	296
Phe Met Met Pro Glu Met Pro Gly Met Pro Ala Met Lys Glu Met Ala	
70 75 80	
CAA GTG AGT GAA AAA AAC GGC CTT TAT GAA GCT AAA ACC AAT CTT TCT	344
Gln Val Ser Glu Lys Asn Gly Leu Tyr Glu Ala Lys Thr Asn Leu Ser	
85 90 95	
ATG AAC GGG ACA TGG CAG GTT AGG GTG GAT ATT AAA TCT AAA GAG GGT	392
Met Asn Gly Thr Trp Gln Val Arg Val Asp Ile Lys Ser Lys Glu Gly	
100 105 110	
CAG GTT TAT CGC GCT AAA ACA AGC CTG GAT TTA TAAGAGCATG CTATCTTTTA	445
Gln Val Tyr Arg Ala Lys Thr Ser Leu Asp Leu	
115 120 125	
TAAGCGCGTT TGATAAAAGG GGC GTT TCAA TAC	478

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

```

Met Lys Lys Leu Ala Ala Leu Phe Leu Val Ser Val Leu Gly Val Met
 1          5          10          15
Gly Leu Asn Ala Trp Glu Gln Thr Leu Lys Ala Asn Asp Leu Glu Val
          20          25          30
Lys Ile Lys Ser Val Gly Asn Pro Ile Lys Gly Asp Asn Thr Phe Ile
          35          40          45
Leu Ser Pro Thr Leu Lys Gly Lys Ala Leu Glu Lys Ala Ile Val Arg
          50          55          60
Val Gln Phe Met Met Pro Glu Met Pro Gly Met Pro Ala Met Lys Glu
          65          70          75          80
Met Ala Gln Val Ser Glu Lys Asn Gly Leu Tyr Glu Ala Lys Thr Asn
          85          90          95
Leu Ser Met Asn Gly Thr Trp Gln Val Arg Val Asp Ile Lys Ser Lys
          100          105          110
Glu Gly Gln Val Tyr Arg Ala Lys Thr Ser Leu Asp Leu
          115          120          125

```

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1064
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

```

AGCGCTTTAA ATAGCACTTA TTTGTCTTTA CAAAACCTTA AAGGATTAGA ATG AAA      56
                                     Met Lys
                                     1

CGG ATT TTA TGG TTA GCC TTG ATT TTA TTT TTT AGC CCC TTA TTC GCT      104
Arg Ile Leu Trp Leu Ala Leu Ile Leu Phe Phe Ser Pro Leu Phe Ala
          5          10          15

AAC GCT CAA AAA ACT CAA GAA ATT AAA AAA ACT AAA GAA GCT AAA AGC      152
Asn Ala Gln Lys Thr Gln Glu Ile Lys Lys Thr Lys Glu Ala Lys Ser
          20          25          30

```

CAA ACC CGT TTT AAT ATT TCC ACC ACT AAG GTC ATA GAA AAA GAA TTT	200
Gln Thr Arg Phe Asn Ile Ser Thr Thr Lys Val Ile Glu Lys Glu Phe	
35 40 45 50	
TCT CAA AGC CGG CGC TAT TAC GCG CTT TTA GAG CCC AAT GAA GCG CTG	248
Ser Gln Ser Arg Arg Tyr Tyr Ala Leu Glu Pro Asn Glu Ala Leu	
55 60 65	
ATT TTT TCT CAA ACC CTG CGT TTT GAT GGC TAT GTG GAA AAG CTT TAT	296
Ile Phe Ser Gln Thr Leu Arg Phe Asp Gly Tyr Val Glu Lys Leu Tyr	
70 75 80	
GCG AAT AAA ACC TAT ACC CCC ATT AAA AAG GGC GAC AGG TTA TTG AGC	344
Ala Asn Lys Thr Tyr Thr Pro Ile Lys Lys Gly Asp Arg Leu Leu Ser	
85 90 95	
GTG TAT TCC CCT GAA TTA GTG AGC GCT CAA AGC GAA TTG CTA TCA TCA	392
Val Tyr Ser Pro Glu Leu Val Ser Ala Gln Ser Glu Leu Leu Ser Ser	
100 105 110	
TTG AAA TTC AAC CAA CAA GTG GGA GCG ATT AAA GAA AAA TTA AAA CTA	440
Leu Lys Phe Asn Gln Gln Val Gly Ala Ile Lys Glu Lys Leu Lys Leu	
115 120 125 130	
TTA GGG TTA GAA AAC TCT AGC ATT GAA AAA ATC ATT AGC AGC CAT AAA	488
Leu Gly Leu Glu Asn Ser Ser Ile Glu Lys Ile Ile Ser Ser His Lys	
135 140 145	
GTC CAA AAT GAA ATG ACT ATT TAC TCT CAC TTC AAC GGC ATT ATT TTT	536
Val Gln Asn Glu Met Thr Ile Tyr Ser His Phe Asn Gly Ile Ile Phe	
150 155 160	
AAA AAA AGC CCG GAT CTC AAT GAG GGG AGC TTC ATT AAA AAA GGG CAA	584
Lys Lys Ser Pro Asp Leu Asn Glu Gly Ser Phe Ile Lys Lys Gly Gln	
165 170 175	
GAG TTG TTT CAA ATC ATA GAT TTA AGC CAA TTG TGG GCG CTG GTT AAA	632
Glu Leu Phe Gln Ile Ile Asp Leu Ser Gln Leu Trp Ala Leu Val Lys	
180 185 190	
GTC AAT CAA GAG GAT TTA GAA TTT TTA AAA AAC ACG CAT AAA GCG ATC	680
Val Asn Gln Glu Asp Leu Glu Phe Leu Lys Asn Thr His Lys Ala Ile	
195 200 205 210	
TTG TTT GTA GAA GGG ATT AAA GGC GAG CAA GAA ATC ACG CTT GAA AAT	728
Leu Phe Val Glu Gly Ile Lys Gly Glu Gln Glu Ile Thr Leu Glu Asn	
215 220 225	
ATC AAC CCC ATC ATC AAC AAA GAA GAT AAA ATG CTA GAA GCG CGC TTC	776
Ile Asn Pro Ile Ile Asn Lys Glu Asp Lys Met Leu Glu Ala Arg Phe	
230 235 240	
AAT GTG CCT AAT GTT AAA CAG ATT TAT TAC CCT AAC ATG TTC GCT CAA	824
Asn Val Pro Asn Val Lys Gln Ile Tyr Tyr Pro Asn Met Phe Ala Gln	
245 250 255	
GTA GAA ATC TTT CAA AAA CCA CAA AAA ATG AAG ATT TTG CCT AAA GAA	872
Val Glu Ile Phe Gln Lys Pro Gln Lys Met Lys Ile Leu Pro Lys Glu	

260		265		270	
GCG GTT TTG ATT AAA GGG GGG AAA GCT ATC GTG TTT AAA AAA GAC GAT	920				
Ala Val Leu Ile Lys Gly Gly Lys Ala Ile Val Phe Lys Lys Asp Asp					
275		280		285	290
TTT GGC TTA AGC CCG TTA GAA ATT AAA GCC GTC CGC TTG AGC GAT GGG	968				
Phe Gly Leu Ser Pro Leu Glu Ile Lys Ala Val Arg Leu Ser Asp Gly					
		295		300	305
AGT TAT GAG ATT TTA GAG GGT TTA AAG GCG GGC GAA GAA GTC GCT AAT	1016				
Ser Tyr Glu Ile Leu Glu Gly Leu Lys Ala Gly Glu Glu Val Ala Asn					
		310		315	320
AAC GCT TTA TTC GTG CTA GAC GCT GAC GCT CAA AAC AAT GGG GAT TAT T	1065				
Asn Ala Leu Phe Val Leu Asp Ala Asp Ala Gln Asn Asn Gly Asp Tyr					
		325		330	335
GAATGATAGA AAAGATCATT GATTTAAGCG TTAAAAACAA ACTCCTTACC AC	1117				

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Met	Lys	Arg	Ile	Leu	Trp	Leu	Ala	Leu	Ile	Leu	Phe	Phe	Ser	Pro	Leu
1				5					10					15	
Phe	Ala	Asn	Ala	Gln	Lys	Thr	Gln	Glu	Ile	Lys	Lys	Thr	Lys	Glu	Ala
			20					25					30		
Lys	Ser	Gln	Thr	Arg	Phe	Asn	Ile	Ser	Thr	Thr	Lys	Val	Ile	Glu	Lys
		35					40					45			
Glu	Phe	Ser	Gln	Ser	Arg	Arg	Tyr	Tyr	Ala	Leu	Leu	Glu	Pro	Asn	Glu
	50					55				60					
Ala	Leu	Ile	Phe	Ser	Gln	Thr	Leu	Arg	Phe	Asp	Gly	Tyr	Val	Glu	Lys
65					70				75					80	
Leu	Tyr	Ala	Asn	Lys	Thr	Tyr	Thr	Pro	Ile	Lys	Lys	Gly	Asp	Arg	Leu
			85						90					95	
Leu	Ser	Val	Tyr	Ser	Pro	Glu	Leu	Val	Ser	Ala	Gln	Ser	Glu	Leu	Leu
		100						105					110		
Ser	Ser	Leu	Lys	Phe	Asn	Gln	Gln	Val	Gly	Ala	Ile	Lys	Glu	Lys	Leu
		115					120					125			
Lys	Leu	Leu	Gly	Leu	Glu	Asn	Ser	Ser	Ile	Glu	Lys	Ile	Ile	Ser	Ser
	130					135					140				
His	Lys	Val	Gln	Asn	Glu	Met	Thr	Ile	Tyr	Ser	His	Phe	Asn	Gly	Ile
145					150					155					160
Ile	Phe	Lys	Lys	Ser	Pro	Asp	Leu	Asn	Glu	Gly	Ser	Phe	Ile	Lys	Lys
			165						170					175	
Gly	Gln	Glu	Leu	Phe	Gln	Ile	Ile	Asp	Leu	Ser	Gln	Leu	Trp	Ala	Leu
		180						185					190		
Val	Lys	Val	Asn	Gln	Glu	Asp	Leu	Glu	Phe	Leu	Lys	Asn	Thr	His	Lys

[illegible]

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...1196
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAAACTTAGA	TAAAATAACA	CGATAAAACC	ATAGTAATAA	AGATAACCCC	ATG	AGA	56									
					Met	Arg										
					1											
TTT	TTT	TGC	TTT	TTC	TTA	TTT	TTT	CTA	ACC	TTT	TCA	AAC	GCA	CAG	ATA	104
Phe	Phe	Cys	Phe	Phe	Leu	Phe	Phe	Leu	Thr	Phe	Ser	Asn	Ala	Gln	Ile	
		5					10					15				
ATG	ATG	ACT	TTT	GAT	TCT	CAA	ACT	AAC	GCC	AAA	CTC	TCG	CGC	TCT	AAC	152
Met	Met	Thr	Phe	Asp	Ser	Gln	Thr	Asn	Ala	Lys	Leu	Ser	Arg	Ser	Asn	
	20					25					30					
GAA	CAG	CTT	TCA	GAC	ATG	CTC	TAT	AAA	CTC	AAT	GAA	AGT	TTA	AGA	ATC	200
Glu	Gln	Leu	Ser	Asp	Met	Leu	Tyr	Lys	Leu	Asn	Glu	Ser	Leu	Arg	Ile	
35					40					45					50	
TAT	CAA	AGC	GTG	CTT	TCC	AAT	AAC	CAA	GAT	CAA	CTC	AAA	GAA	ATC	AAA	248
Tyr	Gln	Ser	Val	Leu	Ser	Asn	Asn	Gln	Asp	Gln	Leu	Lys	Glu	Ile	Lys	
				55				60						65		

AAA GCT AAC AGC ACC CTA AAT AGC CAA AGG CGT TTT TTT AAC GCC AGC	296
Lys Ala Asn Ser Thr Leu Asn Ser Gln Arg Arg Phe Phe Asn Ala Ser	
70 75 80	
CAG ATC CGC CTT ATG GAC ACT GAT GCA CTA TTG AAA CAA AGC GCT TTG	344
Gln Ile Arg Leu Met Asp Thr Asp Ala Leu Leu Lys Gln Ser Ala Leu	
85 90 95	
GAA TTA GAA AAA TTA CAA GCT TTA GAA AAA CAC ATA AAA AAG GGC ATG	392
Glu Leu Glu Lys Leu Gln Ala Leu Glu Lys His Ile Lys Lys Gly Met	
100 105 110	
GAA CAA GAA CGC TTA ATA GAA GAA TCC CAA ACG CTT TTT TTA CAA GAG	440
Glu Gln Glu Arg Leu Ile Glu Glu Ser Gln Thr Leu Phe Leu Gln Glu	
115 120 125 130	
CAT TGC CCT TAT TTG AGC GGC GTT AAG AAT TTA GAA GAG GCT TCA AAC	488
His Cys Pro Tyr Leu Ser Gly Val Lys Asn Leu Glu Glu Ala Ser Asn	
135 140 145	
GCT TTA GAA GTC CAA GAG CAA AAC AAC GCC CTT TTC TTA CTC AAA GAG	536
Ala Leu Glu Val Gln Glu Gln Asn Asn Ala Leu Phe Leu Leu Lys Glu	
150 155 160	
CCT AAA CTC GCC CGT TTG CTC TCA CGA TTG GAT TTG ATG AGC GCT TTA	584
Pro Lys Leu Ala Arg Leu Leu Ser Arg Leu Asp Leu Met Ser Ala Leu	
165 170 175	
AAC GCC TTG TGC GAT CAG GTT TTA GAA AAC CAA GCC CAT AAC CAA CAA	632
Asn Ala Leu Cys Asp Gln Val Leu Glu Asn Gln Ala His Asn Gln Gln	
180 185 190	
TCC CAT AAC AAA ATT TTA GAA TAC AAC GCT CTT AAA AAC CAT GAT TTT	680
Ser His Asn Lys Ile Leu Glu Tyr Asn Ala Leu Lys Asn His Asp Phe	
195 200 205 210	
CAA GCC TAT AAA GCC ATG CGT TTG AAA AAA TTT AAA AAC AAG CTT CAA	728
Gln Ala Tyr Lys Ala Met Arg Leu Lys Lys Phe Lys Asn Lys Leu Gln	
215 220 225	
AGT CAA ATC CAA GCC CAA GAA GAC GCT CTA AAA ACC TTT TTA CCC TTA	776
Ser Gln Ile Gln Ala Gln Glu Asp Ala Leu Lys Thr Phe Leu Pro Leu	
230 235 240	
GAA AAA CGC TTG GAA ACT TTA AAA ACG CAT TTT TTA TGC GAT AAA GAA	824
Glu Lys Arg Leu Glu Thr Leu Lys Thr His Phe Leu Cys Asp Lys Glu	
245 250 255	
AAC CTA AAA TCA TGC GCT AAA GAA TTG CAC CAA CGC TAC CAA AAC GCC	872
Asn Leu Lys Ser Cys Ala Lys Glu Leu His Gln Arg Tyr Gln Asn Ala	
260 265 270	
CTT ATA GAG CGA GAT AAA GAA TTA AAA AAC GCT AAA AAT AAT AAA GAA	920
Leu Ile Glu Arg Asp Lys Glu Leu Lys Asn Ala Lys Asn Asn Lys Glu	
275 280 285 290	
AAG CAT GCT CTA ATC TTA GCC AAT TAC GAG CAT ACT TTA AAA ACC TTG	968
Lys His Ala Leu Ile Leu Ala Asn Tyr Glu His Thr Leu Lys Thr Leu	

				165					170					175	
Ala	Leu	Asn	Ala	Leu	Cys	Asp	Gln	Val	Leu	Glu	Asn	Gln	Ala	His	Asn
			180					185					190		
Gln	Gln	Ser	His	Asn	Lys	Ile	Leu	Glu	Tyr	Asn	Ala	Leu	Lys	Asn	His
		195					200					205			
Asp	Phe	Gln	Ala	Tyr	Lys	Ala	Met	Arg	Leu	Lys	Lys	Phe	Lys	Asn	Lys
	210					215					220				
Leu	Gln	Ser	Gln	Ile	Gln	Ala	Gln	Glu	Asp	Ala	Leu	Lys	Thr	Phe	Leu
225					230					235					240
Pro	Leu	Glu	Lys	Arg	Leu	Glu	Thr	Leu	Lys	Thr	His	Phe	Leu	Cys	Asp
				245					250					255	
Lys	Glu	Asn	Leu	Lys	Ser	Cys	Ala	Lys	Glu	Leu	His	Gln	Arg	Tyr	Gln
			260					265				270			
Asn	Ala	Leu	Ile	Glu	Arg	Asp	Lys	Glu	Leu	Lys	Asn	Ala	Lys	Asn	Asn
	275					280						285			
Lys	Glu	Lys	His	Ala	Leu	Ile	Leu	Ala	Asn	Tyr	Glu	His	Thr	Leu	Lys
	290					295					300				
Thr	Leu	Asn	Ile	Glu	Phe	Leu	Ser	Glu	Leu	Asn	Lys	Gln	Met	Ala	Phe
305					310					315					320
Leu	Asn	Glu	Thr	Met	Ala	Leu	Asn	Ala	Arg	Val	Leu	Ala	Leu	Leu	Ala
				325					330					335	
Lys	Gln	His	Ala	Lys	Thr	Pro	Lys	Pro	Phe	Asn	Leu	Ser	Gly	Gly	Leu
			340					345					350		
Ser	Gly	Asp	Leu	Ser	Gly	Gly	Lys	Ala	Leu	Ile	Lys	Asn	Ile	Arg	Leu
	355					360						365			
Asp	Pro	His	Gly	Phe	Pro	Ser	Phe	Lys	Asn	Phe	Lys	Gln	Glu		
	370					375					380				

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...437
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

TTGTTGAGAA	AATCCGATGT	TTTGAGCGAA	AAATTCAGGA	TCATGAAAAA	ATG	AAA	56									
					Met	Lys										
					1											
AGC	ATC	AGA	AGA	GGC	GAT	GGG	CTG	AAT	GTT	GTC	CCT	TTC	ATT	GAT	ATT	104
Ser	Ile	Arg	Arg	Gly	Asp	Gly	Leu	Asn	Val	Val	Pro	Phe	Ile	Asp	Ile	
		5					10					15				
ATG	CTC	GTT	TTG	CTA	GCG	ATT	GTG	TTG	AGC	ATT	TCT	ACT	TTT	ATT	GCA	152
Met	Leu	Val	Leu	Leu	Ala	Ile	Val	Leu	Ser	Ile	Ser	Thr	Phe	Ile	Ala	
	20					25					30					

CAA GGT AAG ATT AAG GTC AGT CTC CCT AAC GCT AAA AAT GCG GAA AAA	200
Gln Gly Lys Ile Lys Val Ser Leu Pro Asn Ala Lys Asn Ala Glu Lys	
35 40 45 50	
TCC CAG CCA AAC GAT CAA AAA GTG GTG GTC ATC TCT GTA GAT GAG CAT	248
Ser Gln Pro Asn Asp Gln Lys Val Val Ile Ser Val Asp Glu His	
55 60 65	
GAC AAT ATT TTC GTA GAT GAC AAA CCG ATG AAT TTA GAA GCT TTG AGC	296
Asp Asn Ile Phe Val Asp Asp Lys Pro Met Asn Leu Glu Ala Leu Ser	
70 75 80	
GCT GTA GTC AAA CAA ACA GAC CCT AAA ACC CTT ATA GAC TTA AAA AGC	344
Ala Val Val Lys Gln Thr Asp Pro Lys Thr Leu Ile Asp Leu Lys Ser	
85 90 95	
GAC AAA AGC TCT CGT TTT GAA ACT TTT ATC AGC ATT ATG GAT ATT TTA	392
Asp Lys Ser Ser Arg Phe Glu Thr Phe Ile Ser Ile Met Asp Ile Leu	
100 105 110	
AAA GAG CAT AAT CAT GAA AAT TTC TCC ATC TCC ACG CAA GCT CAG TAAAG	442
Lys Glu His Asn His Glu Asn Phe Ser Ile Ser Thr Gln Ala Gln	
115 120 125	
TTTCAACGAG TGTTAGCTTT TTAATCTCTT TTGCCCTATA CGCTATAG	490

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Met Lys Ser Ile Arg Arg Gly Asp Gly Leu Asn Val Val Pro Phe Ile	
1 5 10 15	
Asp Ile Met Leu Val Leu Leu Ala Ile Val Leu Ser Ile Ser Thr Phe	
20 25 30	
Ile Ala Gln Gly Lys Ile Lys Val Ser Leu Pro Asn Ala Lys Asn Ala	
35 40 45	
Glu Lys Ser Gln Pro Asn Asp Gln Lys Val Val Val Ile Ser Val Asp	
50 55 60	
Glu His Asp Asn Ile Phe Val Asp Asp Lys Pro Met Asn Leu Glu Ala	
65 70 75 80	
Leu Ser Ala Val Val Lys Gln Thr Asp Pro Lys Thr Leu Ile Asp Leu	
85 90 95	
Lys Ser Asp Lys Ser Ser Arg Phe Glu Thr Phe Ile Ser Ile Met Asp	
100 105 110	
Ile Leu Lys Glu His Asn His Glu Asn Phe Ser Ile Ser Thr Gln Ala	
115 120 125	
Gln	

GCT AAA GAG GAA GCT AAA GAA AAA AGC GCT CCT AAA CAA GTA ACA ACT	536
Ala Lys Glu Glu Ala Lys Glu Lys Ser Ala Pro Lys Gln Val Thr Thr	
150 155 160	
AAG GAT ATA GTC AAA GAA AAA GAC AAG CAA GAA GAA TCC AAC AAA ACC	584
Lys Asp Ile Val Lys Glu Lys Asp Lys Gln Glu Glu Ser Asn Lys Thr	
165 170 175	
TCT GAG GGG GCC ACT TCT GAA GCT CAA GCT TAT AAC CCA GGG GTG AGC	632
Ser Glu Gly Ala Thr Ser Glu Ala Gln Ala Tyr Asn Pro Gly Val Ser	
180 185 190	
AAC GAA TTT TTA ATG AAG ATC CAA ACC GCT ATT TCT TCT AAA AAC CGC	680
Asn Glu Phe Leu Met Lys Ile Gln Thr Ala Ile Ser Ser Lys Asn Arg	
195 200 205 210	
TAC CCT AAA ATG GCG CAG ATT AGG GGT ATT GAG GGC GAA GTG TTG GTG	728
Tyr Pro Lys Met Ala Gln Ile Arg Gly Ile Glu Gly Glu Val Leu Val	
215 220 225	
AGC TTT ACG ATC AAT GCT GAT GGG AGC GTT ACG GAC ATT AAA GTG GTC	776
Ser Phe Thr Ile Asn Ala Asp Gly Ser Val Thr Asp Ile Lys Val Val	
230 235 240	
AAA AGC AAC ACC ACA GAT ATT TTA AAC CAT GCG GCT TTA GAA GCC ATT	824
Lys Ser Asn Thr Thr Asp Ile Leu Asn His Ala Ala Leu Glu Ala Ile	
245 250 255	
AAA AGC GCG GCA CAT CTA TTC CCT AAA CCA GAA GAA ACC GTG CAT CTA	872
Lys Ser Ala Ala His Leu Phe Pro Lys Pro Glu Glu Thr Val His Leu	
260 265 270	
AAA ATC CCT ATC GCT TAT AGC TTG AAA GAA GAC TGATTAGTCT TTCTTTTAGG	925
Lys Ile Pro Ile Ala Tyr Ser Leu Lys Glu Asp	
275 280 285	
GGCGATTCAA GCCTTAAAAG CCGGGTCAAA ATC	958

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

Met Lys Ile Ser Pro Ser Pro Arg Lys Leu Ser Lys Val Ser Thr Ser
1 5 10 15
Val Ser Phe Leu Ile Ser Phe Ala Leu Tyr Ala Ile Gly Phe Gly Tyr
20 25 30
Phe Leu Leu Arg Glu Asp Ala Pro Glu Pro Leu Ala Gln Ala Gly Thr
35 40 45
Thr Lys Val Thr Met Ser Leu Ala Ser Ile Asn Thr Asn Ser Asn Thr

50		55		60
Lys Thr Asn Ala Glu	Ser Ala Lys Pro Lys	Glu Glu Pro Lys Glu	Lys	
65	70	75	80	
Pro Lys Lys Glu	Pro Lys Lys Glu	Pro Lys Lys Glu	Val Thr	
	85	90	95	
Lys Pro Lys Pro Lys	Pro Lys Pro Lys	Pro Lys Pro Lys	Pro Lys Pro	
	100	105	110	
Lys Pro Glu Pro Lys	Pro Glu Pro Lys	Pro Glu Pro Lys	Pro Glu Pro	
	115	120	125	
Lys Val Glu Glu Val	Lys Lys Glu Glu	Pro Lys Glu Glu	Pro Lys Lys	
	130	135	140	
Glu Glu Ala Lys Glu	Glu Ala Lys Glu	Lys Ser Ala Pro	Lys Gln Val	
145	150	155	160	
Thr Thr Lys Asp Ile	Val Lys Glu Lys	Asp Lys Gln Glu	Glu Ser Asn	
	165	170	175	
Lys Thr Ser Glu Gly	Ala Thr Ser Glu	Ala Gln Ala Tyr	Asn Pro Gly	
	180	185	190	
Val Ser Asn Glu Phe	Leu Met Lys Ile	Gln Thr Ala Ile	Ser Ser Lys	
	195	200	205	
Asn Arg Tyr Pro Lys	Met Ala Gln Ile	Arg Gly Ile Glu	Gly Glu Val	
	210	215	220	
Leu Val Ser Phe Thr	Ile Asn Ala Asp	Gly Ser Val Thr	Asp Ile Lys	
225	230	235	240	
Val Val Lys Ser Asn	Thr Thr Asp Ile	Leu Asn His Ala	Ala Leu Glu	
	245	250	255	
Ala Ile Lys Ser Ala	Ala His Leu Phe	Pro Lys Pro Glu	Glu Thr Val	
	260	265	270	
His Leu Lys Ile Pro	Ile Ala Tyr Ser	Leu Lys Glu Asp		
	275	280	285	

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 757 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...704
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

TTGATGAAAA AAATAACGCT CCTCTTTTAA AACTCTTTT AGAGGATGCC ATG AGA	56
Met Arg	
1	
GTG TCT TCT AAA GAG ATT TTA CTC ATT GTG GGG GGG AGC AGT TTT TAC	104
Val Ser Ser Lys Glu Ile Leu Leu Ile Val Gly Gly Ser Ser Phe Tyr	
5 10 15	
CTC AAA TCC ATT TTA GAA GGT TTG AGC CGC ATG CCA AAA CTG AGC GGT	152

Leu	Lys	Ser	Ile	Leu	Glu	Gly	Leu	Ser	Arg	Met	Pro	Lys	Leu	Ser	Gly	
20						25					30					
GAG	GAG	GTT	GTA	AAA	ATA	GAG	CGA	GAA	ATT	GCC	ACT	CTT	TCT	AAC	CCT	200
Glu	Glu	Val	Val	Lys	Ile	Glu	Arg	Glu	Ile	Ala	Thr	Leu	Ser	Asn	Pro	
35				40				45						50		
TAT	ATA	TTT	TTA	AAA	TCC	ATT	GAC	CCT	AAC	ATG	GCT	TTT	AAA	ATC	CAT	248
Tyr	Ile	Phe	Leu	Lys	Ser	Ile	Asp	Pro	Asn	Met	Ala	Phe	Lys	Ile	His	
			55				60						65			
CCA	AAC	GAC	ACT	TAC	CGC	ACC	CAT	AAG	GCT	TTA	GAA	ATC	TTT	TAT	GCC	296
Pro	Asn	Asp	Thr	Tyr	Arg	Thr	His	Lys	Ala	Leu	Glu	Ile	Phe	Tyr	Ala	
			70				75						80			
ACC	TGC	ACG	CCC	CCA	AGC	GAG	TAT	TTT	AAG	GCC	AAC	CCT	AAA	AAA	CCC	344
Thr	Cys	Thr	Pro	Pro	Ser	Glu	Tyr	Phe	Lys	Ala	Asn	Pro	Lys	Lys	Pro	
		85				90						95				
TTT	GAG	CAT	GCT	ATC	TCC	TTA	TTC	GCT	CTG	TCT	ATT	GAA	AAA	AGC	GCG	392
Phe	Glu	His	Ala	Ile	Ser	Leu	Phe	Ala	Leu	Ser	Ile	Glu	Lys	Ser	Ala	
100					105					110						
CTC	CAT	AAC	AAT	ATC	AAA	CGG	CGC	ACC	AAA	AAC	ATG	CTC	CAT	TCA	GGG	440
Leu	His	Asn	Asn	Ile	Lys	Arg	Arg	Thr	Lys	Asn	Met	Leu	His	Ser	Gly	
115				120					125						130	
CTT	GTT	GAA	GAA	ATC	AAA	GCC	CTC	TAT	ACT	CAA	TAC	CCT	AAA	GAT	TCG	488
Leu	Val	Glu	Glu	Ile	Lys	Ala	Leu	Tyr	Thr	Gln	Tyr	Pro	Lys	Asp	Ser	
			135				140						145			
CAG	CCT	TTT	AAA	GCC	ATA	GGC	GTT	AAA	GAG	AGC	GTT	CTT	TTT	TTA	GAA	536
Gln	Pro	Phe	Lys	Ala	Ile	Gly	Val	Lys	Glu	Ser	Val	Leu	Phe	Leu	Glu	
			150				155						160			
AAA	CGA	CTC	ACT	TTA	AAG	GAG	CTA	GAA	GAA	GCG	ATT	ACC	TCT	AAC	ACC	584
Lys	Arg	Leu	Thr	Leu	Lys	Glu	Leu	Glu	Glu	Ala	Ile	Thr	Ser	Asn	Thr	
		165				170					175					
ATG	AAA	TTA	GCC	AAG	CGC	CAA	AAC	ACT	TTC	AAT	AAA	ACC	CAA	TTC	AAT	632
Met	Lys	Leu	Ala	Lys	Arg	Gln	Asn	Thr	Phe	Asn	Lys	Thr	Gln	Phe	Asn	
180					185						190					
AAC	CTT	TAT	GTG	GGG	AGC	GCT	GAA	GAA	GTT	AGG	CAT	GCG	ATT	TTA	AAA	680
Asn	Leu	Tyr	Val	Gly	Ser	Ala	Glu	Glu	Val	Arg	His	Ala	Ile	Leu	Lys	
195				200					205					210		
CAC	TCA	AAA	AGC	GGC	ATT	AAA	GGA	TAATCTAATG	GATACACAAA	ACTTACCCGA						734
His	Ser	Lys	Ser	Gly	Ile	Lys	Gly									
			215													
TCAAATTATC	CCTATTTT	TGA														757

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Met	Arg	Val	Ser	Ser	Lys	Glu	Ile	Leu	Leu	Ile	Val	Gly	Gly	Ser	Ser
1				5					10					15	
Phe	Tyr	Leu	Lys	Ser	Ile	Leu	Glu	Gly	Leu	Ser	Arg	Met	Pro	Lys	Leu
			20					25					30		
Ser	Gly	Glu	Glu	Val	Val	Lys	Ile	Glu	Arg	Glu	Ile	Ala	Thr	Leu	Ser
		35					40					45			
Asn	Pro	Tyr	Ile	Phe	Leu	Lys	Ser	Ile	Asp	Pro	Asn	Met	Ala	Phe	Lys
	50					55				60					
Ile	His	Pro	Asn	Asp	Thr	Tyr	Arg	Thr	His	Lys	Ala	Leu	Glu	Ile	Phe
65					70				75					80	
Tyr	Ala	Thr	Cys	Thr	Pro	Pro	Ser	Glu	Tyr	Phe	Lys	Ala	Asn	Pro	Lys
			85					90					95		
Lys	Pro	Phe	Glu	His	Ala	Ile	Ser	Leu	Phe	Ala	Leu	Ser	Ile	Glu	Lys
			100					105					110		
Ser	Ala	Leu	His	Asn	Asn	Ile	Lys	Arg	Arg	Thr	Lys	Asn	Met	Leu	His
	115						120					125			
Ser	Gly	Leu	Val	Glu	Glu	Ile	Lys	Ala	Leu	Tyr	Thr	Gln	Tyr	Pro	Lys
	130					135					140				
Asp	Ser	Gln	Pro	Phe	Lys	Ala	Ile	Gly	Val	Lys	Glu	Ser	Val	Leu	Phe
145					150				155					160	
Leu	Glu	Lys	Arg	Leu	Thr	Leu	Lys	Glu	Leu	Glu	Glu	Ala	Ile	Thr	Ser
				165				170						175	
Asn	Thr	Met	Lys	Leu	Ala	Lys	Arg	Gln	Asn	Thr	Phe	Asn	Lys	Thr	Gln
			180					185					190		
Phe	Asn	Asn	Leu	Tyr	Val	Gly	Ser	Ala	Glu	Glu	Val	Arg	His	Ala	Ile
	195					200						205			
Leu	Lys	His	Ser	Lys	Ser	Gly	Ile	Lys	Gly						
	210					215									

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 454 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 51...401
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

CTATATGAAC AAAGCCTTAA AAGACTTGAA AAAAGGAATA ACTCATACCT ATG CGA
Met Arg

56

1

AAC AAT AAA ACG CCT TTT TTG AGC GCG ATT TTT ACG GCA TCA ATT AGG	104
Asn Asn Lys Thr Pro Phe Leu Ser Ala Ile Phe Thr Ala Ser Ile Arg	
5 10 15	
GGT TAC CAA CGC TTT TTT TCG GCT TTC ACC CCT TCA AGC TGC CGG TTT	152
Gly Tyr Gln Arg Phe Phe Ser Ala Phe Thr Pro Ser Ser Cys Arg Phe	
20 25 30	
TAC CCC ACT TGT TCC AAC TAC GCT CTG TGG TTG CTC TGT TTT GAA AGC	200
Tyr Pro Thr Cys Ser Asn Tyr Ala Leu Trp Leu Leu Cys Phe Glu Ser	
35 40 45 50	
CCT TTG AGC GCT ATG GGT AAG ATC GCT ATA AGG ATA CTC TCA TGC AAC	248
Pro Leu Ser Ala Met Gly Lys Ile Ala Ile Arg Ile Leu Ser Cys Asn	
55 60 65	
CCT TTT TGC TCT GGG GGC ATT GCT TAC CCT ACT ACT CGC TTG AAA CGC	296
Pro Phe Cys Ser Gly Gly Ile Ala Tyr Pro Thr Thr Arg Leu Lys Arg	
70 75 80	
CCA AGC CTG ATC CAA TCT CAT AAA GAT TCT AAT CGC AAT TTT AAA ACC	344
Pro Ser Leu Ile Gln Ser His Lys Asp Ser Asn Arg Asn Phe Lys Thr	
85 90 95	
ATC ACT TTT TGG CTC GTT CCC ACA AAA AGC CAC GCA ACT TAC TAC ATC	392
Ile Thr Phe Trp Leu Val Pro Thr Lys Ser His Ala Thr Tyr Tyr Ile	
100 105 110	
ATT AAG GTT TAATCACAAT GGATAAAAAC AACAATAATC TCCGCTTGAT TTTAGCGAT	450
Ile Lys Val	
115	
CGCT	454

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

Met Arg Asn Asn Lys Thr Pro Phe Leu Ser Ala Ile Phe Thr Ala Ser	
1 5 10 15	
Ile Arg Gly Tyr Gln Arg Phe Phe Ser Ala Phe Thr Pro Ser Cys	
20 25 30	
Arg Phe Tyr Pro Thr Cys Ser Asn Tyr Ala Leu Trp Leu Cys Phe	
35 40 45	
Glu Ser Pro Leu Ser Ala Met Gly Lys Ile Ala Ile Arg Ile Leu Ser	
50 55 60	
Cys Asn Pro Phe Cys Ser Gly Gly Ile Ala Tyr Pro Thr Thr Arg Leu	

65					70						75					80
Lys	Arg	Pro	Ser	Leu	Ile	Gln	Ser	His	Lys	Asp	Ser	Asn	Arg	Asn	Phe	
				85					90					95		
Lys	Thr	Ile	Thr	Phe	Trp	Leu	Val	Pro	Thr	Lys	Ser	His	Ala	Thr	Tyr	
			100					105					110			
Tyr	Ile	Ile	Lys	Val												
		115														

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...1100
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

TTATAATAAG AAAGTTTTTA TTATTTTAA TGCTATTTTA GGAGTTCATC	ATG AAA	56
	Met Lys	
	1	
AAA TCC ATT TTA TTG GGC GTT TGC TTG GCT TTT TCT TGC GCT CAT GCC		104
Lys Ser Ile Leu Leu Gly Val Cys Leu Ala Phe Ser Cys Ala His Ala		
5 10 15		
CTA AAC GAT TTA GAA TTG ATC AAA AAA GCG AGG GAA AGC CAG CTA GAA		152
Leu Asn Asp Leu Glu Leu Ile Lys Lys Ala Arg Glu Ser Gln Leu Glu		
20 25 30		
CCC ATG CCT ATG GGC AAA GCG CTC AAA GAA TAC CAG ATT AAA AAG ACC		200
Pro Met Pro Met Gly Lys Ala Leu Lys Glu Tyr Gln Ile Lys Lys Thr		
35 40 45 50		
AGA GAT GTG GGT ATT GGC ACC AAA AAC AGC GAA ATC ATG ACC TCC GCT		248
Arg Asp Val Gly Ile Gly Thr Lys Asn Ser Glu Ile Met Thr Ser Ala		
55 60 65		
CAA GTG GAA TTA GGC AAA ATG CTC TAT TTT GAC CCT AGG ATT TCC ACT		296
Gln Val Glu Leu Gly Lys Met Leu Tyr Phe Asp Pro Arg Ile Ser Thr		
70 75 80		
TCC TAC CTC GTG TCT TGC AAC ACA TGC CAT AAT CTG GGC TTA GGC GGG		344
Ser Tyr Leu Val Ser Cys Asn Thr Cys His Asn Leu Gly Leu Gly Gly		
85 90 95		
GTG GAT TTA GTC CCA AGC GCC ATA GGC TCT CAA TGG AAG AAA AAC CCC		392
Val Asp Leu Val Pro Ser Ala Ile Gly Ser Gln Trp Lys Lys Asn Pro		
100 105 110		

CAC	CTT	TTA	AGC	TCC	CCA	ACG	GTG	TAT	AAC	TCT	GTG	TTT	AAC	GAT	GTG	440
His	Leu	Leu	Ser	Ser	Pro	Thr	Val	Tyr	Asn	Ser	Val	Phe	Asn	Asp	Val	
115					120					125					130	
CAG	TTT	TGG	GAT	GGC	AGG	GTT	ACG	CAT	TTA	AAC	GAA	CAG	GCG	CAA	GGG	488
Gln	Phe	Trp	Asp	Gly	Arg	Val	Thr	His	Leu	Asn	Glu	Gln	Ala	Gln	Gly	
				135					140						145	
CCC	ATC	CAG	TCT	TCT	TTT	GAA	ATG	GGG	GCT	GAT	CCC	AAA	GTG	GTG	GTA	536
Pro	Ile	Gln	Ser	Ser	Phe	Glu	Met	Gly	Ala	Asp	Pro	Lys	Val	Val	Val	
			150					155					160			
GAA	AAA	ATC	AAT	TCC	ATG	CCA	GGC	TAT	GTC	AAG	CTC	TTT	AGA	AAA	GCC	584
Glu	Lys	Ile	Asn	Ser	Met	Pro	Gly	Tyr	Val	Lys	Leu	Phe	Arg	Lys	Ala	
		165					170					175				
TAT	GGC	TCT	AAA	GTC	AAA	ATT	GAT	TTT	AAA	TTG	ATC	GCT	GAT	AGT	ATC	632
Tyr	Gly	Ser	Lys	Val	Lys	Ile	Asp	Phe	Lys	Leu	Ile	Ala	Asp	Ser	Ile	
	180					185					190					
GCT	ATG	TTT	GAA	GCC	ACG	CTT	ATT	ACC	CCA	AGC	CGT	TAC	GAC	GAT	TTT	680
Ala	Met	Phe	Glu	Ala	Thr	Leu	Ile	Thr	Pro	Ser	Arg	Tyr	Asp	Asp	Phe	
195					200					205					210	
TTA	AGA	GGC	AAT	CCT	AAA	GCG	CTC	AGC	AAA	GCC	GAA	AAA	GAG	GGG	CTG	728
Leu	Arg	Gly	Asn	Pro	Lys	Ala	Leu	Ser	Lys	Ala	Glu	Lys	Glu	Gly	Leu	
				215					220					225		
AAT	TTA	TTC	ATT	TCT	AAA	GGC	TGT	GTG	GCT	TGC	CAT	AAC	GGC	ATT	AAT	776
Asn	Leu	Phe	Ile	Ser	Lys	Gly	Cys	Val	Ala	Cys	His	Asn	Gly	Ile	Asn	
			230					235					240			
CTT	GGG	GGA	ACG	ATG	CAG	CCT	TTT	GGG	GTG	GTC	AAA	CCT	TAT	AAA	TTC	824
Leu	Gly	Gly	Thr	Met	Gln	Pro	Phe	Gly	Val	Val	Lys	Pro	Tyr	Lys	Phe	
		245				250						255				
GCT	AAT	GTG	GGC	GAT	TTC	AAA	GGC	GAT	AAA	AAC	GGG	CTT	GTG	AAA	GTG	872
Ala	Asn	Val	Gly	Asp	Phe	Lys	Gly	Asp	Lys	Asn	Gly	Leu	Val	Lys	Val	
	260					265					270					
CCT	ACT	TTA	AGG	AAT	ATC	ACC	GAA	ACG	ATG	CCC	TAT	TTC	CAT	AAC	GGG	920
Pro	Thr	Leu	Arg	Asn	Ile	Thr	Glu	Thr	Met	Pro	Tyr	Phe	His	Asn	Gly	
275					280					285					290	
CAA	TTC	TGG	GAT	GTT	AAG	GAT	GCG	ATT	AAA	GAA	ATG	GGC	TCT	ATC	CAG	968
Gln	Phe	Trp	Asp	Val	Lys	Asp	Ala	Ile	Lys	Glu	Met	Gly	Ser	Ile	Gln	
				295					300					305		
TTA	GGC	ATT	GAA	ATC	AGC	GAT	GAA	GAA	GCG	AAA	AAA	ATT	GAA	ACT	TTC	1016
Leu	Gly	Ile	Glu	Ile	Ser	Asp	Glu	Glu	Ala	Lys	Lys	Ile	Glu	Thr	Phe	
			310					315					320			
TTT	GGA	GCC	TTA	AGG	GGT	AAA	AAA	CCT	AAA	ATA	ATC	TAC	CCA	GAA	CTC	1064
Phe	Gly	Ala	Leu	Arg	Gly	Lys	Lys	Pro	Lys	Ile	Ile	Tyr	Pro	Glu	Leu	
		325				330						335				
CCC	ATA	ATG	ACA	GAC	AAA	ACC	CCT	AAA	CCC	TCT	TTT	TGATT	TAAAA	AAGTCC	1116	
Pro	Ile	Met	Thr	Asp	Lys	Thr	Pro	Lys	Pro	Ser	Phe					

340

345

350

TTTTAGGGGT CTTTGGCGCT AAATCTAAAA AATACTC

1153

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

Met	Lys	Lys	Ser	Ile	Leu	Leu	Gly	Val	Cys	Leu	Ala	Phe	Ser	Cys	Ala	1	5	10	15
His	Ala	Leu	Asn	Asp	Leu	Glu	Leu	Ile	Lys	Lys	Ala	Arg	Glu	Ser	Gln	20	25	30	
Leu	Glu	Pro	Met	Pro	Met	Gly	Lys	Ala	Leu	Lys	Glu	Tyr	Gln	Ile	Lys	35	40	45	
Lys	Thr	Arg	Asp	Val	Gly	Ile	Gly	Thr	Lys	Asn	Ser	Glu	Ile	Met	Thr	50	55	60	
Ser	Ala	Gln	Val	Glu	Leu	Gly	Lys	Met	Leu	Tyr	Phe	Asp	Pro	Arg	Ile	65	70	75	80
Ser	Thr	Ser	Tyr	Leu	Val	Ser	Cys	Asn	Thr	Cys	His	Asn	Leu	Gly	Leu	85	90	95	
Gly	Gly	Val	Asp	Leu	Val	Pro	Ser	Ala	Ile	Gly	Ser	Gln	Trp	Lys	Lys	100	105	110	
Asn	Pro	His	Leu	Leu	Ser	Ser	Pro	Thr	Val	Tyr	Asn	Ser	Val	Phe	Asn	115	120	125	
Asp	Val	Gln	Phe	Trp	Asp	Gly	Arg	Val	Thr	His	Leu	Asn	Glu	Gln	Ala	130	135	140	
Gln	Gly	Pro	Ile	Gln	Ser	Ser	Phe	Glu	Met	Gly	Ala	Asp	Pro	Lys	Val	145	150	155	160
Val	Val	Glu	Lys	Ile	Asn	Ser	Met	Pro	Gly	Tyr	Val	Lys	Leu	Phe	Arg	165	170	175	
Lys	Ala	Tyr	Gly	Ser	Lys	Val	Lys	Ile	Asp	Phe	Lys	Leu	Ile	Ala	Asp	180	185	190	
Ser	Ile	Ala	Met	Phe	Glu	Ala	Thr	Leu	Ile	Thr	Pro	Ser	Arg	Tyr	Asp	195	200	205	
Asp	Phe	Leu	Arg	Gly	Asn	Pro	Lys	Ala	Leu	Ser	Lys	Ala	Glu	Lys	Glu	210	215	220	
Gly	Leu	Asn	Leu	Phe	Ile	Ser	Lys	Gly	Cys	Val	Ala	Cys	His	Asn	Gly	225	230	235	240
Ile	Asn	Leu	Gly	Gly	Thr	Met	Gln	Pro	Phe	Gly	Val	Val	Lys	Pro	Tyr	245	250	255	
Lys	Phe	Ala	Asn	Val	Gly	Asp	Phe	Lys	Gly	Asp	Lys	Asn	Gly	Leu	Val	260	265	270	
Lys	Val	Pro	Thr	Leu	Arg	Asn	Ile	Thr	Glu	Thr	Met	Pro	Tyr	Phe	His	275	280	285	
Asn	Gly	Gln	Phe	Trp	Asp	Val	Lys	Asp	Ala	Ile	Lys	Glu	Met	Gly	Ser	290	295	300	
Ile	Gln	Leu	Gly	Ile	Glu	Ile	Ser	Asp	Glu	Glu	Ala	Lys	Lys	Ile	Glu	305	310	315	320
Thr	Phe	Phe	Gly	Ala	Leu	Arg	Gly	Lys	Lys	Pro	Lys	Ile	Ile	Tyr	Pro				

310

335

350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

[illegible]

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

```

Met Lys Ala Ile Phe Ser Leu Phe Phe Leu Leu Ile Val Leu Lys Ala
 1             5             10             15
Asn Pro Ile Asn Pro Leu Leu Glu Pro Leu Tyr Phe Pro Ser Tyr Ala
      20             25             30
Gln Phe Leu Asn Leu Ala Pro His Phe Val Ile Lys Lys Lys Arg Ala
      35             40             45
Tyr Arg Pro Phe Gln Trp Gly Asn Thr Ile Ile Ile Lys Arg His Asp
      50             55             60
Leu Glu Glu Arg Gln Ser Asn Gln Pro Ser Asp Ile Phe Arg Gln Asn
      65             70             75             80
Ala Glu Ile Asn Val Ser Ser Gln Thr Phe Leu Lys Gly Met Ser Asn
      85             90             95
Ala Ser Ser Arg Thr Val Leu Asp Ser Ala Ala Gln
      100             105

```

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...746
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

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AGCGTGAGCC CAATTACGCC ACGCCTATGT CTAGATAGGG GAGGTTGGAA ATG TTT      56
                                         Met Phe
                                         1

AGT TTT TTA GAA AAA AAC CCG TTC TTT TTC ACT CTT GCG TTT ATT TTT      104
Ser Phe Leu Glu Lys Asn Pro Phe Phe Phe Thr Leu Ala Phe Ile Phe
      5             10             15

GTG TTT GCG ATC GCG GGC TTG GTG GAG ATT TTG CCC AAC TTC TTC AAA      152
Val Phe Ala Ile Ala Gly Leu Val Glu Ile Leu Pro Asn Phe Phe Lys
      20             25             30

TCC GCT CGC CCG ATT GAA GGC TTA CGG CCT TAT ACG GTT TTA GAG ACA      200

```

Ser	Ala	Arg	Pro	Ile	Glu	Gly	Leu	Arg	Pro	Tyr	Thr	Val	Leu	Glu	Thr	
35					40					45					50	
GCG	GGG	AGG	CAA	ATT	TAT	ATC	CAA	GAA	GGT	TGC	TAT	CAT	TGC	CAT	TCC	248
Ala	Gly	Arg	Gln	Ile	Tyr	Ile	Gln	Glu	Gly	Cys	Tyr	His	Cys	His	Ser	
			55					60					65			
CAG	CTT	ATT	CGC	CCT	TTC	CAA	GCT	GAG	GTG	GAT	CGA	TAT	GGC	GCG	TAT	296
Gln	Leu	Ile	Arg	Pro	Phe	Gln	Ala	Glu	Val	Asp	Arg	Tyr	Gly	Ala	Tyr	
			70					75					80			
AGT	TTG	AGT	GGG	GAA	TAC	GCG	TAT	GAC	AGG	CCA	TTT	TTG	TGG	GGT	TCT	344
Ser	Leu	Ser	Gly	Glu	Tyr	Ala	Tyr	Asp	Arg	Pro	Phe	Leu	Trp	Gly	Ser	
		85					90					95				
AAA	AGG	ATT	GGC	CCT	GAT	TTG	CAC	AGG	GTA	GGG	GAT	TAT	CGC	ACA	ACC	392
Lys	Arg	Ile	Gly	Pro	Asp	Leu	His	Arg	Val	Gly	Asp	Tyr	Arg	Thr	Thr	
	100					105					110					
GAT	TGG	CAT	GAA	AAG	CAC	ATG	TTT	GAT	CCT	AAA	AGC	GTT	GTG	CCG	CAC	440
Asp	Trp	His	Glu	Lys	His	Met	Phe	Asp	Pro	Lys	Ser	Val	Val	Pro	His	
	115				120				125						130	
AGC	ATC	ATG	CCC	GCC	TAT	AAG	CAT	TTA	TTT	ACA	AAA	AAG	AGC	GAT	TTT	488
Ser	Ile	Met	Pro	Ala	Tyr	Lys	His	Leu	Phe	Thr	Lys	Lys	Ser	Asp	Phe	
				135					140					145		
GAC	ACC	GCT	TAT	GCA	GAA	GCT	TTG	ACG	CAA	AAA	AAG	GTT	TTT	GGC	GTG	536
Asp	Thr	Ala	Tyr	Ala	Glu	Ala	Leu	Thr	Gln	Lys	Lys	Val	Phe	Gly	Val	
			150					155					160			
CCT	TAT	GAC	ACA	GAA	AAC	GGC	GTG	AAA	TTA	GGG	AGC	GTA	GAA	GAA	GCG	584
Pro	Tyr	Asp	Thr	Glu	Asn	Gly	Val	Lys	Leu	Gly	Ser	Val	Glu	Glu	Ala	
			165				170					175				
AAA	AAA	GCC	TAT	TTA	GAA	GAA	GCT	AAA	AAA	ATC	ACA	GCC	GAT	ATG	AAA	632
Lys	Lys	Ala	Tyr	Leu	Glu	Glu	Ala	Lys	Lys	Ile	Thr	Ala	Asp	Met	Lys	
	180					185					190					
GAC	AAG	AGG	GTG	CTA	GAA	GCG	ATT	GAG	AGA	GGT	GAA	GTG	TTA	GAA	ATT	680
Asp	Lys	Arg	Val	Leu	Glu	Ala	Ile	Glu	Arg	Gly	Glu	Val	Leu	Glu	Ile	
	195				200				205						210	
GTG	GCT	TTG	ATC	GCT	TAT	TTG	AAT	AGC	TTG	GGT	AAT	TCC	AGG	ATC	AAC	728
Val	Ala	Leu	Ile	Ala	Tyr	Leu	Asn	Ser	Leu	Gly	Asn	Ser	Arg	Ile	Asn	
			215					220						225		
GCC	AAT	CAA	AAC	GCT	AAA	TAAGGGGTGA	ATGATGGATT	TAGAAAGTTT	GAGAGGTT							784
Ala	Asn	Gln	Asn	Ala	Lys											
			230													
TTGCGTATGC	GTTTT															799

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 232 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Met	Phe	Ser	Phe	Leu	Glu	Lys	Asn	Pro	Phe	Phe	Phe	Thr	Leu	Ala	Phe	1	5	10	15
Ile	Phe	Val	Phe	Ala	Ile	Ala	Gly	Leu	Val	Glu	Ile	Leu	Pro	Asn	Phe	20	25	30	
Phe	Lys	Ser	Ala	Arg	Pro	Ile	Glu	Gly	Leu	Arg	Pro	Tyr	Thr	Val	Leu	35	40	45	
Glu	Thr	Ala	Gly	Arg	Gln	Ile	Tyr	Ile	Gln	Glu	Gly	Cys	Tyr	His	Cys	50	55	60	
His	Ser	Gln	Leu	Ile	Arg	Pro	Phe	Gln	Ala	Glu	Val	Asp	Arg	Tyr	Gly	65	70	75	80
Ala	Tyr	Ser	Leu	Ser	Gly	Glu	Tyr	Ala	Tyr	Asp	Arg	Pro	Phe	Leu	Trp	85	90	95	
Gly	Ser	Lys	Arg	Ile	Gly	Pro	Asp	Leu	His	Arg	Val	Gly	Asp	Tyr	Arg	100	105	110	
Thr	Thr	Asp	Trp	His	Glu	Lys	His	Met	Phe	Asp	Pro	Lys	Ser	Val	Val	115	120	125	
Pro	His	Ser	Ile	Met	Pro	Ala	Tyr	Lys	His	Leu	Phe	Thr	Lys	Lys	Ser	130	135	140	
Asp	Phe	Asp	Thr	Ala	Tyr	Ala	Glu	Ala	Leu	Thr	Gln	Lys	Lys	Val	Phe	145	150	155	160
Gly	Val	Pro	Tyr	Asp	Thr	Glu	Asn	Gly	Val	Lys	Leu	Gly	Ser	Val	Glu	165	170	175	
Glu	Ala	Lys	Lys	Ala	Tyr	Leu	Glu	Glu	Ala	Lys	Lys	Ile	Thr	Ala	Asp	180	185	190	
Met	Lys	Asp	Lys	Arg	Val	Leu	Glu	Ala	Ile	Glu	Arg	Gly	Glu	Val	Leu	195	200	205	
Glu	Ile	Val	Ala	Leu	Ile	Ala	Tyr	Leu	Asn	Ser	Leu	Gly	Asn	Ser	Arg	210	215	220	
Ile	Asn	Ala	Asn	Gln	Asn	Ala	Lys									225	230		

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...269
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

CTTGGGTAAT TCCAGGATCA ACGCCAATCA AAACGCTAAA TAAGGGGTGA ATG ATG 56
Met Met
1

GAT TTA GAA AGT TTG AGA GGT TTT GCG TAT GCG TTT TTT ACC ATT CTT 104
Asp Leu Glu Ser Leu Arg Gly Phe Ala Tyr Ala Phe Phe Thr Ile Leu
5 10 15

TTT ACG CTC TTT TTG TAT GCC TAT ATT TTT AGC ATG TAT AGA AAG CAA 152
Phe Thr Leu Phe Leu Tyr Ala Tyr Ile Phe Ser Met Tyr Arg Lys Gln
20 25 30

AAA AAA GGC ATT ATG GAT TAT GAG CGA TAC GGA TAC TTA GCG TTA AAT 200
Lys Lys Gly Ile Met Asp Tyr Glu Arg Tyr Gly Tyr Leu Ala Leu Asn
35 40 45 50

GAT GCT TTA GAA GAC GAG TTG ATT GAA CCA CGC CAT AAA AAA GTT CAT 248
Asp Ala Leu Glu Asp Glu Leu Ile Glu Pro Arg His Lys Lys Val His
55 60 65

GAT AAT GGC ATA AAG GAA AGT TGAAATGGAT TTTTAAACG ACCATATAAA TGTT 303
Asp Asn Gly Ile Lys Glu Ser
70

TTTGGCTTGA TTGCAGCGC 322

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

Met Met Asp Leu Glu Ser Leu Arg Gly Phe Ala Tyr Ala Phe Phe Thr
1 5 10 15
Ile Leu Phe Thr Leu Phe Leu Tyr Ala Tyr Ile Phe Ser Met Tyr Arg
20 25 30
Lys Gln Lys Lys Gly Ile Met Asp Tyr Glu Arg Tyr Gly Tyr Leu Ala
35 40 45
Leu Asn Asp Ala Leu Glu Asp Glu Leu Ile Glu Pro Arg His Lys Lys
50 55 60
Val His Asp Asn Gly Ile Lys Glu Ser
65 70

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 51...968

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

TTACTGATTT TTCTTTGTGT GAGCTTTGGC TTAGTTTTGT AAGGAATGAG ATG ATA	56
Met Ile	
1	
AAG AGT TGG ACT AAA AAG TGG TTT TTG ATT TTA TTT TTA ATG GCA AGT	104
Lys Ser Trp Thr Lys Lys Trp Phe Leu Ile Leu Phe Leu Met Ala Ser	
5 10 15	
TGT TCC AGT TAT TTG GTG GCT ACA ACC GGT GAG AAA TAT TTT AAA ATG	152
Cys Ser Ser Tyr Leu Val Ala Thr Thr Gly Glu Lys Tyr Phe Lys Met	
20 25 30	
GCT ACT CAA GCC TTT AAG AGA GGG GAC TAC CAT AAA GCG GTG GCT TTT	200
Ala Thr Gln Ala Phe Lys Arg Gly Asp Tyr His Lys Ala Val Ala Phe	
35 40 45 50	
TAT AAG AGG AGC TGT AAT TTA AGG GTG GGG GTT GGT TGC ACG AGT TTA	248
Tyr Lys Arg Ser Cys Asn Leu Arg Val Gly Val Gly Cys Thr Ser Leu	
55 60 65	
GGC TCT ATG TAT GAA GAT GGC GAT GGC GTG GAT CAG AAT ATT ACA AAA	296
Gly Ser Met Tyr Glu Asp Gly Asp Gly Val Asp Gln Asn Ile Thr Lys	
70 75 80	
GCC GTT TTT TAT TAC AGA AGA GGG TGT AAT TTA AGG AAT CAT CTC GCT	344
Ala Val Phe Tyr Tyr Arg Arg Gly Cys Asn Leu Arg Asn His Leu Ala	
85 90 95	
TGC GCG AGT CTA GGC TCT ATG TAT GAA GAT GGC GAT GGT GTG CAA AAA	392
Cys Ala Ser Leu Gly Ser Met Tyr Glu Asp Gly Asp Gly Val Gln Lys	
100 105 110	
AAC CTT CCA AAG GCT ATC TAT TAT TAC AGG AGA GGG TGC CAC TTA AAG	440
Asn Leu Pro Lys Ala Ile Tyr Tyr Tyr Arg Arg Gly Cys His Leu Lys	
115 120 125 130	
GGT GGG GTG AGC TGT GGG AGT TTA GGT TTT ATG TAT TTT AAT GGC ACG	488
Gly Gly Val Ser Cys Gly Ser Leu Gly Phe Met Tyr Phe Asn Gly Thr	
135 140 145	
GGC GTT AAG CAA AAT TAT GCC AAA GCC CTT TTT CTT TCT AAA TAC GCT	536
Gly Val Lys Gln Asn Tyr Ala Lys Ala Leu Phe Leu Ser Lys Tyr Ala	
150 155 160	
TGC AGT TTG AAT TAC GGC ATT AGT TGT AAC TTT GTA GGG TAT ATG TAT	584
Cys Ser Leu Asn Tyr Gly Ile Ser Cys Asn Phe Val Gly Tyr Met Tyr	
165 170 175	

AGG AAC GCC AAA GGC GTA CAG AAG GAT TTG AAA AAA GCC CTT GCG AAT	632
Arg Asn Ala Lys Gly Val Gln Lys Asp Leu Lys Lys Ala Leu Ala Asn	
180 185 190	
TTT AAA AGA GGG TGC CAT TTG AAA GAC GGA GCG AGT TGT GTG AGC TTG	680
Phe Lys Arg Gly Cys His Leu Lys Asp Gly Ala Ser Cys Val Ser Leu	
195 200 205 210	
GGA TAC ATG TAT GAA GTC GGT ATG GAT GTC AAA CAA AAT GGA GAG CAA	728
Gly Tyr Met Tyr Glu Val Gly Met Asp Val Lys Gln Asn Gly Glu Gln	
215 220 225	
GCC TTG AAT CTT TAT AAA AAG GGT TGT TAT TTA AAA AGG GGG AGC GGT	776
Ala Leu Asn Leu Tyr Lys Lys Gly Cys Tyr Leu Lys Arg Gly Ser Gly	
230 235 240	
TGT CAT AAT GTG GCG GTG ATG TAT TAC ACC GGT AAG GGC GTT CCA AAG	824
Cys His Asn Val Ala Val Met Tyr Tyr Thr Gly Lys Gly Val Pro Lys	
245 250 255	
GAT TTA GAT AAA GCC ATT TCG TAT TAT AAG AAA GGT TGC ACT CTA GGC	872
Asp Leu Asp Lys Ala Ile Ser Tyr Tyr Lys Lys Gly Cys Thr Leu Gly	
260 265 270	
TTT AGT GGT AGC TGT AAA GTG TTA GAA GAA GTG ATT GGC AAG AAG TCT	920
Phe Ser Gly Ser Cys Lys Val Leu Glu Glu Val Ile Gly Lys Lys Ser	
275 280 285 290	
GAT GAT TTG CAA GAT GAC GCG CAA AAC GAC ACG CAA GAT GAT ATG CAA T	969
Asp Asp Leu Gln Asp Asp Ala Gln Asn Asp Thr Gln Asp Asp Met Gln	
295 300 305	
AAGTTAAAGC TTATGGACTA ATGATTAAAA CTCATCTTAT AGAAATCTTT CT	1021

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Met	Ile	Lys	Ser	Trp	Thr	Lys	Lys	Trp	Phe	Leu	Ile	Leu	Phe	Leu	Met
1				5					10					15	
Ala	Ser	Cys	Ser	Ser	Tyr	Leu	Val	Ala	Thr	Thr	Gly	Glu	Lys	Tyr	Phe
			20					25					30		
Lys	Met	Ala	Thr	Gln	Ala	Phe	Lys	Arg	Gly	Asp	Tyr	His	Lys	Ala	Val
		35				40					45				
Ala	Phe	Tyr	Lys	Arg	Ser	Cys	Asn	Leu	Arg	Val	Gly	Val	Gly	Cys	Thr
	50					55				60					
Ser	Leu	Gly	Ser	Met	Tyr	Glu	Asp	Gly	Asp	Gly	Val	Asp	Gln	Asn	Ile
65				70				75						80	
Thr	Lys	Ala	Val	Phe	Tyr	Tyr	Arg	Arg	Gly	Cys	Asn	Leu	Arg	Asn	His



CTATAATGTG	AATTTAATGA	TGAAAATTAG	TTTAGAGTGG	AGAACACACA	ATG	AAA	56									
					Met	Lys										
					1											
AAA	AAT	ATC	TTA	AAT	TTA	GCG	TTA	GTG	GGT	GCG	TTG	AGC	ACG	TCG	TTT	104
Lys	Asn	Ile	Leu	Asn	Leu	Ala	Leu	Val	Gly	Ala	Leu	Ser	Thr	Ser	Phe	
		5					10					15				
TTG	ATG	GCT	AAG	CCG	GCT	CAT	AAC	GCA	AAT	AAC	GCT	ACG	CAT	AAC	ACG	152

Leu	Met	Ala	Lys	Pro	Ala	His	Asn	Ala	Asn	Asn	Ala	Thr	His	Asn	Thr	
20						25					30					
AAA	AAA	ACG	ACT	GAT	TCT	TCA	GCA	GGC	GTG	TTA	GCG	ACA	GTG	GAT	GGC	200
Lys	Lys	Thr	Thr	Asp	Ser	Ser	Ala	Gly	Val	Leu	Ala	Thr	Val	Asp	Gly	
35				40					45					50		
AGA	CCT	ATC	ACT	AAA	AGC	GAT	TTT	GAC	ATG	ATT	AAG	CAA	CGA	AAT	CCT	248
Arg	Pro	Ile	Thr	Lys	Ser	Asp	Phe	Asp	Met	Ile	Lys	Gln	Arg	Asn	Pro	
				55				60						65		
AAT	TTT	GAT	TTT	GAC	AAG	CTT	AAA	GAG	AAA	GAA	AAA	GAA	GCC	TTG	ATT	296
Asn	Phe	Asp	Phe	Asp	Lys	Leu	Lys	Glu	Lys	Glu	Lys	Glu	Ala	Leu	Ile	
			70					75					80			
GAT	CAA	GCT	ATT	CGC	ACC	GCC	CTT	GTA	GAA	AAT	GAA	GCT	AAA	ACC	GAG	344
Asp	Gln	Ala	Ile	Arg	Thr	Ala	Leu	Val	Glu	Asn	Glu	Ala	Lys	Thr	Glu	
	85						90					95				
AAA	TTG	GAC	AGC	ACT	CCA	GAA	TTT	AAA	GCG	ATG	ATG	GAA	GCG	GTT	AAA	392
Lys	Leu	Asp	Ser	Thr	Pro	Glu	Phe	Lys	Ala	Met	Met	Glu	Ala	Val	Lys	
100						105					110					
AAA	CAG	GCT	TTA	GTG	GAA	TTT	TGG	GCT	AAA	AAA	CAG	GCT	GAA	GAA	GTG	440
Lys	Gln	Ala	Leu	Val	Glu	Phe	Trp	Ala	Lys	Lys	Gln	Ala	Glu	Glu	Val	
115					120					125					130	
AAA	AAA	GTC	CAA	ATC	CCA	GAA	AAA	GAA	ATG	CAA	GAT	TTT	TAC	AAC	GCT	488
Lys	Lys	Val	Gln	Ile	Pro	Glu	Lys	Glu	Met	Gln	Asp	Phe	Tyr	Asn	Ala	
				135				140						145		
AAC	AAA	GAT	CAG	CTT	TTT	GTC	AAG	CAA	GAA	GCC	CAT	GCT	AGG	CAT	ATT	536
Asn	Lys	Asp	Gln	Leu	Phe	Val	Lys	Gln	Glu	Ala	His	Ala	Arg	His	Ile	
			150					155					160			
TTA	GTG	AAA	ACC	GAA	GAT	GAG	GCT	AAA	CGG	ATT	ATT	TCT	GAG	ATT	GAC	584
Leu	Val	Lys	Thr	Glu	Asp	Glu	Ala	Lys	Arg	Ile	Ile	Ser	Glu	Ile	Asp	
	165						170					175				
AAA	CAG	CCA	AAG	GCT	AAA	AAA	GAA	GCT	AAA	TTC	ATT	GAG	TTA	GCC	AAT	632
Lys	Gln	Pro	Lys	Ala	Lys	Lys	Glu	Ala	Lys	Phe	Ile	Glu	Leu	Ala	Asn	
180						185					190					
CGG	GAT	ACG	ATT	GAT	CCT	AAC	AGC	AAG	AAC	GCG	CAA	AAT	GGC	GGT	GAT	680
Arg	Asp	Thr	Ile	Asp	Pro	Asn	Ser	Lys	Asn	Ala	Gln	Asn	Gly	Gly	Asp	
195					200					205					210	
TTG	GGG	AAA	TTC	CAA	AAG	AAC	CAA	ATG	GCT	CCG	GAT	TTT	TCT	AAA	GCC	728
Leu	Gly	Lys	Phe	Gln	Lys	Asn	Gln	Met	Ala	Pro	Asp	Phe	Ser	Lys	Ala	
				215				220						225		
GCT	TTC	GCT	TTA	ACT	CCT	GGG	GAT	TAC	ACT	AAA	ACC	CCT	GTT	AAA	ACA	776
Ala	Phe	Ala	Leu	Thr	Pro	Gly	Asp	Tyr	Thr	Lys	Thr	Pro	Val	Lys	Thr	
			230				235						240			
GAG	TTT	GGT	TAT	CAT	ATT	ATC	TAT	TTG	ATT	TCT	AAA	GAT	AGC	CCT	GTA	824
Glu	Phe	Gly	Tyr	His	Ile	Ile	Tyr	Leu	Ile	Ser	Lys	Asp	Ser	Pro	Val	
	245						250					255				

ACT TAT ACT TAT GAA CAG GCT AAA CCT ACC ATT AAG GGG ATG TTA CAA 872
 Thr Tyr Thr Tyr Glu Gln Ala Lys Pro Thr Ile Lys Gly Met Leu Gln
 260 265 270

GAA AAG CTT TTC CAA GAA CGC ATG AAT CAA CGC ATT GAG GAA CTA AGA 920
 Glu Lys Leu Phe Gln Glu Arg Met Asn Gln Arg Ile Glu Glu Leu Arg
 275 280 285 290

AAG CAC GCT AAA ATT GTT ATC AAC AAG TAATTGATGA GGTGTTATCA TGTTAGT 974
 Lys His Ala Lys Ile Val Ile Asn Lys
 295

TAAAGGCAAT GAAATTTTAT TGAAAG 1000

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Met Lys Lys Asn Ile Leu Asn Leu Ala Leu Val Gly Ala Leu Ser Thr
 1 5 10 15
 Ser Phe Leu Met Ala Lys Pro Ala His Asn Ala Asn Asn Ala Thr His
 20 25 30
 Asn Thr Lys Lys Thr Thr Asp Ser Ser Ala Gly Val Leu Ala Thr Val
 35 40 45
 Asp Gly Arg Pro Ile Thr Lys Ser Asp Phe Asp Met Ile Lys Gln Arg
 50 55 60
 Asn Pro Asn Phe Asp Phe Asp Lys Leu Lys Glu Lys Glu Lys Glu Ala
 65 70 75 80
 Leu Ile Asp Gln Ala Ile Arg Thr Ala Leu Val Glu Asn Glu Ala Lys
 85 90 95
 Thr Glu Lys Leu Asp Ser Thr Pro Glu Phe Lys Ala Met Met Glu Ala
 100 105 110
 Val Lys Lys Gln Ala Leu Val Glu Phe Trp Ala Lys Lys Gln Ala Glu
 115 120 125
 Glu Val Lys Lys Val Gln Ile Pro Glu Lys Glu Met Gln Asp Phe Tyr
 130 135 140
 Asn Ala Asn Lys Asp Gln Leu Phe Val Lys Gln Glu Ala His Ala Arg
 145 150 155 160
 His Ile Leu Val Lys Thr Glu Asp Glu Ala Lys Arg Ile Ile Ser Glu
 165 170 175
 Ile Asp Lys Gln Pro Lys Ala Lys Lys Glu Ala Lys Phe Ile Glu Leu
 180 185 190
 Ala Asn Arg Asp Thr Ile Asp Pro Asn Ser Lys Asn Ala Gln Asn Gly
 195 200 205
 Gly Asp Leu Gly Lys Phe Gln Lys Asn Gln Met Ala Pro Asp Phe Ser
 210 215 220
 Lys Ala Ala Phe Ala Leu Thr Pro Gly Asp Tyr Thr Lys Thr Pro Val
 225 230 235 240
 Lys Thr Glu Phe Gly Tyr His Ile Ile Tyr Leu Ile Ser Lys Asp Ser

				245						250						255			
Pro	Val	Thr	Tyr	Thr	Tyr	Glu	Gln	Ala	Lys	Pro	Thr	Ile	Lys	Gly	Met				
			260					265					270						
Leu	Gln	Glu	Lys	Leu	Phe	Gln	Glu	Arg	Met	Asn	Gln	Arg	Ile	Glu	Glu				
		275				280						285							
Leu	Arg	Lys	His	Ala	Lys	Ile	Val	Ile	Asn	Lys									
	290					295													

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...323
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

CAGCGTTGGT GTATTTTGGG GGAAGTTAGG AAAATATTGA AGGAGTATTG ATG AAA	56
Met Lys	
1	
AAG GTT GTT TTT TTA TTG TTA GTT ATA CTA GGG GGT TTA GAA GCG CAA	104
Lys Val Val Phe Leu Leu Leu Val Ile Leu Gly Gly Leu Glu Ala Gln	
5 10 15	
AGT ACT TAT TGC AGT GAT CAT TGC GAA GGC ACG CCA GAT AGC CGT ATC	152
Ser Thr Tyr Cys Ser Asp His Cys Glu Gly Thr Pro Asp Ser Arg Ile	
20 25 30	
CCT CCT ATG GGG TTT CAT TTC AGT TTT GTG CAT TCA GTG AAA TAT TAC	200
Pro Pro Met Gly Phe His Phe Ser Phe Val His Ser Val Lys Tyr Tyr	
35 40 45 50	
TTG CAA GAT CCG CAA GAG CGC GAT CAC AAG CTT GAA AAA TGC CAT CAA	248
Leu Gln Asp Pro Gln Glu Arg Asp His Lys Leu Glu Lys Cys His Gln	
55 60 65	
GCC TTT GAT TCG ACT CTT AAG GTT AAT TTT ATT ACG AAT CTT TTA AAA	296
Ala Phe Asp Ser Thr Leu Lys Val Asn Phe Ile Thr Asn Leu Leu Lys	
70 75 80	
AGG ATT GCA AGC ATG CGC AAA TGG CTT TAGAGCAAGC CCAAAAAGGG ACTCCAT	350
Arg Ile Ala Ser Met Arg Lys Trp Leu	
85 90	
AAAAGGGGTT TCTTTAGGGA TTTTAT	376

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

```

Met Lys Lys Val Val Phe Leu Leu Leu Val Ile Leu Gly Gly Leu Glu
 1             5             10             15
Ala Gln Ser Thr Tyr Cys Ser Asp His Cys Glu Gly Thr Pro Asp Ser
      20             25             30
Arg Ile Pro Pro Met Gly Phe His Phe Ser Phe Val His Ser Val Lys
      35             40             45
Tyr Tyr Leu Gln Asp Pro Gln Glu Arg Asp His Lys Leu Glu Lys Cys
      50             55             60
His Gln Ala Phe Asp Ser Thr Leu Lys Val Asn Phe Ile Thr Asn Leu
      65             70             75             80
Leu Lys Arg Ile Ala Ser Met Arg Lys Trp Leu
      85             90

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(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1127
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

```

TTTTTAGTTA TAATGGCGGA CACCATTAAA ATTAAAACAA AGGTTATTCA ATG AAG      56
                                     Met Lys
                                     1

GTA TTA TCT TAT TTG AAA AAT TTT TAT CTT TTT TTA GCG ATA GGA GCA      104
Val Leu Ser Tyr Leu Lys Asn Phe Tyr Leu Phe Leu Ala Ile Gly Ala
      5             10             15

ATT ATG CAA GCG AGT GAA AAC ATG GGA TCT CAA CAC CAA AAA ACC GAT      152
Ile Met Gln Ala Ser Glu Asn Met Gly Ser Gln His Gln Lys Thr Asp
      20             25             30

GAA AGA GTG ATT TAC TTG GCT GGG GGG TGT TTT TGG GGG CTA GAG GCG      200
Glu Arg Val Ile Tyr Leu Ala Gly Gly Cys Phe Trp Gly Leu Glu Ala
      35             40             45             50

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TAT ATG GAG AGG ATT TAT GGC GTC ATA GAC GCA AGC TCT GGT TAC GCT	248
Tyr Met Glu Arg Ile Tyr Gly Val Ile Asp Ala Ser Ser Gly Tyr Ala	
55 60 65	
AAC GGC AAG ACT TCA AGC ACG AAT TAT GAG AAA TTG CAT GAA AGT GAT	296
Asn Gly Lys Thr Ser Ser Thr Asn Tyr Glu Lys Leu His Glu Ser Asp	
70 75 80	
CAT GCT GAA AGC GTG AAA GTC ATT TAT GAT CCT AAA AAA ATC AGT TTG	344
His Ala Glu Ser Val Lys Val Ile Tyr Asp Pro Lys Lys Ile Ser Leu	
85 90 95	
GAC AAA TTG TTG CGT TAC TAT TTT AAG GTG GTT GAT CCG GTG AGC GTG	392
Asp Lys Leu Leu Arg Tyr Tyr Phe Lys Val Val Asp Pro Val Ser Val	
100 105 110	
AAC AAG CAG GGT AAT GAT GTG GGC AGG CAG TAT CGC ACG GGG ATT TAT	440
Asn Lys Gln Gly Asn Asp Val Gly Arg Gln Tyr Arg Thr Gly Ile Tyr	
115 120 125 130	
TAT GTC AAT AGC GCG GAT AAA GAA GTG ATA GAT CAT GCC TTA AAA GCG	488
Tyr Val Asn Ser Ala Asp Lys Glu Val Ile Asp His Ala Leu Lys Ala	
135 140 145	
TTA CAG AAA GAA GTG AAA GGT AAA ATC GCT ATT GAA GTA GAG CCT TTA	536
Leu Gln Lys Glu Val Lys Gly Lys Ile Ala Ile Glu Val Glu Pro Leu	
150 155 160	
AAA AAT TAT GTG AGG GCT GAA GAG TAT CAT CAG GAT TAT TTG AAG AAA	584
Lys Asn Tyr Val Arg Ala Glu Glu Tyr His Gln Asp Tyr Leu Lys Lys	
165 170 175	
CAC CCT AGT GGT TAT TGC CAT ATT GAT TTG AAA AAG GCG GAT GAA GTG	632
His Pro Ser Gly Tyr Cys His Ile Asp Leu Lys Lys Ala Asp Glu Val	
180 185 190	
ATT GTG GAT GAC GAT AAA TAC ACC AAA CCT AGC GAT GAA GTT TTA AAG	680
Ile Val Asp Asp Asp Lys Tyr Thr Lys Pro Ser Asp Glu Val Leu Lys	
195 200 205 210	
AAA AAA CTC ACC AAA CTC CAG TAT GAG GTT ACG CAA AAC AAA CAC ACT	728
Lys Lys Leu Thr Lys Leu Gln Tyr Glu Val Thr Gln Asn Lys His Thr	
215 220 225	
GAG AAA CCC TTT GAA AAC GAG TAT TAC AAC AAA GAA GAA GAG GGC ATT	776
Glu Lys Pro Phe Glu Asn Glu Tyr Tyr Asn Lys Glu Glu Glu Gly Ile	
230 235 240	
TAT GTG GAT ATT ACC ACA GGC GAG CCG TTA TTT TCT TCA GCG GAT AAA	824
Tyr Val Asp Ile Thr Thr Gly Glu Pro Leu Phe Ser Ser Ala Asp Lys	
245 250 255	
TAC GAC TCC GGT TGC GGG TGG CCA AGC TTT TCT AAG CCT ATC AAT AAA	872
Tyr Asp Ser Gly Cys Gly Trp Pro Ser Phe Ser Lys Pro Ile Asn Lys	
260 265 270	
GAT GTG GTG AAA TAC GAA GAC GAT GAG AGC CTT AAT AGG AAA CGC ATT	920
Asp Val Val Lys Tyr Glu Asp Asp Glu Ser Leu Asn Arg Lys Arg Ile	

275	280	285	290	
GAA GTG TTG AGC CGT ATT GGT AAG GCG CAT TTA GGG CAT GTG TTT AAC				968
Glu Val Leu Ser Arg Ile Gly Lys Ala His Leu Gly His Val Phe Asn	295	300	305	
GAT GGG CCT AAA GAA TTA GGG GGC TTA AGG TAT TGC ATC AAC AGC GCG				1016
Asp Gly Pro Lys Glu Leu Gly Gly Leu Arg Tyr Cys Ile Asn Ser Ala	310	315	320	
GCT TTA AGG TTT ATC CCC TTA AAA GAC ATG GAA AAA GAG GGT TAT GGC				1064
Ala Leu Arg Phe Ile Pro Leu Lys Asp Met Glu Lys Glu Gly Tyr Gly	325	330	335	
GAG TTT ATC CCT TAT ATC AAA AAG GGT GAA TTG AAA AAA TAC ATC AAT				1112
Glu Phe Ile Pro Tyr Ile Lys Lys Gly Glu Leu Lys Lys Tyr Ile Asn	340	345	350	
GAT AAA AAG TCG CAT TAAGGGGTAA TGAATAAGCC CCCTAAGGGG GGTAAAAATG A				1168
Asp Lys Lys Ser His				
355				
GGGGTTTAAG CG				1180

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Met	Lys	Val	Leu	Ser	Tyr	Leu	Lys	Asn	Phe	Tyr	Leu	Phe	Leu	Ala	Ile
1				5					10					15	
Gly	Ala	Ile	Met	Gln	Ala	Ser	Glu	Asn	Met	Gly	Ser	Gln	His	Gln	Lys
			20					25					30		
Thr	Asp	Glu	Arg	Val	Ile	Tyr	Leu	Ala	Gly	Gly	Cys	Phe	Trp	Gly	Leu
		35					40					45			
Glu	Ala	Tyr	Met	Glu	Arg	Ile	Tyr	Gly	Val	Ile	Asp	Ala	Ser	Ser	Gly
	50					55					60				
Tyr	Ala	Asn	Gly	Lys	Thr	Ser	Ser	Thr	Asn	Tyr	Glu	Lys	Leu	His	Glu
65					70					75				80	
Ser	Asp	His	Ala	Glu	Ser	Val	Lys	Val	Ile	Tyr	Asp	Pro	Lys	Lys	Ile
			85						90				95		
Ser	Leu	Asp	Lys	Leu	Leu	Arg	Tyr	Tyr	Phe	Lys	Val	Val	Asp	Pro	Val
			100					105					110		
Ser	Val	Asn	Lys	Gln	Gly	Asn	Asp	Val	Gly	Arg	Gln	Tyr	Arg	Thr	Gly
		115					120					125			
Ile	Tyr	Tyr	Val	Asn	Ser	Ala	Asp	Lys	Glu	Val	Ile	Asp	His	Ala	Leu
	130					135					140				
Lys	Ala	Leu	Gln	Lys	Glu	Val	Lys	Gly	Lys	Ile	Ala	Ile	Glu	Val	Glu
145				150						155				160	
Pro	Leu	Lys	Asn	Tyr	Val	Arg	Ala	Glu	Glu	Tyr	His	Gln	Asp	Tyr	Leu

				165					170					175					
Lys	Lys	His	Pro	Ser	Gly	Tyr	Cys	His	Ile	Asp	Leu	Lys	Lys	Ala	Asp				
			180					185						190					
Glu	Val	Ile	Val	Asp	Asp	Asp	Lys	Tyr	Thr	Lys	Pro	Ser	Asp	Glu	Val				
		195					200					205							
Leu	Lys	Lys	Lys	Leu	Thr	Lys	Leu	Gln	Tyr	Glu	Val	Thr	Gln	Asn	Lys				
	210					215					220								
His	Thr	Glu	Lys	Pro	Phe	Glu	Asn	Glu	Tyr	Tyr	Asn	Lys	Glu	Glu	Glu				
225					230					235					240				
Gly	Ile	Tyr	Val	Asp	Ile	Thr	Thr	Gly	Glu	Pro	Leu	Phe	Ser	Ser	Ala				
			245					250						255					
Asp	Lys	Tyr	Asp	Ser	Gly	Cys	Gly	Trp	Pro	Ser	Phe	Ser	Lys	Pro	Ile				
		260					265						270						
Asn	Lys	Asp	Val	Val	Lys	Tyr	Glu	Asp	Asp	Glu	Ser	Leu	Asn	Arg	Lys				
	275						280					285							
Arg	Ile	Glu	Val	Leu	Ser	Arg	Ile	Gly	Lys	Ala	His	Leu	Gly	His	Val				
	290					295					300								
Phe	Asn	Asp	Gly	Pro	Lys	Glu	Leu	Gly	Gly	Leu	Arg	Tyr	Cys	Ile	Asn				
305					310					315				320					
Ser	Ala	Ala	Leu	Arg	Phe	Ile	Pro	Leu	Lys	Asp	Met	Glu	Lys	Glu	Gly				
			325					330						335					
Tyr	Gly	Glu	Phe	Ile	Pro	Tyr	Ile	Lys	Lys	Gly	Glu	Leu	Lys	Lys	Tyr				
		340					345					350							
Ile	Asn	Asp	Lys	Lys	Ser	His													
		355																	

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 898 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...845
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

TTATTTCTTA TTATTGTAAG GATTTAGGCT ATTGAACTTT AGGAGTTTTA ATG ATA	56
Met Ile	
1	
TTA AGA GCG AGT GTG TTG AGC GCG TTA CTT CTT GTA GGC TTA GGG GCA	104
Leu Arg Ala Ser Val Leu Ser Ala Leu Leu Leu Val Gly Leu Gly Ala	
5 10 15	
GCC CCT AAA CAT TCA GTT TCA GCT AAT GAC AAA CGG ATG CAG GAT AAT	152
Ala Pro Lys His Ser Val Ser Ala Asn Asp Lys Arg Met Gln Asp Asn	
20 25 30	
TTA GTG AGC GTG ATT GAA AAA CAG ACC AAT AAA AAG GTG CGT ATT TTA	200

Leu	Val	Ser	Val	Ile	Glu	Lys	Gln	Thr	Asn	Lys	Lys	Val	Arg	Ile	Leu	
35					40					45					50	
GAA	ATC	AAA	CCT	TTA	AAA	TCT	AGC	CAG	GAT	TTA	AAA	ATG	GTC	GTT	ATT	248
Glu	Ile	Lys	Pro	Leu	Lys	Ser	Ser	Gln	Asp	Leu	Lys	Met	Val	Val	Ile	
				55					60					65		
GAA	GAT	CCG	GAC	ACT	AAA	TAC	AAT	ATC	CCG	CTT	GTG	GTG	AGT	AAG	GAT	296
Glu	Asp	Pro	Asp	Thr	Lys	Tyr	Asn	Ile	Pro	Leu	Val	Val	Ser	Lys	Asp	
			70					75					80			
GGT	AAT	TTA	ATC	ATA	GGG	CTT	AGC	AAC	ATA	TTC	TTT	AGC	AAT	AAA	AGC	344
Gly	Asn	Leu	Ile	Ile	Gly	Leu	Ser	Asn	Ile	Phe	Phe	Ser	Asn	Lys	Ser	
		85					90					95				
GAT	GAT	GTG	CAA	TTA	GTT	GCA	GAA	ACC	AAT	CAA	AAA	GTT	CAA	GCT	CTT	392
Asp	Asp	Val	Gln	Leu	Val	Ala	Glu	Thr	Asn	Gln	Lys	Val	Gln	Ala	Leu	
	100					105					110					
AAC	GCC	ACC	CAA	CAA	AAT	AGC	GCG	AAA	TTG	AAC	GCT	ATT	TTT	AAT	GAA	440
Asn	Ala	Thr	Gln	Gln	Asn	Ser	Ala	Lys	Leu	Asn	Ala	Ile	Phe	Asn	Glu	
	115				120					125					130	
ATA	CCG	GCT	GAT	TAT	GCG	ATA	GAG	TTG	CCC	TCT	ACT	AAC	GCT	GCA	AAT	488
Ile	Pro	Ala	Asp	Tyr	Ala	Ile	Glu	Leu	Pro	Ser	Thr	Asn	Ala	Ala	Asn	
				135					140					145		
AAG	GAT	AAA	ATC	CTT	TAT	ATT	GTC	TCT	GAT	CCC	ATG	TGC	CCA	CAT	TGC	536
Lys	Asp	Lys	Ile	Leu	Tyr	Ile	Val	Ser	Asp	Pro	Met	Cys	Pro	His	Cys	
			150					155					160			
CAA	AAA	GAG	CTC	ACT	AAA	CTT	AGG	GAT	CAT	TTA	AAA	GAA	AAC	ACC	GTG	584
Gln	Lys	Glu	Leu	Thr	Lys	Leu	Arg	Asp	His	Leu	Lys	Glu	Asn	Thr	Val	
		165					170					175				
AGA	ATG	GTC	GTG	GTG	GGG	TGG	CTT	GGG	GTC	AAT	TCA	GCT	AAA	AAA	GCG	632
Arg	Met	Val	Val	Val	Gly	Trp	Leu	Gly	Val	Asn	Ser	Ala	Lys	Lys	Ala	
	180					185					190					
GCT	TTA	ATC	CAA	GAA	GAA	ATG	GCG	AAA	GCT	AGG	GCT	AGG	GGA	GCG	AGC	680
Ala	Leu	Ile	Gln	Glu	Glu	Met	Ala	Lys	Ala	Arg	Ala	Arg	Gly	Ala	Ser	
	195				200					205					210	
GTG	GAA	GAT	AAG	ATC	TCT	ATT	CTT	GAA	AAG	ATT	TAT	TCC	ACC	CAA	TAC	728
Val	Glu	Asp	Lys	Ile	Ser	Ile	Leu	Glu	Lys	Ile	Tyr	Ser	Thr	Gln	Tyr	
				215					220					225		
GAT	ATT	AAC	GCT	CAA	AAA	GAG	CCT	GAA	GAT	TTA	CGC	ACT	AAA	GTG	GAA	776
Asp	Ile	Asn	Ala	Gln	Lys	Glu	Pro	Glu	Asp	Leu	Arg	Thr	Lys	Val	Glu	
			230					235					240			
AAT	ACC	ACT	AAA	AAG	ATT	TTT	GAA	TCT	GGC	GTG	ATT	AAG	GGT	GTG	CCT	824
Asn	Thr	Thr	Lys	Lys	Ile	Phe	Glu	Ser	Gly	Val	Ile	Lys	Gly	Val	Pro	
		245					250					255				
TTC	TTA	TAC	CAT	TAT	AAG	GCA	TGATATAAGG	TTGCTCTCAT	GAAAAAACCC	TATA						879
Phe	Leu	Tyr	His	Tyr	Lys	Ala										
	260					265										

GGAAGATTTTC TGATTATGC

898

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

```

Met Ile Leu Arg Ala Ser Val Leu Ser Ala Leu Leu Leu Val Gly Leu
 1             5             10             15
Gly Ala Ala Pro Lys His Ser Val Ser Ala Asn Asp Lys Arg Met Gln
      20             25             30
Asp Asn Leu Val Ser Val Ile Glu Lys Gln Thr Asn Lys Lys Val Arg
      35             40             45
Ile Leu Glu Ile Lys Pro Leu Lys Ser Ser Gln Asp Leu Lys Met Val
 50             55             60
Val Ile Glu Asp Pro Asp Thr Lys Tyr Asn Ile Pro Leu Val Val Ser
 65             70             75             80
Lys Asp Gly Asn Leu Ile Ile Gly Leu Ser Asn Ile Phe Phe Ser Asn
      85             90             95
Lys Ser Asp Asp Val Gln Leu Val Ala Glu Thr Asn Gln Lys Val Gln
      100             105             110
Ala Leu Asn Ala Thr Gln Gln Asn Ser Ala Lys Leu Asn Ala Ile Phe
      115             120             125
Asn Glu Ile Pro Ala Asp Tyr Ala Ile Glu Leu Pro Ser Thr Asn Ala
 130             135             140
Ala Asn Lys Asp Lys Ile Leu Tyr Ile Val Ser Asp Pro Met Cys Pro
 145             150             155             160
His Cys Gln Lys Glu Leu Thr Lys Leu Arg Asp His Leu Lys Glu Asn
      165             170             175
Thr Val Arg Met Val Val Val Gly Trp Leu Gly Val Asn Ser Ala Lys
      180             185             190
Lys Ala Ala Leu Ile Gln Glu Glu Met Ala Lys Ala Arg Ala Arg Gly
      195             200             205
Ala Ser Val Glu Asp Lys Ile Ser Ile Leu Glu Lys Ile Tyr Ser Thr
 210             215             220
Gln Tyr Asp Ile Asn Ala Gln Lys Glu Pro Glu Asp Leu Arg Thr Lys
 225             230             235             240
Val Glu Asn Thr Thr Lys Lys Ile Phe Glu Ser Gly Val Ile Lys Gly
      245             250             255
Val Pro Phe Leu Tyr His Tyr Lys Ala
      260             265

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(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...707
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

TCTTTTAGAC	GAAAACGCCA	TGATTTTACA	CTGGCAAAAA	GAGGGCTTGC	ATG CGT	56
					Met Arg	
					1	
AAA ATC TTG TTA TTG GGT CTG ATT TTA CAA GCG CTC TTC AGC GAA GAA	104					
Lys Ile Leu Leu Leu Gly Leu Ile Leu Gln Ala Leu Phe Ser Glu Glu						
5 10 15						
GCC GCG CAA GAA TTG TTG CAA TGC TCT GCG ATT TTT GAA TCT AAA AAA	152					
Ala Ala Gln Glu Leu Leu Gln Cys Ser Ala Ile Phe Glu Ser Lys Lys						
20 25 30						
GCC GAA TTG AAA GAC GAT TTG CGC CGA TTG AGT GAA AAA GAG CAG TCT	200					
Ala Glu Leu Lys Asp Asp Leu Arg Arg Leu Ser Glu Lys Glu Gln Ser						
35 40 45 50						
TTA AGG ATC TTG CAA ACC GAA AAC GCC CGC CTT TTA GAT GAA AAA ACC	248					
Leu Arg Ile Leu Gln Thr Glu Asn Ala Arg Leu Leu Asp Glu Lys Thr						
55 60 65						
GAT CTG TTG AAC CAA AAA GAA AAA GAA GTG GAA GAA AAA CTG AAA AAT	296					
Asp Leu Leu Asn Gln Lys Glu Lys Glu Val Glu Glu Lys Leu Lys Asn						
70 75 80						
TTA GCC GCT AAA GAA GAA GCC TTT AAA ACC TTA CAA ACG GAA GAA AAA	344					
Leu Ala Ala Lys Glu Glu Ala Phe Lys Thr Leu Gln Thr Glu Glu Lys						
85 90 95						
AAA CGC CTT AAA AAT TTG ATA GAA GAA AAC GAA GGC ATT TTA AGA GAA	392					
Lys Arg Leu Lys Asn Leu Ile Glu Glu Asn Glu Gly Ile Leu Arg Glu						
100 105 110						
ATC AAG CAG GCT AAA GAC AGC AAG ATT GGC GAG ACT TAT TCT AAA ATG	440					
Ile Lys Gln Ala Lys Asp Ser Lys Ile Gly Glu Thr Tyr Ser Lys Met						
115 120 125 130						
AAA GAT TCT AAA TCG GCT CTG ATT TTA GAA AAT TTA CCC ACT CAA AAC	488					
Lys Asp Ser Lys Ser Ala Leu Ile Leu Glu Asn Leu Pro Thr Gln Asn						
135 140 145						
GCA TTA GAA ATT TTA ATG GCG CTA AAA CCC CAA GAA CTC GGT AAA ATT	536					
Ala Leu Glu Ile Leu Met Ala Leu Lys Pro Gln Glu Leu Gly Lys Ile						
150 155 160						
TTA GCC AAA ATG GAT CCT AAA AAA GCG GCG GCT TTG ACA GAG TTG TGG	584					
Leu Ala Lys Met Asp Pro Lys Lys Ala Ala Ala Leu Thr Glu Leu Trp						
165 170 175						

CAA AAA CCC CCA AAA GAA AAT AAA GAA ATC CCA AAA ACC ACA GCA CCC 632
 Gln Lys Pro Pro Lys Glu Asn Lys Glu Ile Pro Lys Thr Thr Ala Pro
 180 185 190

ACG CCC CCT ATA GCA CCC ACG CCT TTA AAA GAG CCG ATG ATA AAA GAT 680
 Thr Pro Pro Ile Ala Pro Thr Pro Leu Lys Glu Pro Met Ile Lys Asp
 195 200 205 210

CCT AAC ACC AAA GAG CCT GCA GGG GTA TGATGTTTAT TGTAGCGGTT TTGATGC 734
 Pro Asn Thr Lys Glu Pro Ala Gly Val
 215

TGGCGTTTTT AATCTTTGTC CATGAA 760

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Met Arg Lys Ile Leu Leu Leu Gly Leu Ile Leu Gln Ala Leu Phe Ser
 1 5 10 15
 Glu Glu Ala Ala Gln Glu Leu Leu Gln Cys Ser Ala Ile Phe Glu Ser
 20 25 30
 Lys Lys Ala Glu Leu Lys Asp Asp Leu Arg Arg Leu Ser Glu Lys Glu
 35 40 45
 Gln Ser Leu Arg Ile Leu Gln Thr Glu Asn Ala Arg Leu Leu Asp Glu
 50 55 60
 Lys Thr Asp Leu Leu Asn Gln Lys Glu Lys Glu Val Glu Glu Lys Leu
 65 70 75 80
 Lys Asn Leu Ala Ala Lys Glu Glu Ala Phe Lys Thr Leu Gln Thr Glu
 85 90 95
 Glu Lys Lys Arg Leu Lys Asn Leu Ile Glu Glu Asn Glu Gly Ile Leu
 100 105 110
 Arg Glu Ile Lys Gln Ala Lys Asp Ser Lys Ile Gly Glu Thr Tyr Ser
 115 120 125
 Lys Met Lys Asp Ser Lys Ser Ala Leu Ile Leu Glu Asn Leu Pro Thr
 130 135 140
 Gln Asn Ala Leu Glu Ile Leu Met Ala Leu Lys Pro Gln Glu Leu Gly
 145 150 155 160
 Lys Ile Leu Ala Lys Met Asp Pro Lys Lys Ala Ala Ala Leu Thr Glu
 165 170 175
 Leu Trp Gln Lys Pro Pro Lys Glu Asn Lys Glu Ile Pro Lys Thr Thr
 180 185 190
 Ala Pro Thr Pro Pro Ile Ala Pro Thr Pro Leu Lys Glu Pro Met Ile
 195 200 205
 Lys Asp Pro Asn Thr Lys Glu Pro Ala Gly Val
 210 215

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1393 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...1340
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

CTAAAGTGCG	CTAAAATTCA	CTTCAGTGAT	ACAAAAAAGG	AAATAAAATA	ATG AAT	56
					Met Asn	
					1	
ATT CAA ATA AAG AAA AGG TTT TTA GCA AAT TTG TTG CTT TTT AGC CTG						104
Ile Gln Ile Lys Lys Arg Phe Leu Ala Asn Leu Leu Leu Phe Ser Leu	5	10		15		
TTT TGC CTT AAG GCT GAA ACC CTT TCA GAA GAT CAT CAA ATC CTG TTG						152
Phe Cys Leu Lys Ala Glu Thr Leu Ser Glu Asp His Gln Ile Leu Leu	20	25		30		
AGT TCA GAC GCT TTC CAT AGA GGG GAT TTT GCT GCC GCT CAA AAA GGC						200
Ser Ser Asp Ala Phe His Arg Gly Asp Phe Ala Ala Ala Gln Lys Gly	35	40		45	50	
TAT ATG AAT CTC TAT AAG CAA ACC AAT AAG GTG GTG TAT GCT AAA GAA						248
Tyr Met Asn Leu Tyr Lys Gln Thr Asn Lys Val Val Tyr Ala Lys Glu	55	60		65		
GCG GCC ATT TCA GCG GCG AGC TTA GGG GAT ATT AAA ACC GCT ATG CAT						296
Ala Ala Ile Ser Ala Ala Ser Leu Gly Asp Ile Lys Thr Ala Met His	70	75		80		
TTA GCC ATG CTC TAT CAA AAA ATC ACC AAT AAT CGT AAT GAT GTT TCT						344
Leu Ala Met Leu Tyr Gln Lys Ile Thr Asn Asn Arg Asn Asp Val Ser	85	90		95		
ATC AAT AAG ATT TTA GTG GAT GGC TAT GCG CAA ATG GGG CAG ATT GAT						392
Ile Asn Lys Ile Leu Val Asp Gly Tyr Ala Gln Met Gly Gln Ile Asp	100	105		110		
AAG GCG ATT GAA TTG CTG CAC AAA ATC CGT AAA GAA GAA AAG ACC ATA						440
Lys Ala Ile Glu Leu Leu His Lys Ile Arg Lys Glu Glu Lys Thr Ile	115	120		125	130	
GCC ACA GAC AAT GTG TTA GGG ACT TTG TAT TTG ACT CAA AAG CGT TTG						488
Ala Thr Asp Asn Val Leu Gly Thr Leu Tyr Leu Thr Gln Lys Arg Leu	135	140		145		
GAT AAG GCT TTC CCA TTG TTG AAT AAG TTT TAT AAC CAA GTG CAT GAT						536

Asp	Lys	Ala	Phe	Pro	Leu	Leu	Asn	Lys	Phe	Tyr	Asn	Gln	Val	His	Asp	
			150					155					160			
GAA	GAC	AGC	CTA	GAA	AAA	CTC	ATT	ACG	ATC	TAT	TTT	TTG	CAA	AAT	CGT	584
Glu	Asp	Ser	Leu	Glu	Lys	Leu	Ile	Thr	Ile	Tyr	Phe	Leu	Gln	Asn	Arg	
		165					170					175				
AAA	AAA	GAG	GGC	TTG	GAT	TTG	TTG	CAA	TCT	CAT	ATA	GAC	AGG	TAT	GGT	632
Lys	Lys	Glu	Gly	Leu	Asp	Leu	Leu	Gln	Ser	His	Ile	Asp	Arg	Tyr	Gly	
	180					185					190					
TGC	TCA	GAG	CAA	TTG	TGC	CAA	AAA	GCG	CTC	AAC	ACT	TTC	ACG	CAA	TTT	680
Cys	Ser	Glu	Gln	Leu	Cys	Gln	Lys	Ala	Leu	Asn	Thr	Phe	Thr	Gln	Phe	
195					200					205					210	
AAC	GAG	CTT	GAT	TTG	GCT	AAA	ACG	ACT	TTT	GCT	CGT	TTG	TAT	GAA	AAA	728
Asn	Glu	Leu	Asp	Leu	Ala	Lys	Thr	Thr	Phe	Ala	Arg	Leu	Tyr	Glu	Lys	
				215					220					225		
AAC	CCT	ATT	GTT	CAA	AAT	GCT	CAG	TTT	TAC	ATA	GGG	GTA	TTA	ATC	TTG	776
Asn	Pro	Ile	Val	Gln	Asn	Ala	Gln	Phe	Tyr	Ile	Gly	Val	Leu	Ile	Leu	
			230				235						240			
TTA	AAA	GAG	TTT	GAT	AAG	GCC	CAG	AAA	ATC	GCA	GAA	TTA	TTC	CCT	TTT	824
Leu	Lys	Glu	Phe	Asp	Lys	Ala	Gln	Lys	Ile	Ala	Glu	Leu	Phe	Pro	Phe	
		245					250					255				
GAC	AGG	CGT	TTG	TTG	TTA	GAC	TTA	TAC	ACC	GCA	CAA	AAA	AAA	TTC	GAT	872
Asp	Arg	Arg	Leu	Leu	Leu	Asp	Leu	Tyr	Thr	Ala	Gln	Lys	Lys	Phe	Asp	
	260					265					270					
CAA	GCT	TCC	AAA	CAA	GCT	TCT	TTG	ATC	TAT	CAA	GAA	AAA	AAA	GAC	CCT	920
Gln	Ala	Ser	Lys	Gln	Ala	Ser	Leu	Ile	Tyr	Gln	Glu	Lys	Lys	Asp	Pro	
275					280					285					290	
AAA	TTC	TTA	GGA	TTA	GAG	GCC	ATT	TAT	CAT	TAT	GAA	AGC	TTG	AGT	GCG	968
Lys	Phe	Leu	Gly	Leu	Glu	Ala	Ile	Tyr	His	Tyr	Glu	Ser	Leu	Ser	Ala	
				295				300						305		
AAT	AAG	AAA	AAG	CTC	ACC	AAA	GAA	GAG	ATG	TTG	CCT	ATC	ATT	CAA	AAA	1016
Asn	Lys	Lys	Lys	Leu	Thr	Lys	Glu	Glu	Met	Leu	Pro	Ile	Ile	Gln	Lys	
			310					315					320			
TTA	GAG	CAA	GCC	ACC	AAA	GAG	CGC	CAA	GCA	TGG	CTC	GCT	AAA	ACC	AAA	1064
Leu	Glu	Gln	Ala	Thr	Lys	Glu	Arg	Gln	Ala	Trp	Leu	Ala	Lys	Thr	Lys	
		325					330					335				
GAT	AAA	GAA	GAC	GCG	CAA	GAC	GCT	TTC	TTT	TAT	AAT	TTT	TTA	GGG	TAT	1112
Asp	Lys	Glu	Asp	Ala	Gln	Asp	Ala	Phe	Phe	Tyr	Asn	Phe	Leu	Gly	Tyr	
	340					345					350					
TCC	TTA	ATA	GAT	TAT	GAC	ATG	GAT	ATT	AAA	AGG	GGC	ATG	GAT	TTT	GTG	1160
Ser	Leu	Ile	Asp	Tyr	Asp	Met	Asp	Ile	Lys	Arg	Gly	Met	Asp	Phe	Val	
355					360					365					370	
AGG	AAA	GCC	TTA	GCG	TTG	GAT	TCT	GGA	TCA	GTG	CTT	TAT	TTG	GAT	TCT	1208
Arg	Lys	Ala	Leu	Ala	Leu	Asp	Ser	Gly	Ser	Val	Leu	Tyr	Leu	Asp	Ser	
				375					380					385		

TTA GCA TGG GGT TAT TAC AAA TTA GGG AAT TGT TTG GAA GCT AAA AAA 1256
 Leu Ala Trp Gly Tyr Tyr Lys Leu Gly Asn Cys Leu Glu Ala Lys Lys
 390 395 400

ATC TTT TCT AGC ATC GCT AAA GAG TCT ATC CAA GCC GAA CCT GAA TTG 1304
 Ile Phe Ser Ser Ile Ala Lys Glu Ser Ile Gln Ala Glu Pro Glu Leu
 405 410 415

AAA GAA CAC AAT AAA ATC ATT CAA GAA TGC AAG AAA TAGGGATTTT AGAAAA 1356
 Lys Glu His Asn Lys Ile Ile Gln Glu Cys Lys Lys
 420 425 430

TTTACAAAAA AGCTTAGCCT TAAAAGAGGG CATGCTT 1393

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Met Asn Ile Gln Ile Lys Lys Arg Phe Leu Ala Asn Leu Leu Leu Phe
 1 5 10 15
 Ser Leu Phe Cys Leu Lys Ala Glu Thr Leu Ser Glu Asp His Gln Ile
 20 25 30
 Leu Leu Ser Ser Asp Ala Phe His Arg Gly Asp Phe Ala Ala Ala Gln
 35 40 45
 Lys Gly Tyr Met Asn Leu Tyr Lys Gln Thr Asn Lys Val Val Tyr Ala
 50 55 60
 Lys Glu Ala Ala Ile Ser Ala Ala Ser Leu Gly Asp Ile Lys Thr Ala
 65 70 75 80
 Met His Leu Ala Met Leu Tyr Gln Lys Ile Thr Asn Asn Arg Asn Asp
 85 90 95
 Val Ser Ile Asn Lys Ile Leu Val Asp Gly Tyr Ala Gln Met Gly Gln
 100 105 110
 Ile Asp Lys Ala Ile Glu Leu Leu His Lys Ile Arg Lys Glu Glu Lys
 115 120 125
 Thr Ile Ala Thr Asp Asn Val Leu Gly Thr Leu Tyr Leu Thr Gln Lys
 130 135 140
 Arg Leu Asp Lys Ala Phe Pro Leu Leu Asn Lys Phe Tyr Asn Gln Val
 145 150 155 160
 His Asp Glu Asp Ser Leu Glu Lys Leu Ile Thr Ile Tyr Phe Leu Gln
 165 170 175
 Asn Arg Lys Lys Glu Gly Leu Asp Leu Leu Gln Ser His Ile Asp Arg
 180 185 190
 Tyr Gly Cys Ser Glu Gln Leu Cys Gln Lys Ala Leu Asn Thr Phe Thr
 195 200 205
 Gln Phe Asn Glu Leu Asp Leu Ala Lys Thr Thr Phe Ala Arg Leu Tyr
 210 215 220
 Glu Lys Asn Pro Ile Val Gln Asn Ala Gln Phe Tyr Ile Gly Val Leu
 225 230 235 240
 Ile Leu Leu Lys Glu Phe Asp Lys Ala Gln Lys Ile Ala Glu Leu Phe

				245					250					255			
Pro	Phe	Asp	Arg	Arg	Leu	Leu	Leu	Asp	Leu	Tyr	Thr	Ala	Gln	Lys	Lys		
			260					265					270				
Phe	Asp	Gln	Ala	Ser	Lys	Gln	Ala	Ser	Leu	Ile	Tyr	Gln	Glu	Lys	Lys		
		275					280					285					
Asp	Pro	Lys	Phe	Leu	Gly	Leu	Glu	Ala	Ile	Tyr	His	Tyr	Glu	Ser	Leu		
	290					295				300							
Ser	Ala	Asn	Lys	Lys	Lys	Leu	Thr	Lys	Glu	Glu	Met	Leu	Pro	Ile	Ile		
305					310					315					320		
Gln	Lys	Leu	Glu	Gln	Ala	Thr	Lys	Glu	Arg	Gln	Ala	Trp	Leu	Ala	Lys		
				325				330						335			
Thr	Lys	Asp	Lys	Glu	Asp	Ala	Gln	Asp	Ala	Phe	Phe	Tyr	Asn	Phe	Leu		
		340						345					350				
Gly	Tyr	Ser	Leu	Ile	Asp	Tyr	Asp	Met	Asp	Ile	Lys	Arg	Gly	Met	Asp		
		355					360					365					
Phe	Val	Arg	Lys	Ala	Leu	Ala	Leu	Asp	Ser	Gly	Ser	Val	Leu	Tyr	Leu		
	370					375					380						
Asp	Ser	Leu	Ala	Trp	Gly	Tyr	Tyr	Lys	Leu	Gly	Asn	Cys	Leu	Glu	Ala		
385					390					395					400		
Lys	Lys	Ile	Phe	Ser	Ser	Ile	Ala	Lys	Glu	Ser	Ile	Gln	Ala	Glu	Pro		
			405					410					415				
Glu	Leu	Lys	Glu	His	Asn	Lys	Ile	Ile	Gln	Glu	Cys	Lys	Lys				
			420					425					430				

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1090 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1037
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

TTACCCTAAA	ACGCTATTTT	TAAAATAATC	CATTAAAATA	AAGGCGAGGA	ATG AAA	56
					Met Lys	
					1	
AGA TTT GTT TTG TTT TTA TTG TTC ATG TGC GTT TGC GTT CAA GCT TAC						104
Arg Phe Val Leu Phe Leu Leu Phe Met Cys Val Cys Val Gln Ala Tyr						
	5		10		15	
GCC GAG CAA GAT TAC TTT TTT AGG GAT TTT AAA TCT AGA GAT TTG CCC						152
Ala Glu Gln Asp Tyr Phe Phe Arg Asp Phe Lys Ser Arg Asp Leu Pro						
	20		25		30	
CAA AAA CTC CAT CTT GAT AAA AAG CTC TCC CAA ACA ATA CAG CCA TGC						200
Gln Lys Leu His Leu Asp Lys Lys Leu Ser Gln Thr Ile Gln Pro Cys						
	35		40		45	50

ATG CAA CTT AAC GCA TCA AAA CAC TAC ACT TCT ACC GGG GTT AGA GAG	248
Met Gln Leu Asn Ala Ser Lys His Tyr Thr Ser Thr Gly Val Arg Glu	
55 60 65	
CCT GAT AAA TGC ACA AAG AGT TTT AAA AAA TCC GCT CTC ATG TCC TAT	296
Pro Asp Lys Cys Thr Lys Ser Phe Lys Lys Ser Ala Leu Met Ser Tyr	
70 75 80	
GAC TTA GCG CTA GGT TAT TTG GTG AGT AAG AAT AAG CAA TAC GGC TTA	344
Asp Leu Ala Leu Gly Tyr Leu Val Ser Lys Asn Lys Gln Tyr Gly Leu	
85 90 95	
AAG GCT ATA GAA ATT TTA AAC GCT TGG GCT AAA GAG CTT CAA AGC GTG	392
Lys Ala Ile Glu Ile Leu Asn Ala Trp Ala Lys Glu Leu Gln Ser Val	
100 105 110	
GAT ACT TAT CAG AGC GAG GAT AAT ATC AAT TTT TAC ATG CCT TAT ATG	440
Asp Thr Tyr Gln Ser Glu Asp Asn Ile Asn Phe Tyr Met Pro Tyr Met	
115 120 125 130	
AAC ATG GCT TAT TGG TTT GTC AAA AAG GCG TTT CCT AGC CCA GAA TAT	488
Asn Met Ala Tyr Trp Phe Val Lys Lys Ala Phe Pro Ser Pro Glu Tyr	
135 140 145	
GAA GAT TTC ATT AAG CGG ATG CGC CAG TAT TCT CAA TCA GCT CTT AAC	536
Glu Asp Phe Ile Lys Arg Met Arg Gln Tyr Ser Gln Ser Ala Leu Asn	
150 155 160	
ACT AAC CAT GGG GCG TGG GGC ATT CTT TTT GAT GTG AGT TCT GCG CTA	584
Thr Asn His Gly Ala Trp Gly Ile Leu Phe Asp Val Ser Ser Ala Leu	
165 170 175	
GCG TTA GAC GAT AAT GCC CTT TTG CAC AAT AGC GCT AAT CGG TGG CAG	632
Ala Leu Asp Asp Asn Ala Leu Leu His Asn Ser Ala Asn Arg Trp Gln	
180 185 190	
GAG TGG GTG TTT AAA GCC ATA GAT GAG AAT GGG GTT ATT GNT AGC GCG	680
Glu Trp Val Phe Lys Ala Ile Asp Glu Asn Gly Val Ile Xaa Ser Ala	
195 200 205 210	
ATC ACT AGG AGC GAT ACG AGC GAT TAT CAT GGC GGC CCT ACA AAG GGC	728
Ile Thr Arg Ser Asp Thr Ser Asp Tyr His Gly Gly Pro Thr Lys Gly	
215 220 225	
ATT AAG GGG ATA GCT TAT ACC AAT TTC GCG CTT CTT GCG CTA ACC ATA	776
Ile Lys Gly Ile Ala Tyr Thr Asn Phe Ala Leu Leu Ala Leu Thr Ile	
230 235 240	
TCA GGC GAA TTG CTT TTT GAG AAC GGG TAT GAT TTG TGG GGT AGT GGA	824
Ser Gly Glu Leu Leu Phe Glu Asn Gly Tyr Asp Leu Trp Gly Ser Gly	
245 250 255	
GCT GGG AAA AGG CTC TCT GTG GCG TAT AAC AAA GTT GCA ACA TGG ATT	872
Ala Gly Lys Arg Leu Ser Val Ala Tyr Asn Lys Val Ala Thr Trp Ile	
260 265 270	
TTA AAC CCT GAA ACT TTC CCT TAT TTC CAG CCT AAC CTT ATC GGG GTG	920
Leu Asn Pro Glu Thr Phe Pro Tyr Phe Gln Pro Asn Leu Ile Gly Val	

275		280		285		290	
CAT AAC AAC GCC TAT TTC ATT ATT TTA GCC AAG CAT TAT TCT AGC CCT							968
His Asn Asn Ala Tyr Phe Ile Ile Leu Ala Lys His Tyr Ser Ser Pro							
	295			300		305	
AGT GCA AAT GAG CTT TTA AAG CAA GGC GAT TTA CAC GAA GAT GGT TTC							1016
Ser Ala Asn Glu Leu Leu Lys Gln Gly Asp Leu His Glu Asp Gly Phe							
	310			315		320	
AGG CTG AAA CTC CGA TCG CCA TGAATTTTTC TGTATCCAAG GTTAGCCTTA AGGA							1071
Arg Leu Lys Leu Arg Ser Pro							
	325						
TGGCCATGCG CTTTAACCT							1090

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Met	Lys	Arg	Phe	Val	Leu	Phe	Leu	Leu	Phe	Met	Cys	Val	Cys	Val	Gln
1				5					10					15	
Ala	Tyr	Ala	Glu	Gln	Asp	Tyr	Phe	Phe	Arg	Asp	Phe	Lys	Ser	Arg	Asp
		20						25					30		
Leu	Pro	Gln	Lys	Leu	His	Leu	Asp	Lys	Lys	Leu	Ser	Gln	Thr	Ile	Gln
		35					40					45			
Pro	Cys	Met	Gln	Leu	Asn	Ala	Ser	Lys	His	Tyr	Thr	Ser	Thr	Gly	Val
	50					55				60					
Arg	Glu	Pro	Asp	Lys	Cys	Thr	Lys	Ser	Phe	Lys	Lys	Ser	Ala	Leu	Met
65					70				75					80	
Ser	Tyr	Asp	Leu	Ala	Leu	Gly	Tyr	Leu	Val	Ser	Lys	Asn	Lys	Gln	Tyr
			85					90					95		
Gly	Leu	Lys	Ala	Ile	Glu	Ile	Leu	Asn	Ala	Trp	Ala	Lys	Glu	Leu	Gln
		100					105					110			
Ser	Val	Asp	Thr	Tyr	Gln	Ser	Glu	Asp	Asn	Ile	Asn	Phe	Tyr	Met	Pro
	115					120					125				
Tyr	Met	Asn	Met	Ala	Tyr	Trp	Phe	Val	Lys	Lys	Ala	Phe	Pro	Ser	Pro
	130					135					140				
Glu	Tyr	Glu	Asp	Phe	Ile	Lys	Arg	Met	Arg	Gln	Tyr	Ser	Gln	Ser	Ala
145					150				155					160	
Leu	Asn	Thr	Asn	His	Gly	Ala	Trp	Gly	Ile	Leu	Phe	Asp	Val	Ser	Ser
			165					170					175		
Ala	Leu	Ala	Leu	Asp	Asp	Asn	Ala	Leu	Leu	His	Asn	Ser	Ala	Asn	Arg
		180					185					190			
Trp	Gln	Glu	Trp	Val	Phe	Lys	Ala	Ile	Asp	Glu	Asn	Gly	Val	Ile	Xaa
	195					200					205				
Ser	Ala	Ile	Thr	Arg	Ser	Asp	Thr	Ser	Asp	Tyr	His	Gly	Gly	Pro	Thr
	210					215				220					
Lys	Gly	Ile	Lys	Gly	Ile	Ala	Tyr	Thr	Asn	Phe	Ala	Leu	Leu	Ala	Leu

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225          230          235          240
Thr Ile Ser Gly Glu Leu Leu Phe Glu Asn Gly Tyr Asp Leu Trp Gly
          245          250          255
Ser Gly Ala Gly Lys Arg Leu Ser Val Ala Tyr Asn Lys Val Ala Thr
          260          265          270
Trp Ile Leu Asn Pro Glu Thr Phe Pro Tyr Phe Gln Pro Asn Leu Ile
          275          280          285
Gly Val His Asn Asn Ala Tyr Phe Ile Ile Leu Ala Lys His Tyr Ser
          290          295          300
Ser Pro Ser Ala Asn Glu Leu Leu Lys Gln Gly Asp Leu His Glu Asp
305          310          315          320
Gly Phe Arg Leu Lys Leu Arg Ser Pro
          325

```

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...320
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

```

TTAACGATCG CAAAAGCCGA TGAAAGTTTT GATGAAATCA TAAAAGGTGT  GTG AAT  56
                                     Val Asn
                                     1

TTT TTG AAA AAG CCA AAG TAT TAT AAA TTC ATA GAG GGG GCG AAT TAT  104
Phe Leu Lys Lys Pro Lys Tyr Tyr Lys Phe Ile Glu Gly Ala Asn Tyr
      5                      10                      15

TTG AGC TTG GGG CTT TCT ATG GTG GTA GCG ATC CTT ATG GGC GTG GCT  152
Leu Ser Leu Gly Leu Ser Met Val Val Ala Ile Leu Met Gly Val Ala
      20                      25                      30

ATA GGC TAT GGG CTT AAA AAA CTC ACT CAT ATT TCG TGG CTT TTT TGG  200
Ile Gly Tyr Gly Leu Lys Lys Leu Thr His Ile Ser Trp Leu Phe Trp
      35                      40                      45                      50

CTT GGG GTT ATT TGG GGC GTC TTA GCG AGC TTT CTC AAT GTC TAT AAA  248
Leu Gly Val Ile Trp Gly Val Leu Ala Ser Phe Leu Asn Val Tyr Lys
      55                      60                      65

GCT TAT AAA AAC ATG CAA AAA GAC TAT GAA GAA CTA GCC AAA GAC CCT  296
Ala Tyr Lys Asn Met Gln Lys Asp Tyr Glu Glu Leu Ala Lys Asp Pro
      70                      75                      80

AAA TAC ACA CAA AAT AAA ACA AAA TAAATCCAAT CAAATCCCAT GTGCCAAATC  350
Lys Tyr Thr Gln Asn Lys Thr Lys

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85

90

CAATGCTTGC TTATTTTACT TTC

373

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Val	Asn	Phe	Leu	Lys	Lys	Pro	Lys	Tyr	Tyr	Lys	Phe	Ile	Glu	Gly	Ala	
1				5					10					15		
Asn	Tyr	Leu	Ser	Leu	Gly	Leu	Ser	Met	Val	Val	Ala	Ile	Leu	Met	Gly	
			20					25					30			
Val	Ala	Ile	Gly	Tyr	Gly	Leu	Lys	Lys	Leu	Thr	His	Ile	Ser	Trp	Leu	
		35				40						45				
Phe	Trp	Leu	Gly	Val	Ile	Trp	Gly	Val	Leu	Ala	Ser	Phe	Leu	Asn	Val	
	50				55						60					
Tyr	Lys	Ala	Tyr	Lys	Asn	Met	Gln	Lys	Asp	Tyr	Glu	Glu	Leu	Ala	Lys	
65				70					75						80	
Asp	Pro	Lys	Tyr	Thr	Gln	Asn	Lys	Thr	Lys							
			85						90							

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...590
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

TTGGTTGGTT	GTTTTTATCA	TAGAGTGTA	TTTAAAATAA	GGATCATTTG	ATG TTA	56
					Met Leu	
					1	
AAC AAG TTT	AAA AAA ATC	GTT GGC GTT	AGT GTG TTA	GTG GGC TGT	TTA	104
Asn Lys Phe	Lys Lys Ile	Val Gly Val	Ser Val Leu	Val Gly Cys	Leu	
	5		10		15	
GGG GTT TTG	CAA GCT AAA	AAC AGC TTA	TTT GTC TTA	CCT TAT GAG	CAA	152

Gly	Val	Leu	Gln	Ala	Lys	Asn	Ser	Leu	Phe	Val	Leu	Pro	Tyr	Glu	Gln		
20						25					30						
AAA	GAC	GCT	CTC	AAT	TCT	TTA	GTT	TCT	GGC	ATT	AGT	AAC	GCC	AGA	GAG	200	
Lys	Asp	Ala	Leu	Asn	Ser	Leu	Val	Ser	Gly	Ile	Ser	Asn	Ala	Arg	Glu		
35				40					45						50		
AGC	GTG	AAA	ATC	GCT	ATC	TAT	AGT	TTC	ACG	CAC	AGA	GAT	ATT	GCA	AGA	248	
Ser	Val	Lys	Ile	Ala	Ile	Tyr	Ser	Phe	Thr	His	Arg	Asp	Ile	Ala	Arg		
				55					60					65			
GCG	ATT	AAA	AGC	GTA	GCG	AGT	AGG	GGG	ATT	AAG	GTG	CAA	ATC	ATT	TAT	296	
Ala	Ile	Lys	Ser	Val	Ala	Ser	Arg	Gly	Ile	Lys	Val	Gln	Ile	Ile	Tyr		
			70					75					80				
GAT	TAT	GAA	AGC	AAT	CAT	CAT	AAC	AAG	CAA	TCC	ACT	ATT	GGC	TAT	CTG	344	
Asp	Tyr	Glu	Ser	Asn	His	His	Asn	Lys	Gln	Ser	Thr	Ile	Gly	Tyr	Leu		
		85					90					95					
GAC	AAA	TAC	CCT	AAC	ACG	AAA	GTG	TGC	TTA	TTG	AAA	GGG	CTT	AAG	GCT	392	
Asp	Lys	Tyr	Pro	Asn	Thr	Lys	Val	Cys	Leu	Leu	Lys	Gly	Leu	Lys	Ala		
	100					105						110					
AAA	AAC	GGG	AAT	TAT	TAC	GGC	ATC	ATG	CAC	CAA	AAA	GTA	GCG	ATC	ATT	440	
Lys	Asn	Gly	Asn	Tyr	Tyr	Gly	Ile	Met	His	Gln	Lys	Val	Ala	Ile	Ile		
	115					120				125					130		
GAT	GAT	AAG	ATC	GTG	TTT	TTA	GGC	TCA	GCG	AAT	TGG	AGC	AAA	AAC	GCT	488	
Asp	Asp	Lys	Ile	Val	Phe	Leu	Gly	Ser	Ala	Asn	Trp	Ser	Lys	Asn	Ala		
				135					140					145			
TTT	GAA	AAC	AAT	TAT	GAA	GTG	CTT	TTA	AAA	ACC	GAT	GAC	ACA	GAA	ACG	536	
Phe	Glu	Asn	Asn	Tyr	Glu	Val	Leu	Leu	Lys	Thr	Asp	Asp	Thr	Glu	Thr		
			150					155					160				
ATC	CTC	AAA	GCC	AAG	AGC	TAT	TAC	CAA	AAG	ATG	TTA	GGG	AGT	TGC	GTT	584	
Ile	Leu	Lys	Ala	Lys	Ser	Tyr	Tyr	Gln	Lys	Met	Leu	Gly	Ser	Cys	Val		
		165					170					175					
GGG	TTT	TAAAAGCCCT	TTAGAAGTGG	TAATTATACC	CCACATAAAA	GGCAAAGACC	CT									642	
Gly	Phe																
	180																
A																	643

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

```

Met Leu Asn Lys Phe Lys Lys Ile Val Gly Val Ser Val Leu Val Gly
 1          5          10          15
Cys Leu Gly Val Leu Gln Ala Lys Asn Ser Leu Phe Val Leu Pro Tyr
      20          25          30
Glu Gln Lys Asp Ala Leu Asn Ser Leu Val Ser Gly Ile Ser Asn Ala
      35          40          45
Arg Glu Ser Val Lys Ile Ala Ile Tyr Ser Phe Thr His Arg Asp Ile
      50          55          60
Ala Arg Ala Ile Lys Ser Val Ala Ser Arg Gly Ile Lys Val Gln Ile
      65          70          75          80
Ile Tyr Asp Tyr Glu Ser Asn His His Asn Lys Gln Ser Thr Ile Gly
      85          90          95
Tyr Leu Asp Lys Tyr Pro Asn Thr Lys Val Cys Leu Leu Lys Gly Leu
      100          105          110
Lys Ala Lys Asn Gly Asn Tyr Tyr Gly Ile Met His Gln Lys Val Ala
      115          120          125
Ile Ile Asp Asp Lys Ile Val Phe Leu Gly Ser Ala Asn Trp Ser Lys
      130          135          140
Asn Ala Phe Glu Asn Asn Tyr Glu Val Leu Leu Lys Thr Asp Asp Thr
      145          150          155          160
Glu Thr Ile Leu Lys Ala Lys Ser Tyr Tyr Gln Lys Met Leu Gly Ser
      165          170          175
Cys Val Gly Phe
      180

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(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...761
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

```

TATAAGAGAG TATAATTCAA GGCTTAAAT AACTCAAGTA AGGCTAGTGG ATG AAA      56
                                     Met Lys
                                     1

AAA GCG CTT TAT TTA GGG GCT GTT GCG TTT AGC GTT GCA TTC AGC ATG      104
Lys Ala Leu Tyr Leu Gly Ala Val Ala Phe Ser Val Ala Phe Ser Met
      5          10          15

GCA TCA GCC AAT GAG CCA AAA ATT GAT TTT AAC CCT CCC AAT TAT GTA      152
Ala Ser Ala Asn Glu Pro Lys Ile Asp Phe Asn Pro Pro Asn Tyr Val
      20          25          30

GAA GAA ACC CCC TCT AAA GAA TTT ATC CCT GAA TTG AAC AAG TTA GGG      200
Glu Glu Thr Pro Ser Lys Glu Phe Ile Pro Glu Leu Asn Lys Leu Gly

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35	40	45	50	
AGT TTT GGG CAG GGT GAG CGC CCC TTG TTT GCG GAC AGG AGG GCG				248
Ser Leu Phe Gly Gln Gly Glu Arg Pro Leu Phe Ala Asp Arg Arg Ala	55	60	65	
ATG AAG CCT AAC GAT TTG ATC ACA ATC ATT GTT TCT GAA AAA GCG AGC				296
Met Lys Pro Asn Asp Leu Ile Thr Ile Ile Val Ser Glu Lys Ala Ser	70	75	80	
GCG AAT TAT TCC AGC TCT AAA GAT TAT AAA AGC GCT TCA GGG GGT AAT				344
Ala Asn Tyr Ser Ser Ser Lys Asp Tyr Lys Ser Ala Ser Gly Gly Asn	85	90	95	
TCC ACG CCC CCA AGA CTC ACT TAT AAC GGG CTA GAT GAA AGA AAG AAA				392
Ser Thr Pro Pro Arg Leu Thr Tyr Asn Gly Leu Asp Glu Arg Lys Lys	100	105	110	
AAA GAA GCG GAG TAT TTA GAC GAT AAG AAT AAT TAC AAT TTC ACC AAA				440
Lys Glu Ala Glu Tyr Leu Asp Asp Lys Asn Asn Tyr Asn Phe Thr Lys	115	120	125	130
TCC AGC AAT AAC ACG AAT TTT AAA GGC GGT GGC TCG CAA AAA AAG AGC				488
Ser Ser Asn Asn Thr Asn Phe Lys Gly Gly Gly Ser Gln Lys Lys Ser	135	140	145	
GAA GAT TTA GAG ATT GTG TTG AGC GCT CGA ATC ATT AAG GTG CTA GAA				536
Glu Asp Leu Glu Ile Val Leu Ser Ala Arg Ile Ile Lys Val Leu Glu	150	155	160	
AAC GGG AAT TAT TTC ATC TAT GGG AAT AAG GAA GTG CTA GTG GAT GGG				584
Asn Gly Asn Tyr Phe Ile Tyr Gly Asn Lys Glu Val Leu Val Asp Gly	165	170	175	
GAA AAG CAA ATC CTT AAG GTG AGT GGG GTG ATC CGC CCT TAT GAT ATT				632
Glu Lys Gln Ile Leu Lys Val Ser Gly Val Ile Arg Pro Tyr Asp Ile	180	185	190	
GAA AGG AAT AAC ACC ATC CAA TCC AAG TTT TTA GCC GAC GCT AAG ATT				680
Glu Arg Asn Asn Thr Ile Gln Ser Lys Phe Leu Ala Asp Ala Lys Ile	195	200	205	210
GAA TAC ACG AAT TTA GGG CAT TTG AGC GAT TCC AAT AAG AAG AAA TTC				728
Glu Tyr Thr Asn Leu Gly His Leu Ser Asp Ser Asn Lys Lys Lys Phe	215	220	225	
GCT GCT GAT GCG ATG GAA ACC CAA ATG CCT TAT TAAAAAGAGC AAAGCCTAGC				781
Ala Ala Asp Ala Met Glu Thr Gln Met Pro Tyr	230	235		
ATGAGAGCGA TCGCTATTGT TTTAGCCAGA AGT				814

(2) INFORMATION FOR SEQ ID NO:262:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Met	Lys	Lys	Ala	Leu	Tyr	Leu	Gly	Ala	Val	Ala	Phe	Ser	Val	Ala	Phe
1				5					10					15	
Ser	Met	Ala	Ser	Ala	Asn	Glu	Pro	Lys	Ile	Asp	Phe	Asn	Pro	Pro	Asn
			20					25					30		
Tyr	Val	Glu	Glu	Thr	Pro	Ser	Lys	Glu	Phe	Ile	Pro	Glu	Leu	Asn	Lys
		35					40					45			
Leu	Gly	Ser	Leu	Phe	Gly	Gln	Gly	Glu	Arg	Pro	Leu	Phe	Ala	Asp	Arg
	50					55					60				
Arg	Ala	Met	Lys	Pro	Asn	Asp	Leu	Ile	Thr	Ile	Ile	Val	Ser	Glu	Lys
65					70					75				80	
Ala	Ser	Ala	Asn	Tyr	Ser	Ser	Ser	Lys	Asp	Tyr	Lys	Ser	Ala	Ser	Gly
			85						90					95	
Gly	Asn	Ser	Thr	Pro	Pro	Arg	Leu	Thr	Tyr	Asn	Gly	Leu	Asp	Glu	Arg
			100					105					110		
Lys	Lys	Lys	Glu	Ala	Glu	Tyr	Leu	Asp	Asp	Lys	Asn	Asn	Tyr	Asn	Phe
		115					120					125			
Thr	Lys	Ser	Ser	Asn	Asn	Thr	Asn	Phe	Lys	Gly	Gly	Gly	Ser	Gln	Lys
	130					135					140				
Lys	Ser	Glu	Asp	Leu	Glu	Ile	Val	Leu	Ser	Ala	Arg	Ile	Ile	Lys	Val
145					150					155				160	
Leu	Glu	Asn	Gly	Asn	Tyr	Phe	Ile	Tyr	Gly	Asn	Lys	Glu	Val	Leu	Val
			165						170					175	
Asp	Gly	Glu	Lys	Gln	Ile	Leu	Lys	Val	Ser	Gly	Val	Ile	Arg	Pro	Tyr
			180					185					190		
Asp	Ile	Glu	Arg	Asn	Asn	Thr	Ile	Gln	Ser	Lys	Phe	Leu	Ala	Asp	Ala
	195					200						205			
Lys	Ile	Glu	Tyr	Thr	Asn	Leu	Gly	His	Leu	Ser	Asp	Ser	Asn	Lys	Lys
	210				215						220				
Lys	Phe	Ala	Ala	Asp	Ala	Met	Glu	Thr	Gln	Met	Pro	Tyr			
225				230						235					

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 850 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 51...797

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

TTGGGTAAGA TTAGGAATTG ATTTTAAAGA AAAAGAAAGA AAGGAATTTA ATG AAA

56

Met Lys
1

AAA GGT AGT TTG GCA ATC GTT TTA GGA TCG CTA TTA GCG AGT GGG GCG	104
Lys Gly Ser Leu Ala Ile Val Leu Gly Ser Leu Leu Ala Ser Gly Ala	
5 10 15	
TTT TAT ACG GCT CTA GCT GAT GGA ATG CCT GCA AAA CAG CAG CAC AAT	152
Phe Tyr Thr Ala Leu Ala Asp Gly Met Pro Ala Lys Gln Gln His Asn	
20 25 30	
AAT ACG GGC GAG TCA GTG GAG TTG CAT TTC CAC TAT CCT ATT AAA GGC	200
Asn Thr Gly Glu Ser Val Glu Leu His Phe His Tyr Pro Ile Lys Gly	
35 40 45 50	
AAG CAA GAG CCT AAA AAC AGC CAT TTA GTC GTT TTG ATC GAA CCT AAA	248
Lys Gln Glu Pro Lys Asn Ser His Leu Val Val Leu Ile Glu Pro Lys	
55 60 65	
ATA GAG ATC AAT AAA GTT ATC CCT GAA AGT TAT CAA AAA GAG TTT GAG	296
Ile Glu Ile Asn Lys Val Ile Pro Glu Ser Tyr Gln Lys Glu Phe Glu	
70 75 80	
AAG TCT TTG TTT CTC CAG TTG AGT AGT TTT TTA GAG AGA AAA GGC TAT	344
Lys Ser Leu Phe Leu Gln Leu Ser Ser Phe Leu Glu Arg Lys Gly Tyr	
85 90 95	
AGC GTT TCG CAA TTT AAA GAT GCT AGC GAA ATC CCT CAA GAC ATC AAA	392
Ser Val Ser Gln Phe Lys Asp Ala Ser Glu Ile Pro Gln Asp Ile Lys	
100 105 110	
GAA AAA GCG TTG CTC GTT TTA CGC ATG GAT GGG AAT GTG GCT ATC TTG	440
Glu Lys Ala Leu Leu Val Leu Arg Met Asp Gly Asn Val Ala Ile Leu	
115 120 125 130	
GAA GAT ATT GTA GAA GAG AGC GAT GCG CTT AGC GAA GAA AAA GTG ATA	488
Glu Asp Ile Val Glu Glu Ser Asp Ala Leu Ser Glu Glu Lys Val Ile	
135 140 145	
GAC ATG TCT TCA GGG TAT TTG AAC TTG AAT TTT GTT GAG CCA AAA AGT	536
Asp Met Ser Ser Gly Tyr Leu Asn Leu Asn Phe Val Glu Pro Lys Ser	
150 155 160	
GAA GAT ATT ATC CAT AGT TTT GGT ATT GAT GTT TCA AAG ATT AAG GCT	584
Glu Asp Ile Ile His Ser Phe Gly Ile Asp Val Ser Lys Ile Lys Ala	
165 170 175	
GTG ATT GAA AGA GTG GAA TTG CGG CGC ACC AAT TCT GGA GGT TTT GTC	632
Val Ile Glu Arg Val Glu Leu Arg Arg Thr Asn Ser Gly Gly Phe Val	
180 185 190	
CCC AAA ACT TTT GTG CAT AGG ATT AAG GAA ACC GAT CAT GAT CAA GCC	680
Pro Lys Thr Phe Val His Arg Ile Lys Glu Thr Asp His Asp Gln Ala	
195 200 205 210	
ATT AGA AAA ATC ATG AAT CAA GCC TAT CAC AAA GTG ATG GTG CAT ATT	728
Ile Arg Lys Ile Met Asn Gln Ala Tyr His Lys Val Met Val His Ile	
215 220 225	

ACC AAA GAG TTA AGC AAA AAA CAC ATG GAA CAT TAT GAA AAA GTT TCT 776
 Thr Lys Glu Leu Ser Lys Lys His Met Glu His Tyr Glu Lys Val Ser
 230 235 240

AGT GAA ATG AAA AAA CGA AAG TAGTTTTTAA GAAACGAAAA GCTTAAAAAT CATT 831
 Ser Glu Met Lys Lys Arg Lys
 245

GAGAGCTATT TTTAAAAAA 850

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Met Lys Lys Gly Ser Leu Ala Ile Val Leu Gly Ser Leu Leu Ala Ser
 1 5 10 15
 Gly Ala Phe Tyr Thr Ala Leu Ala Asp Gly Met Pro Ala Lys Gln Gln
 20 25 30
 His Asn Asn Thr Gly Glu Ser Val Glu Leu His Phe His Tyr Pro Ile
 35 40 45
 Lys Gly Lys Gln Glu Pro Lys Asn Ser His Leu Val Val Leu Ile Glu
 50 55 60
 Pro Lys Ile Glu Ile Asn Lys Val Ile Pro Glu Ser Tyr Gln Lys Glu
 65 70 75 80
 Phe Glu Lys Ser Leu Phe Leu Gln Leu Ser Phe Leu Glu Arg Lys
 85 90 95
 Gly Tyr Ser Val Ser Gln Phe Lys Asp Ala Ser Glu Ile Pro Gln Asp
 100 105 110
 Ile Lys Glu Lys Ala Leu Leu Val Leu Arg Met Asp Gly Asn Val Ala
 115 120 125
 Ile Leu Glu Asp Ile Val Glu Glu Ser Asp Ala Leu Ser Glu Glu Lys
 130 135 140
 Val Ile Asp Met Ser Ser Gly Tyr Leu Asn Leu Asn Phe Val Glu Pro
 145 150 155 160
 Lys Ser Glu Asp Ile Ile His Ser Phe Gly Ile Asp Val Ser Lys Ile
 165 170 175
 Lys Ala Val Ile Glu Arg Val Glu Leu Arg Arg Thr Asn Ser Gly Gly
 180 185 190
 Phe Val Pro Lys Thr Phe Val His Arg Ile Lys Glu Thr Asp His Asp
 195 200 205
 Gln Ala Ile Arg Lys Ile Met Asn Gln Ala Tyr His Lys Val Met Val
 210 215 220
 His Ile Thr Lys Glu Leu Ser Lys Lys His Met Glu His Tyr Glu Lys
 225 230 235 240
 Val Ser Ser Glu Met Lys Lys Arg Lys
 245

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...788
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

TACAAATAGG TATAATCACC AATTCCAATC ATTTAATCAA AGGGAGTTCT ATG AAA	56
Met Lys	
1	
AAT ACT TTC AAA GCG TTT GCC TTT TTA ATT GTA TTT TTT TCA AGC GCT	104
Asn Thr Phe Lys Ala Phe Ala Phe Leu Ile Val Phe Phe Ser Ser Ala	
5 10 15	
TTA TTA GCG CAG GAT TTA AAA ATC GCT GCT GCT GCT AAT CTT ACA CGC	152
Leu Leu Ala Gln Asp Leu Lys Ile Ala Ala Ala Ala Asn Leu Thr Arg	
20 25 30	
GCT TTA AAA GCC CTT GTT AAA GAA TTT CAA AAA GAA CAC CCC AAA GAC	200
Ala Leu Lys Ala Leu Val Lys Glu Phe Gln Lys Glu His Pro Lys Asp	
35 40 45 50	
ACT GTT AAT ATT AGC TTT AAT TCT TCA GGC AAA CTC TAC GCT CAA ATC	248
Thr Val Asn Ile Ser Phe Asn Ser Ser Gly Lys Leu Tyr Ala Gln Ile	
55 60 65	
ATT CAA AAC GCC CCT TTT GAT TTA TTC ATT TCA GCA GAT ATG ATT AGA	296
Ile Gln Asn Ala Pro Phe Asp Leu Phe Ile Ser Ala Asp Met Ile Arg	
70 75 80	
CCT AAA AAG CTT TAT GAT AAA AAA ATA ACC CCT TTT AAA GAA GAA GTC	344
Pro Lys Lys Leu Tyr Asp Lys Lys Ile Thr Pro Phe Lys Glu Glu Val	
85 90 95	
TAT GCT AAA GGC GTG TTG GTT TTA TGG AGT GAA GAT CTA AAA ATG GAT	392
Tyr Ala Lys Gly Val Leu Val Leu Trp Ser Glu Asp Leu Lys Met Asp	
100 105 110	
TCT TTA GAA ATT CTT AAA AAT CCT AAA ATC AAG CGT ATC GCT ATG GCT	440
Ser Leu Glu Ile Leu Lys Asn Pro Lys Ile Lys Arg Ile Ala Met Ala	
115 120 125 130	
AAT CCT AAA CTA GCC CCT TAT GGA AAA GCC AGC ATG GAA GTC TTA GAG	488
Asn Pro Lys Leu Ala Pro Tyr Gly Lys Ala Ser Met Glu Val Leu Glu	
135 140 145	
AAT TTA AAA CTC ACT CCC AGT CTT AAA TCT AAA ATC GTT TAT GGC GCT	536

Asn	Leu	Lys	Leu	Thr	Pro	Ser	Leu	Lys	Ser	Lys	Ile	Val	Tyr	Gly	Ala		
			150					155					160				
TCT	ATT	TCT	CAA	GCC	CAT	CAA	TTT	GTC	GCT	ACT	AAA	AAC	GCT	CAA	ATA	584	
Ser	Ile	Ser	Gln	Ala	His	Gln	Phe	Val	Ala	Thr	Lys	Asn	Ala	Gln	Ile		
		165					170					175					
GGC	TTT	GGA	GCG	TTA	TCC	TTG	ATG	GAT	AAA	AAA	GAT	AAA	AAC	CTC	TCT	632	
Gly	Phe	Gly	Ala	Leu	Ser	Leu	Met	Asp	Lys	Lys	Asp	Lys	Asn	Leu	Ser		
	180					185					190						
TAT	TTC	ATC	ATT	GAT	AAA	GCC	CTT	TAT	AAC	CCT	ATT	GAA	CAA	GCC	TTG	680	
Tyr	Phe	Ile	Ile	Asp	Lys	Ala	Leu	Tyr	Asn	Pro	Ile	Glu	Gln	Ala	Leu		
195					200				205					210			
ATT	ATC	ACT	AAA	AAT	GGG	GCT	AAC	AAC	CCT	TTA	GCC	AAA	GTC	TTT	AAA	728	
Ile	Ile	Thr	Lys	Asn	Gly	Ala	Asn	Asn	Pro	Leu	Ala	Lys	Val	Phe	Lys		
				215				220						225			
GAT	TTT	TTA	TTC	AGC	CCT	AAA	GCC	AGA	GCT	ATT	TTT	AAA	GAA	TAC	GGC	776	
Asp	Phe	Leu	Phe	Ser	Pro	Lys	Ala	Arg	Ala	Ile	Phe	Lys	Glu	Tyr	Gly		
			230					235					240				
TAT	ATT	GTG	GAT	TAAAACGCAT	AAAAAAGGCG	AGCAATGGAT	CATGAGTTTT	TGATT	833								
Tyr	Ile	Val	Asp														
		245															
ACCATGCG																841	

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Met	Lys	Asn	Thr	Phe	Lys	Ala	Phe	Ala	Phe	Leu	Ile	Val	Phe	Phe	Ser		
1				5					10					15			
Ser	Ala	Leu	Leu	Ala	Gln	Asp	Leu	Lys	Ile	Ala	Ala	Ala	Ala	Asn	Leu		
		20					25					30					
Thr	Arg	Ala	Leu	Lys	Ala	Leu	Val	Lys	Glu	Phe	Gln	Lys	Glu	His	Pro		
	35					40					45						
Lys	Asp	Thr	Val	Asn	Ile	Ser	Phe	Asn	Ser	Ser	Gly	Lys	Leu	Tyr	Ala		
	50				55				60								
Gln	Ile	Ile	Gln	Asn	Ala	Pro	Phe	Asp	Leu	Phe	Ile	Ser	Ala	Asp	Met		
65				70					75					80			
Ile	Arg	Pro	Lys	Lys	Leu	Tyr	Asp	Lys	Lys	Ile	Thr	Pro	Phe	Lys	Glu		
			85					90						95			
Glu	Val	Tyr	Ala	Lys	Gly	Val	Leu	Val	Leu	Trp	Ser	Glu	Asp	Leu	Lys		
		100				105						110					
Met	Asp	Ser	Leu	Glu	Ile	Leu	Lys	Asn	Pro	Lys	Ile	Lys	Arg	Ile	Ala		
	115					120						125					

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Met Ala Asn Pro Lys Leu Ala Pro Tyr Gly Lys Ala Ser Met Glu Val
  130                      135                      140
Leu Glu Asn Leu Lys Leu Thr Pro Ser Leu Lys Ser Lys Ile Val Tyr
 145                      150                      155                      160
Gly Ala Ser Ile Ser Gln Ala His Gln Phe Val Ala Thr Lys Asn Ala
                      165                      170                      175
Gln Ile Gly Phe Gly Ala Leu Ser Leu Met Asp Lys Lys Asp Lys Asn
                      180                      185                      190
Leu Ser Tyr Phe Ile Ile Asp Lys Ala Leu Tyr Asn Pro Ile Glu Gln
                      195                      200                      205
Ala Leu Ile Ile Thr Lys Asn Gly Ala Asn Asn Pro Leu Ala Lys Val
                      210                      215                      220
Phe Lys Asp Phe Leu Phe Ser Pro Lys Ala Arg Ala Ile Phe Lys Glu
 225                      230                      235                      240
Tyr Gly Tyr Ile Val Asp
                      245

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(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...1406
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

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AGCCATTTTA TGGCATTAA AAAAGTTTAA AAATGTTTAA AAGGAATTTT ATG TTA      56
                                   Met Leu
                                   1
AGG CTT TTG ATA GGA CTT CTT CTA ATG AGT TTT ATA AGC TTG CAA TCA      104
Arg Leu Leu Ile Gly Leu Leu Leu Met Ser Phe Ile Ser Leu Gln Ser
   5                      10                      15
GCC TCT TGG CAA GAA CCC TTA AGA GTG AGT ATA GAA TTT GTG GAT TTG      152
Ala Ser Trp Gln Glu Pro Leu Arg Val Ser Ile Glu Phe Val Asp Leu
  20                      25                      30
CCT AAA AAA ATC ATT CGT TTT CCG GCT CAT GAT TTG CAA GTG GGG GAG      200
Pro Lys Lys Ile Ile Arg Phe Pro Ala His Asp Leu Gln Val Gly Glu
 35                      40                      45                      50
TTT GGT TTT GTC GTT ACT AAA CTT TCA GAT TAT GAA ATC GTT AAT TCT      248
Phe Gly Phe Val Val Thr Lys Leu Ser Asp Tyr Glu Ile Val Asn Ser
                      55                      60                      65
GAA GTG GTC ATT ATT GCC GTT GAA AAT GGC GTC GCA ACG GCT AAA TTC      296
Glu Val Val Ile Ile Ala Val Glu Asn Gly Val Ala Thr Ala Lys Phe

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70										75					80					
AGA	GCG	TTT	GAG	TCT	ATG	AAA	CAA	AGG	CAT	TTA	CCC	ACT	CCA	AGA	ATG	344				
Arg	Ala	Phe	Glu	Ser	Met	Lys	Gln	Arg	His	Leu	Pro	Thr	Pro	Arg	Met					
	85						90					95								
GTC	GCT	AGA	AAG	GGT	GAT	TTA	GTC	TAT	TTT	AGG	CAA	TTC	AAC	AAC	CAA	392				
Val	Ala	Arg	Lys	Gly	Asp	Leu	Val	Tyr	Phe	Arg	Gln	Phe	Asn	Asn	Gln					
	100					105					110									
GCG	TTT	TTA	ATC	GCT	CCT	AAT	GAT	GAA	CTC	TAT	GAG	CAA	ATC	AGA	GCG	440				
Ala	Phe	Leu	Ile	Ala	Pro	Asn	Asp	Glu	Leu	Tyr	Glu	Gln	Ile	Arg	Ala					
115					120					125					130					
ACT	AAC	ACC	GAT	ATT	AAT	TTT	ATT	AGT	TCT	GAT	TTG	TTG	GTT	ACT	TTT	488				
Thr	Asn	Thr	Asp	Ile	Asn	Phe	Ile	Ser	Ser	Asp	Leu	Leu	Val	Thr	Phe					
				135					140					145						
TTG	AAT	GGG	TTT	GAC	CCA	AAA	ATC	GCT	AAT	TTA	AGG	AAA	GCG	TGC	AAC	536				
Leu	Asn	Gly	Phe	Asp	Pro	Lys	Ile	Ala	Asn	Leu	Arg	Lys	Ala	Cys	Asn					
			150					155					160							
GTT	TAT	AGC	GTG	GGG	GTG	ATT	TAT	ATT	GTA	ACC	ACC	AAC	ACG	CTC	AAT	584				
Val	Tyr	Ser	Val	Gly	Val	Ile	Tyr	Ile	Val	Thr	Thr	Asn	Thr	Leu	Asn					
		165					170					175								
ATT	TTA	AGT	TGT	GAG	AGT	TTT	GAA	ATT	TTA	GAA	AAA	AGA	GAG	CTG	GAT	632				
Ile	Leu	Ser	Cys	Glu	Ser	Phe	Glu	Ile	Leu	Glu	Lys	Arg	Glu	Leu	Asp					
	180					185					190									
ACA	AGC	GGC	GTT	ACT	AAA	ACT	TCC	ACG	CCG	TTT	TTT	TCT	AGG	GTT	GAG	680				
Thr	Ser	Gly	Val	Thr	Lys	Thr	Ser	Thr	Pro	Phe	Phe	Ser	Arg	Val	Glu					
195					200					205					210					
GGT	ATT	GAT	GCA	GGC	ACG	CTA	GGG	AAA	CTT	TTT	TCA	GGC	AGT	CAG	TCT	728				
Gly	Ile	Asp	Ala	Gly	Thr	Leu	Gly	Lys	Leu	Phe	Ser	Gly	Ser	Gln	Ser					
				215					220					225						
AAA	AAT	TAC	TTC	GCT	TAC	TAT	GAC	GCT	TTA	GTG	AAG	AAA	GAA	AAA	CGC	776				
Lys	Asn	Tyr	Phe	Ala	Tyr	Tyr	Asp	Ala	Leu	Val	Lys	Lys	Glu	Lys	Arg					
			230				235						240							
AAA	GAA	GTG	AGG	ATT	AAA	AAG	AGG	GAA	GAA	AAG	ATT	GAT	TCT	AGA	GAA	824				
Lys	Glu	Val	Arg	Ile	Lys	Lys	Arg	Glu	Glu	Lys	Ile	Asp	Ser	Arg	Glu					
		245					250					255								
ATT	AAA	CGA	GAA	ATC	AAG	CAA	GAG	GCC	ATT	AAA	GAG	CCT	AAA	AAA	GCC	872				
Ile	Lys	Arg	Glu	Ile	Lys	Gln	Glu	Ala	Ile	Lys	Glu	Pro	Lys	Lys	Ala					
	260					265					270									
AAT	CAA	GGC	ACA	CAA	AAC	GCT	CCT	ACT	TTA	GAA	GAG	AAA	AAC	TAC	CAA	920				
Asn	Gln	Gly	Thr	Gln	Asn	Ala	Pro	Thr	Leu	Glu	Glu	Lys	Asn	Tyr	Gln					
275					280					285					290					
AAA	GCA	GAG	CGC	AAA	CTT	GAT	GCT	AAA	GAA	GAA	AGG	CGT	TAT	TTG	AGA	968				
Lys	Ala	Glu	Arg	Lys	Leu	Asp	Ala	Lys	Glu	Glu	Arg	Arg	Tyr	Leu	Arg					
				295					300					305						

GAT GAA AGG AAA AAA GCC AAA GCC ACC AAA AAG GCT ATG GAA TTT GAA	1016
Asp Glu Arg Lys Lys Ala Lys Ala Thr Lys Lys Ala Met Glu Phe Glu	
310 315 320	
GAA AGA GAA AAA GAG CAT GAT GAA AGG GAC GAA CAA GAG ACT GAA GGA	1064
Glu Arg Glu Lys Glu His Asp Glu Arg Asp Glu Gln Glu Thr Glu Gly	
325 330 335	
AGA AGA AAA GCT TTA GAA ATG GAT AAA GGC GAT AAA AAA GAA GAA AGA	1112
Arg Arg Lys Ala Leu Glu Met Asp Lys Gly Asp Lys Lys Glu Glu Arg	
340 345 350	
GTC AAA CCC AAA GAA AAT GAG CGA GAA ATC AAG CAA GAA GCC ATT AAA	1160
Val Lys Pro Lys Glu Asn Glu Arg Glu Ile Lys Gln Glu Ala Ile Lys	
355 360 365 370	
GAG CCA AGT GAT GGA AAT AAC GCC ACC CAA CAA GGC GAA AAA CAA AAC	1208
Glu Pro Ser Asp Gly Asn Asn Ala Thr Gln Gln Gly Glu Lys Gln Asn	
375 380 385	
GCT CCT AAA GAG AAC AAC GCT CAA AAA GAA GAG AAT AAA CCA AAT TCT	1256
Ala Pro Lys Glu Asn Asn Ala Gln Lys Glu Glu Asn Lys Pro Asn Ser	
390 395 400	
AAA GAA GAA AAA CGC CGC TTG AAA GAA GAA AAG AAA AAA GCC AAA GCC	1304
Lys Glu Glu Lys Arg Arg Leu Lys Glu Glu Lys Lys Lys Ala Lys Ala	
405 410 415	
GAA CAA AGA GCG AGA GAA TTT GAA CAA AGA GCG AGA GAG CAT CAA GAA	1352
Glu Gln Arg Ala Arg Glu Phe Glu Gln Arg Ala Arg Glu His Gln Glu	
420 425 430	
AGA GAT GAA AAA GAG CTT GAA GAG CGA AGA AAG GCG CTA GAA GCG GGT	1400
Arg Asp Glu Lys Glu Leu Glu Glu Arg Arg Lys Ala Leu Glu Ala Gly	
435 440 445 450	
AAA AAA TAACATGTTA GACCAACAAC ACATCCAATA CTTTAAAAAC CTAGTAGGGG GA	1458
Lys Lys	
G	1459

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

Met	Leu	Arg	Leu	Leu	Ile	Gly	Leu	Leu	Leu	Met	Ser	Phe	Ile	Ser	Leu
1				5					10					15	
Gln	Ser	Ala	Ser	Trp	Gln	Glu	Pro	Leu	Arg	Val	Ser	Ile	Glu	Phe	Val
			20					25					30		

Asp	Leu	Pro	Lys	Lys	Ile	Ile	Arg	Phe	Pro	Ala	His	Asp	Leu	Gln	Val		
	35						40					45					
Gly	Glu	Phe	Gly	Phe	Val	Val	Thr	Lys	Leu	Ser	Asp	Tyr	Glu	Ile	Val		
	50					55					60						
Asn	Ser	Glu	Val	Val	Ile	Ile	Ala	Val	Glu	Asn	Gly	Val	Ala	Thr	Ala		
65					70					75					80		
Lys	Phe	Arg	Ala	Phe	Glu	Ser	Met	Lys	Gln	Arg	His	Leu	Pro	Thr	Pro		
				85					90					95			
Arg	Met	Val	Ala	Arg	Lys	Gly	Asp	Leu	Val	Tyr	Phe	Arg	Gln	Phe	Asn		
			100					105					110				
Asn	Gln	Ala	Phe	Leu	Ile	Ala	Pro	Asn	Asp	Glu	Leu	Tyr	Glu	Gln	Ile		
		115					120					125					
Arg	Ala	Thr	Asn	Thr	Asp	Ile	Asn	Phe	Ile	Ser	Ser	Asp	Leu	Leu	Val		
	130					135					140						
Thr	Phe	Leu	Asn	Gly	Phe	Asp	Pro	Lys	Ile	Ala	Asn	Leu	Arg	Lys	Ala		
145					150					155					160		
Cys	Asn	Val	Tyr	Ser	Val	Gly	Val	Ile	Tyr	Ile	Val	Thr	Thr	Asn	Thr		
				165					170					175			
Leu	Asn	Ile	Leu	Ser	Cys	Glu	Ser	Phe	Glu	Ile	Leu	Glu	Lys	Arg	Glu		
			180					185					190				
Leu	Asp	Thr	Ser	Gly	Val	Thr	Lys	Thr	Ser	Thr	Pro	Phe	Phe	Ser	Arg		
	195						200					205					
Val	Glu	Gly	Ile	Asp	Ala	Gly	Thr	Leu	Gly	Lys	Leu	Phe	Ser	Gly	Ser		
	210					215					220						
Gln	Ser	Lys	Asn	Tyr	Phe	Ala	Tyr	Tyr	Asp	Ala	Leu	Val	Lys	Lys	Glu		
225					230					235					240		
Lys	Arg	Lys	Glu	Val	Arg	Ile	Lys	Lys	Arg	Glu	Glu	Lys	Ile	Asp	Ser		
				245					250					255			
Arg	Glu	Ile	Lys	Arg	Glu	Ile	Lys	Gln	Glu	Ala	Ile	Lys	Glu	Pro	Lys		
			260					265					270				
Lys	Ala	Asn	Gln	Gly	Thr	Gln	Asn	Ala	Pro	Thr	Leu	Glu	Glu	Lys	Asn		
	275						280					285					
Tyr	Gln	Lys	Ala	Glu	Arg	Lys	Leu	Asp	Ala	Lys	Glu	Glu	Arg	Arg	Tyr		
	290					295					300						
Leu	Arg	Asp	Glu	Arg	Lys	Lys	Ala	Lys	Ala	Thr	Lys	Lys	Ala	Met	Glu		
305					310					315					320		
Phe	Glu	Glu	Arg	Glu	Lys	Glu	His	Asp	Glu	Arg	Asp	Glu	Gln	Glu	Thr		
				325					330					335			
Glu	Gly	Arg	Arg	Lys	Ala	Leu	Glu	Met	Asp	Lys	Gly	Asp	Lys	Lys	Glu		
			340					345					350				
Glu	Arg	Val	Lys	Pro	Lys	Glu	Asn	Glu	Arg	Glu	Ile	Lys	Gln	Glu	Ala		
		355					360					365					
Ile	Lys	Glu	Pro	Ser	Asp	Gly	Asn	Asn	Ala	Thr	Gln	Gln	Gly	Glu	Lys		
	370					375					380						
Gln	Asn	Ala	Pro	Lys	Glu	Asn	Asn	Ala	Gln	Lys	Glu	Glu	Asn	Lys	Pro		
385					390					395					400		
Asn	Ser	Lys	Glu	Glu	Lys	Arg	Arg	Leu	Lys	Glu	Glu	Lys	Lys	Lys	Ala		
				405					410					415			
Lys	Ala	Glu	Gln	Arg	Ala	Arg	Glu	Phe	Glu	Gln	Arg	Ala	Arg	Glu	His		
			420					425					430				
Gln	Glu	Arg	Asp	Glu	Lys	Glu	Leu	Glu	Glu	Arg	Arg	Lys	Ala	Leu	Glu		
		435					440					445					
Ala	Gly	Lys	Lys														
	450																

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 995 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 74...943
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GGCCTATGAC	GATTGTCTCG	CTTTTAGAAA	ACACTCTAAT	CGCTTTTGAA	AAACAACAAA	60
GGAAGGGATT	TTA ATG AAA TTT TTA CGC TCT GTT TAT GCA TTT TGC TCC	109				
	Met Lys Phe Leu Arg Ser Val Tyr Ala Phe Cys Ser					
	1 5 10					
AGT TGG GTA GGG ACG ATT GTT ATT GTG CTG TTG GTT ATC TTT TTT ATC	157					
Ser Trp Val Gly Thr Ile Val Ile Val Leu Leu Val Ile Phe Phe Ile						
	15 20 25					
GCG CAA GCC TTT ATC ATT CCC TCT CGC TCT ATG GTT GGC ACG CTC TAT	205					
Ala Gln Ala Phe Ile Ile Pro Ser Arg Ser Met Val Gly Thr Leu Tyr						
	30 35 40					
GAG GGC GAC ATG CTC TTT GTC AAA AAG TTT TCT TAC GGC ATA CCC ATT	253					
Glu Gly Asp Met Leu Phe Val Lys Lys Phe Ser Tyr Gly Ile Pro Ile						
	45 50 55 60					
CCT AAA ATC CCA TGG ATT GAG CTT CCT GTT ATG CCT GAT TTT AAA AAT	301					
Pro Lys Ile Pro Trp Ile Glu Leu Pro Val Met Pro Asp Phe Lys Asn						
	65 70 75					
AAC GGA CAT TTG ATA GAG GGG GAT CGC CCT AAG CGT GGC GAA GTG GTG	349					
Asn Gly His Leu Ile Glu Gly Asp Arg Pro Lys Arg Gly Glu Val Val						
	80 85 90					
GTG TTT ATC CCT CCC CAT GAA AAA AAG TCT TAC TAT GTT AAA AGG AAT	397					
Val Phe Ile Pro Pro His Glu Lys Lys Ser Tyr Tyr Val Lys Arg Asn						
	95 100 105					
TTT GCC ATT GGA GGC GAT GAG GTG TTG TTC ACT AAT GAG GGT TTT TAT	445					
Phe Ala Ile Gly Gly Asp Glu Val Leu Phe Thr Asn Glu Gly Phe Tyr						
	110 115 120					
TTG CAC CCT TTT GAG AGC GAC ACG GAC AAA AAT TAC ATC GCT AAA CAT	493					
Leu His Pro Phe Glu Ser Asp Thr Asp Lys Asn Tyr Ile Ala Lys His						
	125 130 135 140					
TAC CCT AAC GCC ATG ACA AAA GAA TTT ATG GGT AAA ATT TTT GTT TTA	541					
Tyr Pro Asn Ala Met Thr Lys Glu Phe Met Gly Lys Ile Phe Val Leu						
	145 150 155					
AAC CCT TAT AAA AAT GAG CAT CCG GGT ATC CAT TAC CAA AAA GAC AAT	589					

Asn	Pro	Tyr	Lys	Asn	Glu	His	Pro	Gly	Ile	His	Tyr	Gln	Lys	Asp	Asn		
			160					165					170				
GAA	ACC	TTC	CAC	TTA	ATG	GAG	CAA	TTA	GCC	ACT	CAA	GGC	GCA	GAA	GCT		637
Glu	Thr	Phe	His	Leu	Met	Glu	Gln	Leu	Ala	Thr	Gln	Gly	Ala	Glu	Ala		
		175					180					185					
AAT	ATC	AGC	ATG	CAA	CTC	ATT	CAA	ATG	GAG	GGC	GAA	AAG	GTG	TTT	TAT		685
Asn	Ile	Ser	Met	Gln	Leu	Ile	Gln	Met	Glu	Gly	Glu	Lys	Val	Phe	Tyr		
	190					195					200						
AAG	AAA	ATC	AAT	GAC	GAT	GAA	TTT	TTC	ATG	ATC	GGC	GAC	AAC	AGA	GAC		733
Lys	Lys	Ile	Asn	Asp	Asp	Glu	Phe	Phe	Met	Ile	Gly	Asp	Asn	Arg	Asp		
205					210				215					220			
AAT	TCT	AGC	GAC	TCG	CGC	TTT	TGG	GGG	AGT	GTG	GCT	TAT	AAA	AAC	ATC		781
Asn	Ser	Ser	Asp	Ser	Arg	Phe	Trp	Gly	Ser	Val	Ala	Tyr	Lys	Asn	Ile		
			225					230						235			
GTG	GGT	TCG	CCA	TGG	TTT	GTT	TAT	TTC	AGT	TTG	AGT	TTA	AAA	AAT	AGC		829
Val	Gly	Ser	Pro	Trp	Phe	Val	Tyr	Phe	Ser	Leu	Ser	Leu	Lys	Asn	Ser		
			240					245					250				
CTA	GAA	ATG	GAT	GCA	GAA	AAT	AAC	CCT	AAA	AAA	CGC	TAT	CTG	GTG	CGT		877
Leu	Glu	Met	Asp	Ala	Glu	Asn	Asn	Pro	Lys	Lys	Arg	Tyr	Leu	Val	Arg		
		255					260					265					
TGG	GAA	CGC	ATG	TTT	AAA	AGC	GTT	GGA	GGC	TTA	GAA	AAA	ATC	ATT	AAA		925
Trp	Glu	Arg	Met	Phe	Lys	Ser	Val	Gly	Gly	Leu	Glu	Lys	Ile	Ile	Lys		
	270					275				280							
AAA	GAA	AAC	GCA	ACG	CAT	TAAGGTTTTT	TGTGCAATTT	TTTGATTCT	CTTTAGAA								981
Lys	Glu	Asn	Ala	Thr	His												
285					290												
AGTTTTATTA	CCAC																995

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

Met	Lys	Phe	Leu	Arg	Ser	Val	Tyr	Ala	Phe	Cys	Ser	Ser	Trp	Val	Gly		
1			5					10					15				
Thr	Ile	Val	Ile	Val	Leu	Leu	Val	Ile	Phe	Phe	Ile	Ala	Gln	Ala	Phe		
		20						25				30					
Ile	Ile	Pro	Ser	Arg	Ser	Met	Val	Gly	Thr	Leu	Tyr	Glu	Gly	Asp	Met		
		35				40					45						
Leu	Phe	Val	Lys	Lys	Phe	Ser	Tyr	Gly	Ile	Pro	Ile	Pro	Lys	Ile	Pro		
50						55					60						

Trp Ile Glu Leu Pro Val Met Pro Asp Phe Lys Asn Asn Gly His Leu
 65 70 75 80
 Ile Glu Gly Asp Arg Pro Lys Arg Gly Glu Val Val Val Phe Ile Pro
 85 90 95
 Pro His Glu Lys Lys Ser Tyr Tyr Val Lys Arg Asn Phe Ala Ile Gly
 100 105 110
 Gly Asp Glu Val Leu Phe Thr Asn Glu Gly Phe Tyr Leu His Pro Phe
 115 120 125
 Glu Ser Asp Thr Asp Lys Asn Tyr Ile Ala Lys His Tyr Pro Asn Ala
 130 135 140
 Met Thr Lys Glu Phe Met Gly Lys Ile Phe Val Leu Asn Pro Tyr Lys
 145 150 155 160
 Asn Glu His Pro Gly Ile His Tyr Gln Lys Asp Asn Glu Thr Phe His
 165 170 175
 Leu Met Glu Gln Leu Ala Thr Gln Gly Ala Glu Ala Asn Ile Ser Met
 180 185 190
 Gln Leu Ile Gln Met Glu Gly Glu Lys Val Phe Tyr Lys Lys Ile Asn
 195 200 205
 Asp Asp Glu Phe Phe Met Ile Gly Asp Asn Arg Asp Asn Ser Ser Asp
 210 215 220
 Ser Arg Phe Trp Gly Ser Val Ala Tyr Lys Asn Ile Val Gly Ser Pro
 225 230 235 240
 Trp Phe Val Tyr Phe Ser Leu Ser Leu Lys Asn Ser Leu Glu Met Asp
 245 250 255
 Ala Glu Asn Asn Pro Lys Lys Arg Tyr Leu Val Arg Trp Glu Arg Met
 260 265 270
 Phe Lys Ser Val Gly Gly Leu Glu Lys Ile Ile Lys Lys Glu Asn Ala
 275 280 285
 Thr His
 290

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 548...2419
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

GATACAATTC	CAAATTTAAA	AAACAAACGA	TTTAATTCAA	ATTTAAGGAA	AAATTTTGAT	60
TACAGTGGTT	AAACGAAACG	GGCGCATTGA	GCCTTTGGAC	ATTACCAAAA	TCCAAAAATA	120
CACTAAGGAC	GCTACGGACA	ATTTAGAGGG	CGTGAGCCAA	AGTGAGCTGG	AAGTGGATGC	180
GAGGTTGCAA	TTCAAGGACA	AGATCACTAC	TGAAGAAATC	CAACAAACTT	TGATTAAAC	240
CGCTGTGGAT	AAGATAGATA	TTGACACGCC	TAATTGGAGT	TTTGTCGCCT	CAAGGCTTTT	300
TTTGATATGAT	TTATACCATA	AAGTAAGTGG	TTTTACAGGG	TATAGGCATT	TGAAAGAGTA	360
TTTTGAAAAC	GCTGAAGAAA	AGGGCCGCAT	CCTTAAGGGC	TTTAAGGAAA	AATTTGATCT	420
AGAGTTTTTA	AATAGCCAGA	TCAAGCCTGA	AAGGGATTTC	CAATTCAATT	ATTTAGGGAT	480

TAAAACCTTG TATGATCGCT ATTTGTAAAGACGCTAAC AACAAACCCTA TTGAATTGCC	540
CCAACAC ATG TTT ATG AGC ATT GCG ATG TTT TTA GCA CAA AAC GAA CAA	589
Met Phe Met Ser Ile Ala Met Phe Leu Ala Gln Asn Glu Gln	
1 5 10	
GAA CCC AAT AAA ATC GCC TTA GAA TTT TAT GAA GTT TTG AGC AAG TTT	637
Glu Pro Asn Lys Ile Ala Leu Glu Phe Tyr Glu Val Leu Ser Lys Phe	
15 20 25 30	
GAA GCG ATG TGC GCG ACC CCC ACT CTA GCG AAC GCC CGC ACC ACC AAA	685
Glu Ala Met Cys Ala Thr Pro Thr Leu Ala Asn Ala Arg Thr Thr Lys	
35 40 45	
CAC CAG CTC AGC TCA TGC TAT ATT GGC AGC ACG CCG GAT AAT ATT GAG	733
His Gln Leu Ser Ser Cys Tyr Ile Gly Ser Thr Pro Asp Asn Ile Glu	
50 55 60	
GGG ATT TTT GAC AGC TAT AAG GAA ATG GCG CTG TTG TCC AAA TAC GGC	781
Gly Ile Phe Asp Ser Tyr Lys Glu Met Ala Leu Leu Ser Lys Tyr Gly	
65 70 75	
GGA GGG ATT GGC TGG GAT TTT TCT TTG GTG CGC TCT ATT GGG AGT TAT	829
Gly Gly Ile Gly Trp Asp Phe Ser Leu Val Arg Ser Ile Gly Ser Tyr	
80 85 90	
ATT GAT GGG CAT AAA AAT GCG AGC GCT GGC ACG ATC CCT TTT TTA AAA	877
Ile Asp Gly His Lys Asn Ala Ser Ala Gly Thr Ile Pro Phe Leu Lys	
95 100 105 110	
ATC GCT AAC GAT GTG GCG ATT GCG GTG GAT CAA TTA GGC ACA CGA AAG	925
Ile Ala Asn Asp Val Ala Ile Ala Val Asp Gln Leu Gly Thr Arg Lys	
115 120 125	
GGC GCG ATT GCG GTG TAT TTG GAA ATT TGG CAC ATT GAT GTG ATG GAG	973
Gly Ala Ile Ala Val Tyr Leu Glu Ile Trp His Ile Asp Val Met Glu	
130 135 140	
TTC ATT GAT TTA AGG AAA AAT AGC GGC GAT GAA AGG CGA AGA GCG CAT	1021
Phe Ile Asp Leu Arg Lys Asn Ser Gly Asp Glu Arg Arg Arg Ala His	
145 150 155	
GAT TTA TTC CCG GCT CTT TGG GTG TGC GAT TTG TTT TTG AAA AGG GTT	1069
Asp Leu Phe Pro Ala Leu Trp Val Cys Asp Leu Phe Leu Lys Arg Val	
160 165 170	
TTA GAA GAT GCG ATG TGG ACT TTA TTT GAC CCT TAT GAG TGT AAG GAT	1117
Leu Glu Asp Ala Met Trp Thr Leu Phe Asp Pro Tyr Glu Cys Lys Asp	
175 180 185 190	
TTG ACT GAG CTT TAT GGG CAG GAT TTT GAA AAA CGC TAT TTA GAG TAT	1165
Leu Thr Glu Leu Tyr Gly Gln Asp Phe Glu Lys Arg Tyr Leu Glu Tyr	
195 200 205	
GAA AAA GAT CCC AAG ATC ATT AAG GAA TAC ATT AAC GCT AAA GAT TTA	1213
Glu Lys Asp Pro Lys Ile Ile Lys Glu Tyr Ile Asn Ala Lys Asp Leu	
210 215 220	
TGG AAA AAA ATC TTA ATG AAT TAT TTT GAA GCC GGT TTG CCT TTC TTA	1261

Trp	Lys	Lys	Ile	Leu	Met	Asn	Tyr	Phe	Glu	Ala	Gly	Leu	Pro	Phe	Leu	
		225					230					235				
GCC	TTT	AAA	GAT	AAC	GCC	AAT	CGG	TGC	AAC	CCA	AAC	GCT	CAT	GCA	GGA	1309
Ala	Phe	Lys	Asp	Asn	Ala	Asn	Arg	Cys	Asn	Pro	Asn	Ala	His	Ala	Gly	
	240					245					250					
ATC	ATT	CGA	TCC	AGC	AAT	CTA	TGC	ACG	GAG	ATT	TTC	CAA	AAT	ACC	GCG	1357
Ile	Ile	Arg	Ser	Ser	Asn	Leu	Cys	Thr	Glu	Ile	Phe	Gln	Asn	Thr	Ala	
255					260					265					270	
CCT	AAC	CAC	TAC	TAC	ATG	CAA	ATA	GAA	TAC	ACC	GAC	GGC	ACC	ATA	GAG	1405
Pro	Asn	His	Tyr	Tyr	Met	Gln	Ile	Glu	Tyr	Thr	Asp	Gly	Thr	Ile	Glu	
				275					280					285		
TTT	TTT	GAA	GAA	AAA	GAG	TTG	GTA	ACG	ACA	GAT	AGT	AAT	ATC	ACT	AAA	1453
Phe	Phe	Glu	Glu	Lys	Glu	Leu	Val	Thr	Thr	Asp	Ser	Asn	Ile	Thr	Lys	
			290					295					300			
TGC	GCT	AAC	AAG	CTC	ACT	AGC	ACC	GAT	ATT	CTA	AAG	GGC	AAG	CCA	ATC	1501
Cys	Ala	Asn	Lys	Leu	Thr	Ser	Thr	Asp	Ile	Leu	Lys	Gly	Lys	Pro	Ile	
		305					310					315				
TAT	ATC	GCT	ACT	AAA	GTC	GCT	AAA	GAC	GGG	CAA	ACG	GCG	GTG	TGC	AAT	1549
Tyr	Ile	Ala	Thr	Lys	Val	Ala	Lys	Asp	Gly	Gln	Thr	Ala	Val	Cys	Asn	
	320					325					330					
CTG	GCG	AGC	ATC	AAT	TTA	AGC	AAA	ATC	AAC	ACT	GAA	GAA	GAC	ATT	AAA	1597
Leu	Ala	Ser	Ile	Asn	Leu	Ser	Lys	Ile	Asn	Thr	Glu	Glu	Asp	Ile	Lys	
335					340					345					350	
AGG	GTT	GTG	CCG	ATC	ATG	GTC	AGG	CTT	TTA	GAC	AAT	GTG	ATT	GAT	TTG	1645
Arg	Val	Val	Pro	Ile	Met	Val	Arg	Leu	Leu	Asp	Asn	Val	Ile	Asp	Leu	
				355					360					365		
AAT	TTC	TAC	CCT	AAC	CGC	AAA	GTC	AAA	GCC	ACT	AAT	TTA	CAA	AAT	AGG	1693
Asn	Phe	Tyr	Pro	Asn	Arg	Lys	Val	Lys	Ala	Thr	Asn	Leu	Gln	Asn	Arg	
			370					375					380			
GCC	ATA	GGG	TTA	GGG	GTT	ATG	GGT	GAA	GCG	CAA	ATG	CTC	GCA	GAA	CAC	1741
Ala	Ile	Gly	Leu	Gly	Val	Met	Gly	Glu	Ala	Gln	Met	Leu	Ala	Glu	His	
		385					390					395				
CAA	ATC	GCT	TGG	GGG	TCT	AAA	GAG	CAT	TTA	GAA	AAA	ATT	GAC	GCT	TTA	1789
Gln	Ile	Ala	Trp	Gly	Ser	Lys	Glu	His	Leu	Glu	Lys	Ile	Asp	Ala	Leu	
	400					405					410					
ATG	GAG	CAA	ATC	AGC	TAC	CAT	GCG	ATT	GAC	ACG	AGC	GCG	AAT	TTA	GCG	1837
Met	Glu	Gln	Ile	Ser	Tyr	His	Ala	Ile	Asp	Thr	Ser	Ala	Asn	Leu	Ala	
415					420					425					430	
AAA	GAA	AAA	GGG	GTT	TAT	AAG	GAT	TTT	GAA	AAT	TCA	GAA	TGG	AGT	AAG	1885
Lys	Glu	Lys	Gly	Val	Tyr	Lys	Asp	Phe	Glu	Asn	Ser	Glu	Trp	Ser	Lys	
			435						440					445		
GGG	ATT	TTC	CCC	ATT	GAT	AAA	GCC	AAT	AAT	GAA	GCC	TTA	AAG	CTC	ACC	1933
Gly	Ile	Phe	Pro	Ile	Asp	Lys	Ala	Asn	Asn	Glu	Ala	Leu	Lys	Leu	Thr	
			450					455					460			

GAA AAA GGG CTT TTT AAT CAC GCT TGC GAT TGG CAA GGT TTG AGG GAA	1981
Glu Lys Gly Leu Phe Asn His Ala Cys Asp Trp Gln Gly Leu Arg Glu	
465 470 475	
AAA GTC AAA GCC AAT GGC ATG CGT AAT GGC TAT TTA ATG GCG ATC GCT	2029
Lys Val Lys Ala Asn Gly Met Arg Asn Gly Tyr Leu Met Ala Ile Ala	
480 485 490	
CCC ACA AGC TCC ATT TCT ATT TTA GTA GGC ACA ACC CAA ACG ATT GAA	2077
Pro Thr Ser Ser Ile Ser Ile Leu Val Gly Thr Thr Gln Thr Ile Glu	
495 500 505 510	
CCC ATT TAT AAG AAA AAA TGG TTT GAA GAA AAT TTG AGC GGG CTT ATT	2125
Pro Ile Tyr Lys Lys Lys Trp Phe Glu Glu Asn Leu Ser Gly Leu Ile	
515 520 525	
CCT GTT GTG GTG CCT AAT TTG AAT GTA GAA ACC TGG AAT TTT TAC ACA	2173
Pro Val Val Val Pro Asn Leu Asn Val Glu Thr Trp Asn Phe Tyr Thr	
530 535 540	
TCA GCC TAT GAT ATT GAC GCT AAA GAT TTG ATT AAA GCA GCG GCC GTG	2221
Ser Ala Tyr Asp Ile Asp Ala Lys Asp Leu Ile Lys Ala Ala Ala Val	
545 550 555	
CGC CAA AAG TGG ATT GAT CAA GGC CAA AGC CTT AAT GTG TTT TTA CGC	2269
Arg Gln Lys Trp Ile Asp Gln Gly Gln Ser Leu Asn Val Phe Leu Arg	
560 565 570	
ATA GAA AAC GCC AGC GGT AAA ACC TTG CAT GAC ATC TAC ACG CTC GCT	2317
Ile Glu Asn Ala Ser Gly Lys Thr Leu His Asp Ile Tyr Thr Leu Ala	
575 580 585 590	
TGG AAA TTA GGA CTC AAA TCC ACT TAT TAT TTG CGC AGC GAA AGC CCT	2365
Trp Lys Leu Gly Leu Lys Ser Thr Tyr Tyr Leu Arg Ser Glu Ser Pro	
595 600 605	
AGC ATA GAT GAA AAA AGC GTG TTG GAT CGA TCG GTG GAG TGT TTT AAT	2413
Ser Ile Asp Glu Lys Ser Val Leu Asp Arg Ser Val Glu Cys Phe Asn	
610 615 620	
TGC CAA TAATATAAGC TTAAATAAGC TAATCTTTGC TAAAATGAGA TTTAAATTA TT	2471
Cys Gln	

TA

2473

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

Met Phe Met Ser Ile Ala Met Phe Leu Ala Gln Asn Glu Gln Glu Pro
 1 5 10 15
 Asn Lys Ile Ala Leu Glu Phe Tyr Glu Val Leu Ser Lys Phe Glu Ala
 20 25 30
 Met Cys Ala Thr Pro Thr Leu Ala Asn Ala Arg Thr Thr Lys His Gln
 35 40 45
 Leu Ser Ser Cys Tyr Ile Gly Ser Thr Pro Asp Asn Ile Glu Gly Ile
 50 55 60
 Phe Asp Ser Tyr Lys Glu Met Ala Leu Leu Ser Lys Tyr Gly Gly Gly
 65 70 75 80
 Ile Gly Trp Asp Phe Ser Leu Val Arg Ser Ile Gly Ser Tyr Ile Asp
 85 90 95
 Gly His Lys Asn Ala Ser Ala Gly Thr Ile Pro Phe Leu Lys Ile Ala
 100 105 110
 Asn Asp Val Ala Ile Ala Val Asp Gln Leu Gly Thr Arg Lys Gly Ala
 115 120 125
 Ile Ala Val Tyr Leu Glu Ile Trp His Ile Asp Val Met Glu Phe Ile
 130 135 140
 Asp Leu Arg Lys Asn Ser Gly Asp Glu Arg Arg Arg Ala His Asp Leu
 145 150 155 160
 Phe Pro Ala Leu Trp Val Cys Asp Leu Phe Leu Lys Arg Val Leu Glu
 165 170 175
 Asp Ala Met Trp Thr Leu Phe Asp Pro Tyr Glu Cys Lys Asp Leu Thr
 180 185 190
 Glu Leu Tyr Gly Gln Asp Phe Glu Lys Arg Tyr Leu Glu Tyr Glu Lys
 195 200 205
 Asp Pro Lys Ile Ile Lys Glu Tyr Ile Asn Ala Lys Asp Leu Trp Lys
 210 215 220
 Lys Ile Leu Met Asn Tyr Phe Glu Ala Gly Leu Pro Phe Leu Ala Phe
 225 230 235 240
 Lys Asp Asn Ala Asn Arg Cys Asn Pro Asn Ala His Ala Gly Ile Ile
 245 250 255
 Arg Ser Ser Asn Leu Cys Thr Glu Ile Phe Gln Asn Thr Ala Pro Asn
 260 265 270
 His Tyr Tyr Met Gln Ile Glu Tyr Thr Asp Gly Thr Ile Glu Phe Phe
 275 280 285
 Glu Glu Lys Glu Leu Val Thr Thr Asp Ser Asn Ile Thr Lys Cys Ala
 290 295 300
 Asn Lys Leu Thr Ser Thr Asp Ile Leu Lys Gly Lys Pro Ile Tyr Ile
 305 310 315 320
 Ala Thr Lys Val Ala Lys Asp Gly Gln Thr Ala Val Cys Asn Leu Ala
 325 330 335
 Ser Ile Asn Leu Ser Lys Ile Asn Thr Glu Glu Asp Ile Lys Arg Val
 340 345 350
 Val Pro Ile Met Val Arg Leu Leu Asp Asn Val Ile Asp Leu Asn Phe
 355 360 365
 Tyr Pro Asn Arg Lys Val Lys Ala Thr Asn Leu Gln Asn Arg Ala Ile
 370 375 380
 Gly Leu Gly Val Met Gly Glu Ala Gln Met Leu Ala Glu His Gln Ile
 385 390 395 400
 Ala Trp Gly Ser Lys Glu His Leu Glu Lys Ile Asp Ala Leu Met Glu
 405 410 415
 Gln Ile Ser Tyr His Ala Ile Asp Thr Ser Ala Asn Leu Ala Lys Glu
 420 425 430
 Lys Gly Val Tyr Lys Asp Phe Glu Asn Ser Glu Trp Ser Lys Gly Ile
 435 440 445
 Phe Pro Ile Asp Lys Ala Asn Asn Glu Ala Leu Lys Leu Thr Glu Lys
 450 455 460

Gly Leu Phe Asn His Ala Cys Asp Trp Gln Gly Leu Arg Glu Lys Val
 465 470 475 480
 Lys Ala Asn Gly Met Arg Asn Gly Tyr Leu Met Ala Ile Ala Pro Thr
 485 490 495
 Ser Ser Ile Ser Ile Leu Val Gly Thr Gln Thr Ile Glu Pro Ile
 500 505 510
 Tyr Lys Lys Lys Trp Phe Glu Glu Asn Leu Ser Gly Leu Ile Pro Val
 515 520 525
 Val Val Pro Asn Leu Asn Val Glu Thr Trp Asn Phe Tyr Thr Ser Ala
 530 535 540
 Tyr Asp Ile Asp Ala Lys Asp Leu Ile Lys Ala Ala Ala Val Arg Gln
 545 550 555 560
 Lys Trp Ile Asp Gln Gly Gln Ser Leu Asn Val Phe Leu Arg Ile Glu
 565 570 575
 Asn Ala Ser Gly Lys Thr Leu His Asp Ile Tyr Thr Leu Ala Trp Lys
 580 585 590
 Leu Gly Leu Lys Ser Thr Tyr Tyr Leu Arg Ser Glu Ser Pro Ser Ile
 595 600 605
 Asp Glu Lys Ser Val Leu Asp Arg Ser Val Glu Cys Phe Asn Cys Gln
 610 615 620

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 56...1390
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

GCAAAATTCT AGCCTTAAAT CTTTGATGAA ACGAAGTCAA ATTATAAGAT AAGGC ATG 58
 Met
 1
 TTA AAA TTC CCT AAA ATG AGT TTA AGG ATT TTA ATG CTT TCT GTC ATC 106
 Leu Lys Phe Pro Lys Met Ser Leu Arg Ile Leu Met Leu Ser Val Ile
 5 10 15
 ATA CTG GCC GCT GGT AAA GGC ACT CGC ATG CGT TCT AGC CTG CCT AAA 154
 Ile Leu Ala Ala Gly Lys Gly Thr Arg Met Arg Ser Ser Leu Pro Lys
 20 25 30
 ACT TTA CAC ACC ATT TGT GGG GAG CCT ATG TTG TTT TAC ATT TTA GAA 202
 Thr Leu His Thr Ile Cys Gly Glu Pro Met Leu Phe Tyr Ile Leu Glu
 35 40 45
 ACG GCT TTT TCA ATC AGC GAT GAT GTG CAT CTT ATC TTA CAC CAC CAA 250
 Thr Ala Phe Ser Ile Ser Asp Asp Val His Leu Ile Leu His His Gln

50	55	60	65	
CAA GAA CGC ATT AAA GAA GCG GTG TTG GAG CGT TTT AAG GGC GTC ATT				298
Gln Glu Arg Ile Lys Glu Ala Val Leu Glu Arg Phe Lys Gly Val Ile	70	75	80	
TTT CAC ACT CAA ATT GTG GAA AAA TAT TCA GGG ACA GGT GGG GCT ATC				346
Phe His Thr Gln Ile Val Glu Lys Tyr Ser Gly Thr Gly Gly Ala Ile	85	90	95	
ATG CAA AAA GAT AAA ACG CCT ATT TCT ACG AAA CAT GAG CGG GTT TTG				394
Met Gln Lys Asp Lys Thr Pro Ile Ser Thr Lys His Glu Arg Val Leu	100	105	110	
ATT TTG AAT GCG GAC ATG CCT TTA ATC ACT AAA GAC GCT CTC GCC CCC				442
Ile Leu Asn Ala Asp Met Pro Leu Ile Thr Lys Asp Ala Leu Ala Pro	115	120	125	
TTA TTA GAA AGC AAG AAT AAC GCT ATA GGC TTA CTC CAT TTA GCT GAC				490
Leu Leu Glu Ser Lys Asn Asn Ala Ile Gly Leu Leu His Leu Ala Asp	130	135	140	145
CCT AAA GGT TAT GGG CGC GTT GTT TTA GAA AAC CAT CAG GTT AAA AAG				538
Pro Lys Gly Tyr Gly Arg Val Val Leu Glu Asn His Gln Val Lys Lys	150	155	160	
ATT GTA GAA GAA AAG GAC GCT AAT GAT GAA GAA AAA GAA ATT AAA AGC				586
Ile Val Glu Glu Lys Asp Ala Asn Asp Glu Glu Lys Glu Ile Lys Ser	165	170	175	
GTG AAT GCT GGC GTG TAT GGG TTT GAA AGG GAT TTT TTA GAA AAA TAC				634
Val Asn Ala Gly Val Tyr Gly Phe Glu Arg Asp Phe Leu Glu Lys Tyr	180	185	190	
TTA CCC AAG CTC CAT GAC CAA AAC GCC CAA AAA GAA TAC TAC CTC ACG				682
Leu Pro Lys Leu His Asp Gln Asn Ala Gln Lys Glu Tyr Tyr Leu Thr	195	200	205	
GAT TTA ATC GCT CTA GGG ATC AAT GAA AAC GAA ACA ATT GAC GCT ATT				730
Asp Leu Ile Ala Leu Gly Ile Asn Glu Asn Glu Thr Ile Asp Ala Ile	210	215	220	225
TTC TTA AAA GAA GAG TGT TTT TTA GGG GTG AAT AGC CAA ACA GAA AGG				778
Phe Leu Lys Glu Glu Cys Phe Leu Gly Val Asn Ser Gln Thr Glu Arg	230	235	240	
GCG AAA GCT GAA GAA ATC ATG CTA GAA AGA CTG CGC AAA AAC GCC ATG				826
Ala Lys Ala Glu Glu Ile Met Leu Glu Arg Leu Arg Lys Asn Ala Met	245	250	255	
GAC TTG GGG GTA GTG ATG CAA TTG CCT AAT AGC ATT TAT TTA GAA AAA				874
Asp Leu Gly Val Val Met Gln Leu Pro Asn Ser Ile Tyr Leu Glu Lys	260	265	270	
GGC GTG AGT TTT AAG GGG GAG TGC GTT TTA GAG CAA GGG GTG CGT TTG				922
Gly Val Ser Phe Lys Gly Glu Cys Val Leu Glu Gln Gly Val Arg Leu	275	280	285	

ATT GGG AAT TGT TTG ATA GAA AAC GCG CAT ATT AAG GCT TAT AGC GTG	970
Ile Gly Asn Cys Leu Ile Glu Asn Ala His Ile Lys Ala Tyr Ser Val	
290 295 300 305	
ATA GAA GAG AGC CAG ATT GTT AAT AGC AGT GTG GGG CCG TTT GCC CAT	1018
Ile Glu Glu Ser Gln Ile Val Asn Ser Ser Val Gly Pro Phe Ala His	
310 315 320	
GCG CGC CCT AAA AGC GTG ATT TGT AAT AGC CAT GTG GGG AAT TTT GTA	1066
Ala Arg Pro Lys Ser Val Ile Cys Asn Ser His Val Gly Asn Phe Val	
325 330 335	
GAG ACT AAA AAC GCT AAA CTT CAA GGC ACT AAA GCA GGG CAT TTG AGC	1114
Glu Thr Lys Asn Ala Lys Leu Gln Gly Thr Lys Ala Gly His Leu Ser	
340 345 350	
TAT TTA GGG GAT TGT GAG ATA GGG AAA AAC ACA AAT GTA GGG GCT GGC	1162
Tyr Leu Gly Asp Cys Glu Ile Gly Lys Asn Thr Asn Val Gly Ala Gly	
355 360 365	
GTG ATC ACT TGC AAT TAC GAT GGT AAA AAG AAA CAC CAA ACA ATC ATC	1210
Val Ile Thr Cys Asn Tyr Asp Gly Lys Lys Lys His Gln Thr Ile Ile	
370 375 380 385	
GGT GAA AAT GTC TTT ATA GGG AGC GAT AGC CAG CTA GTC GCC CCC ATA	1258
Gly Glu Asn Val Phe Ile Gly Ser Asp Ser Gln Leu Val Ala Pro Ile	
390 395 400	
AAT ATC GGC TCT AAT GTC TTA ATC GGC AGC GGC ACC ACT ATC ACT AAA	1306
Asn Ile Gly Ser Asn Val Leu Ile Gly Ser Gly Thr Thr Ile Thr Lys	
405 410 415	
GAC ATT CCT AGC GGT TCG TTG AGC CTT TCA CGC GCC CCT CAA ACC AAC	1354
Asp Ile Pro Ser Gly Ser Leu Ser Leu Ser Arg Ala Pro Gln Thr Asn	
420 425 430	
ATT GAA AAC GGG TAT TTT AAG TTT TTT AAG AAA CCT TAATTTGTTT GAATAA	1406
Ile Glu Asn Gly Tyr Phe Lys Phe Phe Lys Lys Pro	
435 440 445	
TGAAAAATCC TAAATATTA ATCATTACT TTAA	1440

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Met	Leu	Lys	Phe	Pro	Lys	Met	Ser	Leu	Arg	Ile	Leu	Met	Leu	Ser	Val
1				5					10					15	
Ile	Ile	Leu	Ala	Ala	Gly	Lys	Gly	Thr	Arg	Met	Arg	Ser	Ser	Leu	Pro

[REDACTED]

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 771 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 227...715
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

GCAAAGATAA	AAAACAAACG	GGTTTTGGTG	AAATTTTCTG	GGGAAGCGTT	AGCTGGNGGA	60
CAACCAGTTT	GGGATTGACA	TTCATGTGTT	AGATCACATC	GCTAAAGAGA	TCAAAAAGTTT	120
AGTGGAAAAAC	GATATTGAAG	TGGGTATTGT	GATTGGTGGA	GGCAATATTA	TTAGGGGGGT	180
TAGCGCGGCT	CAAGGGGGGA	TTATTAGGCG	CACCAGTGGG	GATTAT ATG	GGC ATG	235
				Met Gly Met		
				1		
TTA GCC ACC GTG ATT AAT GCG GTA GCG ATG CAA GAA GCT TTA GAG CAT						283
Leu Ala Thr Val Ile Asn Ala Val Ala Met Gln Glu Ala Leu Glu His						
5		10		15		
ATC GGC TTA GAC ACA AGG GTG CAG AGC GCG ATT GAA ATC AAA GAG ATT						331
Ile Gly Leu Asp Thr Arg Val Gln Ser Ala Ile Glu Ile Lys Glu Ile						
20	25		30		35	
TGT GAA AGT TAC ATT TAC AGA AAA GCG ATC AGG CAT TTA GAA AAG GGT						379
Cys Glu Ser Tyr Ile Tyr Arg Lys Ala Ile Arg His Leu Glu Lys Gly						
	40		45		50	
AGG GTG GTG ATT TTT GGC GCA GGC ACG GGA AAC CCG TTT TTC ACT ACG						427
Arg Val Val Ile Phe Gly Ala Gly Thr Gly Asn Pro Phe Phe Thr Thr						
	55		60		65	
GAT ACG GCT GCC ACT TTA AGA GCG ATT GAA ATT GGA TCG GAT TTA ATC						475
Asp Thr Ala Ala Thr Leu Arg Ala Ile Glu Ile Gly Ser Asp Leu Ile						
	70		75		80	
ATT AAA GCG ACT AAA GTG GAT GGC ATT TAC GAC AAA GAT CCT AAC AAG						523
Ile Lys Ala Thr Lys Val Asp Gly Ile Tyr Asp Lys Asp Pro Asn Lys						
	85		90		95	
TTT AAA GAC GCT AAA AAA TTA GAC ACT TTA AGC TAT AAC GAT GCC TTG						571
Phe Lys Asp Ala Lys Lys Leu Asp Thr Leu Ser Tyr Asn Asp Ala Leu						
100		105		110		115
ATA GGG GAT ATT GAA GTG ATG GAC GAT ACC GCT ATT TCT TTA GCT AAA						619
Ile Gly Asp Ile Glu Val Met Asp Asp Thr Ala Ile Ser Leu Ala Lys						
	120		125		130	
GAC AAT AAG CTC CCC ATT GTG GTG TGT AAC ATG TTC AAA AAA GGG AAT						667
Asp Asn Lys Leu Pro Ile Val Val Cys Asn Met Phe Lys Lys Gly Asn						
	135		140		145	

TTA TTG CAA GTG ATC AAG CAC CAA CAA GGC GTA TTT TCT ATG GTA AAA T 716
 Leu Leu Gln Val Ile Lys His Gln Gln Gly Val Phe Ser Met Val Lys
 150 155 160

AAGCCCTTTA ACATTGGATA GAACTCAAAA TAAAAGGATC AGTTTGAAAA AAGAG 771

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

Met	Gly	Met	Leu	Ala	Thr	Val	Ile	Asn	Ala	Val	Ala	Met	Gln	Glu	Ala
1				5					10					15	
Leu	Glu	His	Ile	Gly	Leu	Asp	Thr	Arg	Val	Gln	Ser	Ala	Ile	Glu	Ile
			20					25					30		
Lys	Glu	Ile	Cys	Glu	Ser	Tyr	Ile	Tyr	Arg	Lys	Ala	Ile	Arg	His	Leu
		35					40					45			
Glu	Lys	Gly	Arg	Val	Val	Ile	Phe	Gly	Ala	Gly	Thr	Gly	Asn	Pro	Phe
	50					55					60				
Phe	Thr	Thr	Asp	Thr	Ala	Ala	Thr	Leu	Arg	Ala	Ile	Glu	Ile	Gly	Ser
65					70				75					80	
Asp	Leu	Ile	Ile	Lys	Ala	Thr	Lys	Val	Asp	Gly	Ile	Tyr	Asp	Lys	Asp
				85					90					95	
Pro	Asn	Lys	Phe	Lys	Asp	Ala	Lys	Lys	Leu	Asp	Thr	Leu	Ser	Tyr	Asn
			100					105					110		
Asp	Ala	Leu	Ile	Gly	Asp	Ile	Glu	Val	Met	Asp	Asp	Thr	Ala	Ile	Ser
		115					120					125			
Leu	Ala	Lys	Asp	Asn	Lys	Leu	Pro	Ile	Val	Val	Cys	Asn	Met	Phe	Lys
	130					135					140				
Lys	Gly	Asn	Leu	Leu	Gln	Val	Ile	Lys	His	Gln	Gln	Gly	Val	Phe	Ser
145					150					155					160
Met	Val	Lys													

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 659 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 56...607
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

TCATGTAAAA TAAAGGGTTT TATTAAAGAT GAGAGATTGT TTTAAGGTTT GAATA ATG	58
Met	
1	
AGA GCT TTT TTA AAG ATT TTA ATG GTT TTG ATT TTT ATG AGC GTT GCT	106
Arg Ala Phe Leu Lys Ile Leu Met Val Leu Ile Phe Met Ser Val Ala	
5 10 15	
TAT GCT AAA AAT CCT TCA ACG CTT TCT AAA GAA GAA GAG GTT TTG CAG	154
Tyr Ala Lys Asn Pro Ser Thr Leu Ser Lys Glu Glu Glu Val Leu Gln	
20 25 30	
CAT TTG CAA AGT TTT AGC GCG CAT TTC AAG CAG GTT TTA AAA AAT GAA	202
His Leu Gln Ser Phe Ser Ala His Phe Lys Gln Val Leu Lys Asn Glu	
35 40 45	
AAA CCT TTA GTT TAT TAC GGG GTT TTA AAG GCT AAA GCC CCT AAT TGG	250
Lys Pro Leu Val Tyr Tyr Gly Val Leu Lys Ala Lys Ala Pro Asn Trp	
50 55 60 65	
GCT TTA TGG GTT TAT GAA AAG CCT TTA AAA AAA GAA ATT TAC ATG AAC	298
Ala Leu Trp Val Tyr Glu Lys Pro Leu Lys Lys Glu Ile Tyr Met Asn	
70 75 80	
GAT AAA GAA GTG GTA ATT TAT GAG CCT AAT TTG TTT CAA GCG ACC ATC	346
Asp Lys Glu Val Val Ile Tyr Glu Pro Asn Leu Phe Gln Ala Thr Ile	
85 90 95	
ACG CCC TTA AAA GAC AAG ACG GAT TTT TTC ACC ATT CTC AAG CGT TTA	394
Thr Pro Leu Lys Asp Lys Thr Asp Phe Phe Thr Ile Leu Lys Arg Leu	
100 105 110	
AAA AAG CAA GAT GAC GGA TCT TTT AAA ACG ACT ATC AAC AAA ACC ACT	442
Lys Lys Gln Asp Asp Gly Ser Phe Lys Thr Thr Ile Asn Lys Thr Thr	
115 120 125	
TAT CGT TTG GTT TTT AAA GAC GGC AAG CCT TTT TCA TTG GAA TTT AAA	490
Tyr Arg Leu Val Phe Lys Asp Gly Lys Pro Phe Ser Leu Glu Phe Lys	
130 135 140 145	
GAT GGA ATG AAC AAT CTT GTA ACG ATC ACT TTT TCT CAA GCA GAA ATC	538
Asp Gly Met Asn Asn Leu Val Thr Ile Thr Phe Ser Gln Ala Glu Ile	
150 155 160	
AAC CCC ACC ATT GCT AAT GAA ATC TTT GTT TTT AAG CCT AAA GAT GAA	586
Asn Pro Thr Ile Ala Asn Glu Ile Phe Val Phe Lys Pro Lys Asp Glu	
165 170 175	
AAC ATT GAT ATT GTG CGC CAA TGATTTTAA TGATTCATTG CATCTTGTTA GCAA	641
Asn Ile Asp Ile Val Arg Gln	
180	
AAGTTAGCTA AAATAGAC	659

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

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Met Arg Ala Phe Leu Lys Ile Leu Met Val Leu Ile Phe Met Ser Val
 1           5           10           15
Ala Tyr Ala Lys Asn Pro Ser Thr Leu Ser Lys Glu Glu Glu Val Leu
 20           25           30
Gln His Leu Gln Ser Phe Ser Ala His Phe Lys Gln Val Leu Lys Asn
 35           40           45
Glu Lys Pro Leu Val Tyr Tyr Gly Val Leu Lys Ala Lys Ala Pro Asn
 50           55           60
Trp Ala Leu Trp Val Tyr Glu Lys Pro Leu Lys Lys Glu Ile Tyr Met
 65           70           75           80
Asn Asp Lys Glu Val Val Ile Tyr Glu Pro Asn Leu Phe Gln Ala Thr
 85           90           95
Ile Thr Pro Leu Lys Asp Lys Thr Asp Phe Phe Thr Ile Leu Lys Arg
100           105           110
Leu Lys Lys Gln Asp Asp Gly Ser Phe Lys Thr Thr Ile Asn Lys Thr
115           120           125
Thr Tyr Arg Leu Val Phe Lys Asp Gly Lys Pro Phe Ser Leu Glu Phe
130           135           140
Lys Asp Gly Met Asn Asn Leu Val Thr Ile Thr Phe Ser Gln Ala Glu
145           150           155           160
Ile Asn Pro Thr Ile Ala Asn Glu Ile Phe Val Phe Lys Pro Lys Asp
165           170           175
Glu Asn Ile Asp Ile Val Arg Gln
180

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(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3035 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 729...2981
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

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GAAACGATCG CAGAAAGCAA TGAAAGCACG GTAGTAGCGG AATTTTCATAG CAGTAATGAA      60
AAAAAAGCGC TTATGAGAGC GAAGCAGAGC TAGAAAGGGC GTTTATTAAG CTTTtagAAA      120
AACAAAGGCTA TGAATTTAAA AAAATCCACA AAGAAGAAGA ATTAAAAGAC AATTtAAAAG      180

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AGCAGTTAGA	AAAGCTTAAT	GATCATTCTT	TCACGCCTAA	AGAATGGGAC	ACTCTTTATT	240									
CTCAATTCAT	CGCTAATAAA	AACGATGACT	ATAAGGCTAA	AACGAAAAAG	ATCCAAGAAG	300									
ATCCGATTTT	TAATCTCACG	CTAGAGAACG	GGAAAACCAA	AAACATTAAA	ATCATTGATA	360									
AGAAAAATAT	CCATAGAAAC	GCCTTGCAAG	TGATCCACCA	ATACAGCAAT	AAAGGGGGGA	420									
AGTATCAAAA	CCGCTATGAT	GTGAGTATCC	TTGTGAATGG	CTTGCCTTTA	GTGCATGTGG	480									
AATTGAAAAA	AAGAGGCGTG	GCGATCAGGG	AGGCGTTCAA	CCAGATCAAG	CGCTATAAAA	540									
GGGATAGTTT	TAGCGCTGAA	GACGGGCTTT	TTGATTTTGT	GCAGATTTT	GTCATCAGTA	600									
ACGGCACGAG	CTCTAAATAC	TATTCAAACA	CCACAAGAAT	AGCCCAGCTG	GAAAAAAACC	660									
ATAAAGCCGA	TACTTTTGAA	TTCACGAATT	ATTGGGCGGA	TAGCAAGAAT	CACAATATTG	720									
AGGATTTA	ATG	GAT	TTT	GCT	AAG	GCG	TTT	TTT	GCA	AAG	CGC	AGC	CTT	TTG	770
	Met	Asp	Phe	Ala	Lys	Ala	Phe	Phe	Ala	Lys	Arg	Ser	Leu	Leu	
	1					5								10	

AAC	GTT	TTA	ACG	TGC	TAT	TGC	GTT	TTC	ACA	AGC	GAA	GAG	GTT	TTA	TTG	818
Asn	Val	Leu	Thr	Cys	Tyr	Cys	Val	Phe	Thr	Ser	Glu	Glu	Val	Leu	Leu	
15					20					25					30	

GTG	ATG	CGG	CCT	TAT	CAA	ATC	GTG	GCG	GCC	GAA	AGG	ATT	TTG	GAA	AAG	866
Val	Met	Arg	Pro	Tyr	Gln	Ile	Val	Ala	Ala	Glu	Arg	Ile	Leu	Glu	Lys	
				35					40					45		

ATC	AAA	ACC	GCG	CAA	AAT	AGT	AAA	ACG	AAA	AAT	CAA	AGC	AAA	GGC	TAT	914
Ile	Lys	Thr	Ala	Gln	Asn	Ser	Lys	Thr	Lys	Asn	Gln	Ser	Lys	Gly	Tyr	
			50					55						60		

ATC	TGG	CAC	ACG	ACA	GGG	AGC	GGT	AAA	ACC	CTA	ACG	AGC	TTT	AAA	AGC	962
Ile	Trp	His	Thr	Thr	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ser	Phe	Lys	Ser	
		65					70					75				

GCA	ACG	TTG	GCT	AAA	GAA	TTA	GAG	AGC	GTT	TCA	AAA	GTC	TTG	TTC	GTG	1010
Ala	Thr	Leu	Ala	Lys	Glu	Leu	Glu	Ser	Val	Ser	Lys	Val	Leu	Phe	Val	
	80					85					90					

GTG	GAC	AGG	AAG	GAT	TTG	GAC	TAT	CAA	ACC	ATG	AAA	GAA	TAC	GAT	AAA	1058
Val	Asp	Arg	Lys	Asp	Leu	Asp	Tyr	Gln	Thr	Met	Lys	Glu	Tyr	Asp	Lys	
95					100					105					110	

TTC	CAA	AAA	GAT	TGC	GCT	AAT	TCC	AAC	ACA	AGC	ACT	AAG	ATT	TTA	AAA	1106
Phe	Gln	Lys	Asp	Cys	Ala	Asn	Ser	Asn	Thr	Ser	Thr	Lys	Ile	Leu	Lys	
				115					120					125		

GAA	CAG	CTT	GAA	GAT	TCT	AAC	GCT	AAA	ATC	ATT	ATC	ACC	ACG	ATC	CAA	1154
Glu	Gln	Leu	Glu	Asp	Ser	Asn	Ala	Lys	Ile	Ile	Ile	Thr	Thr	Ile	Gln	
			130					135					140			

AAA	TTA	GAC	AAA	TTC	GTT	AAA	TCC	CAT	AAA	GGG	CAT	GCG	ATT	TTT	AAT	1202
Lys	Leu	Asp	Lys	Phe	Val	Lys	Ser	His	Lys	Gly	His	Ala	Ile	Phe	Asn	
		145					150					155				

GAA	GAA	GTT	GTG	ATG	ATT	TTT	GAT	GAA	TGC	CAC	AGG	AGT	CAG	TTA	GGC	1250
Glu	Glu	Val	Val	Met	Ile	Phe	Asp	Glu	Cys	His	Arg	Ser	Gln	Leu	Gly	
	160					165					170					

TCT	ATG	CAT	CAA	GCC	ATC	ACT	AAA	GCG	TTT	AAA	AAA	TAC	CAC	CTT	TTT	1298
Ser	Met	His	Gln	Ala	Ile	Thr	Lys	Ala	Phe	Lys	Lys	Tyr	His	Leu	Phe	
175					180					185					190	

GGC	TTT	ACT	GGC	ACG	CCC	ATT	TTT	GCA	GCT	AAT	TGC	GAT	AAA	AAC	AAC	1346
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Gly	Phe	Thr	Gly	Thr	Pro	Ile	Phe	Ala	Ala	Asn	Cys	Asp	Lys	Asn	Asn	
				195					200					205		
CCT	TTA	GGC	ACG	ACA	GAG	CAA	AAG	TTT	GGG	AAA	TGC	CTC	CAC	CAA	TAC	1394
Pro	Leu	Gly	Thr	Thr	Glu	Gln	Lys	Phe	Gly	Lys	Cys	Leu	His	Gln	Tyr	
			210					215					220			
ACC	ATT	ATT	GAT	GCG	ATC	AGG	GAT	AAA	AAC	GTT	TTG	CCC	TTT	AGA	GTG	1442
Thr	Ile	Ile	Asp	Ala	Ile	Arg	Asp	Lys	Asn	Val	Leu	Pro	Phe	Arg	Val	
		225					230					235				
GAA	TAC	CAC	AAC	ACC	ATT	AAA	GCT	AAA	GAG	GAC	ATT	AAG	GAT	AAT	AAG	1490
Glu	Tyr	His	Asn	Thr	Ile	Lys	Ala	Lys	Glu	Asp	Ile	Lys	Asp	Asn	Lys	
	240					245					250					
GTT	AGA	GCG	GTT	GAT	GAA	AAA	AAC	GCC	CTT	TTG	GAT	ACT	AGG	AGG	ATC	1538
Val	Arg	Ala	Val	Asp	Glu	Lys	Asn	Ala	Leu	Leu	Asp	Thr	Arg	Arg	Ile	
255					260					265					270	
AAA	GAA	ATC	ACT	AAA	TGC	ATT	TTA	GAG	CGT	TTC	AAT	CAA	GCC	ACT	AAA	1586
Lys	Glu	Ile	Thr	Lys	Cys	Ile	Leu	Glu	Arg	Phe	Asn	Gln	Ala	Thr	Lys	
				275				280						285		
AAT	AAA	AAA	TTC	AAT	TCC	ATT	CTG	GCA	TGC	TCT	AGC	ATA	GAA	GCG	CTG	1634
Asn	Lys	Lys	Phe	Asn	Ser	Ile	Leu	Ala	Cys	Ser	Ser	Ile	Glu	Ala	Leu	
			290					295					300			
AAA	AAA	TAC	TAC	CAA	GCC	TTT	AAA	GAA	GAA	AAA	CAC	GAT	CTT	AAA	ATC	1682
Lys	Lys	Tyr	Tyr	Gln	Ala	Phe	Lys	Glu	Glu	Lys	His	Asp	Leu	Lys	Ile	
		305					310					315				
GCT	GCC	ATT	TTT	AGC	TAT	AGC	GCT	AAT	GAG	GAA	ATT	GAC	ACG	CTA	GAA	1730
Ala	Ala	Ile	Phe	Ser	Tyr	Ser	Ala	Asn	Glu	Glu	Ile	Asp	Thr	Leu	Glu	
	320					325					330					
GAT	GAA	AAC	AAT	GAA	AGC	GCT	TGC	CGG	CTA	GAC	AAA	AGC	TCA	AGG	GAT	1778
Asp	Glu	Asn	Asn	Glu	Ser	Ala	Cys	Arg	Leu	Asp	Lys	Ser	Ser	Arg	Asp	
335					340					345					350	
TTT	TTA	GAG	GGC	GCG	ATT	GCG	GAT	TAT	AAT	GGG	ATG	TTT	GGC	GTT	TCT	1826
Phe	Leu	Glu	Gly	Ala	Ile	Ala	Asp	Tyr	Asn	Gly	Met	Phe	Gly	Val	Ser	
				355					360					365		
TTT	GAC	ACT	TCG	GAT	CAA	AAA	TTC	CAA	AGT	TAT	TAC	AAG	GAT	CTT	TCT	1874
Phe	Asp	Thr	Ser	Asp	Gln	Lys	Phe	Gln	Ser	Tyr	Tyr	Lys	Asp	Leu	Ser	
			370					375					380			
CAA	AAA	ATG	AAA	GAG	CGT	AAA	ATC	GAT	CTT	TTA	ATG	GTG	GTG	AAC	ATG	1922
Gln	Lys	Met	Lys	Glu	Arg	Lys	Ile	Asp	Leu	Leu	Met	Val	Val	Asn	Met	
		385					390					395				
TTT	TTG	ACC	GGG	TTT	GAC	GCT	ACA	AGG	CTC	AAC	ACC	CTT	TGG	GTG	GAT	1970
Phe	Leu	Thr	Gly	Phe	Asp	Ala	Thr	Arg	Leu	Asn	Thr	Leu	Trp	Val	Asp	
	400					405					410					
AAA	AAT	CTC	AAA	TAC	CAT	GGG	CTA	ATT	CAA	GCT	TTT	TCA	CGC	GCA	AAC	2018
Lys	Asn	Leu	Lys	Tyr	His	Gly	Leu	Ile	Gln	Ala	Phe	Ser	Arg	Ala	Asn	
415					420					425					430	

CGC	ATT	TTA	GAT	AGC	GTT	AAA	ACG	CAT	GGG	AAT	ATC	GTG	TGT	TTT	AGG	2066
Arg	Ile	Leu	Asp	Ser	Val	Lys	Thr	His	Gly	Asn	Ile	Val	Cys	Phe	Arg	
				435					440						445	
GAT	TTA	GAA	CAG	GAT	TTG	AAT	GAC	GCT	CTC	ATG	CTT	TTT	GGC	AAC	AAG	2114
Asp	Leu	Glu	Gln	Asp	Leu	Asn	Asp	Ala	Leu	Met	Leu	Phe	Gly	Asn	Lys	
			450					455					460			
GAC	GCT	CAA	TCT	ATT	GCG	CTG	TTA	AGA	AAA	TAT	GAA	GAT	TAT	TTG	AAA	2162
Asp	Ala	Gln	Ser	Ile	Ala	Leu	Leu	Arg	Lys	Tyr	Glu	Asp	Tyr	Leu	Lys	
		465					470					475				
GGC	TAC	ACG	GAT	AAC	AAC	AAA	GAA	TAC	GAG	GGC	TAT	GAG	GGT	TTG	ATT	2210
Gly	Tyr	Thr	Asp	Asn	Asn	Lys	Glu	Tyr	Glu	Gly	Tyr	Glu	Gly	Leu	Ile	
	480					485					490					
AAA	AGG	CTT	TTA	ACC	GAA	TTC	CCA	TTA	AAA	GAG	CCA	ATC	GTT	TCA	GAA	2258
Lys	Arg	Leu	Leu	Thr	Glu	Phe	Pro	Leu	Lys	Glu	Pro	Ile	Val	Ser	Glu	
495					500					505					510	
AGC	CAG	AAA	AAG	GAT	TTT	ATT	AAG	CTT	TTT	GGC	AAG	ATT	TTG	AAA	TTA	2306
Ser	Gln	Lys	Lys	Asp	Phe	Ile	Lys	Leu	Phe	Gly	Lys	Ile	Leu	Lys	Leu	
				515					520					525		
GAA	AAT	ATT	TTA	AAC	AGC	TTT	GAA	AAT	TTC	AAA	AAA	GAC	GAT	TAC	ATC	2354
Glu	Asn	Ile	Leu	Asn	Ser	Phe	Glu	Asn	Phe	Lys	Lys	Asp	Asp	Tyr	Ile	
			530					535					540			
AAT	CCC	AGG	GAT	TTT	CAA	GAC	TAT	CAA	AGC	AAA	TAC	CTT	GAT	TTT	TAC	2402
Asn	Pro	Arg	Asp	Phe	Gln	Asp	Tyr	Gln	Ser	Lys	Tyr	Leu	Asp	Phe	Tyr	
		545					550					555				
GAT	GCA	ATG	AGA	TCA	GAA	AAA	GGG	AAG	GAT	AAA	GAA	GAG	ATT	AAT	GAT	2450
Asp	Ala	Met	Arg	Ser	Glu	Lys	Gly	Lys	Asp	Lys	Glu	Glu	Ile	Asn	Asp	
	560					565					570					
GAT	TTG	ATT	TTT	GAA	ATT	GAA	CTC	ATC	AAA	CAA	GTG	GAA	GTC	AAT	ATT	2498
Asp	Leu	Ile	Phe	Glu	Ile	Glu	Leu	Ile	Lys	Gln	Val	Glu	Val	Asn	Ile	
575					580					585					590	
GAC	TAT	ATT	TTG	AAT	TTG	ATT	GAA	GAG	TTC	GCT	AAA	GAG	CAT	GGG	GTG	2546
Asp	Tyr	Ile	Leu	Asn	Leu	Ile	Glu	Glu	Phe	Ala	Lys	Glu	His	Gly	Val	
				595				600						605		
GAA	ATC	CAA	GGC	GTT	AAA	ACC	AAA	ATA	GAG	CCA	ATC	ATC	AAC	TCC	AGC	2594
Glu	Ile	Gln	Gly	Val	Lys	Thr	Lys	Ile	Glu	Pro	Ile	Ile	Asn	Ser	Ser	
		610						615					620			
ATA	GAG	TTA	AGG	AAT	AAA	AAA	GAT	TTG	ATC	ATG	GAT	TTC	ATT	GAC	AAA	2642
Ile	Glu	Leu	Arg	Asn	Lys	Lys	Asp	Leu	Ile	Met	Asp	Phe	Ile	Asp	Lys	
		625					630					635				
TAC	AAC	AAA	GAC	CAA	GAA	GTC	CAT	GCG	CAT	TTT	CAA	GAT	TAT	ATC	CAC	2690
Tyr	Asn	Lys	Asp	Gln	Glu	Val	His	Ala	His	Phe	Gln	Asp	Tyr	Ile	His	
	640					645					650					
CAA	AAA	AGA	GAA	GAG	GAA	TTC	CAA	AAT	ATC	ATA	GAA	GAA	AAC	CGC	TTG	2738
Gln	Lys	Arg	Glu	Glu	Glu	Phe	Gln	Asn	Ile	Ile	Glu	Glu	Asn	Arg	Leu	

655	660	665	670	
AAT GAA GAA AAA GCC TAT TCG TTC ATG CAG CAT GCC TTT AAA GGG GGC				2786
Asn Glu Glu Lys Ala Tyr Ser Phe Met Gln His Ala Phe Lys Gly Gly	675	680	685	
GAA ATC AGT TTT AGT GGG ACG GAA TTC CCT AAA ATC ATT GAA GAA AAA				2834
Glu Ile Ser Phe Ser Gly Thr Glu Phe Pro Lys Ile Ile Glu Glu Lys	690	695	700	
CCC TCC ATG TTT GGT AAA AAT TCG CGC TAT CAA GAG GTG AAA GAA AAA				2882
Pro Ser Met Phe Gly Lys Asn Ser Arg Tyr Gln Glu Val Lys Glu Lys	705	710	715	
GTC GCT GCA AGC CTT TCT CGT TTT TTC CAC CGC TTT TGT GAT CTC ACT				2930
Val Ala Ala Ser Leu Ser Arg Phe Phe His Arg Phe Cys Asp Leu Thr	720	725	730	
AGC GCT ATA TTT AAG AAA AAT GAG GTT AAA AAA GAT GAG GTT AAT GAA				2978
Ser Ala Ile Phe Lys Lys Asn Glu Val Lys Lys Asp Glu Val Asn Glu	735	740	745	750
AAA TAGTTCATGA ACGCTTTTGC ATTAAGGCTC AAAAAAGCG CCGTTTAATG GATT				3035
Lys				

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Met	Asp	Phe	Ala	Lys	Ala	Phe	Phe	Ala	Lys	Arg	Ser	Leu	Leu	Asn	Val
1				5					10					15	
Leu	Thr	Cys	Tyr	Cys	Val	Phe	Thr	Ser	Glu	Glu	Val	Leu	Leu	Val	Met
			20					25					30		
Arg	Pro	Tyr	Gln	Ile	Val	Ala	Ala	Glu	Arg	Ile	Leu	Glu	Lys	Ile	Lys
		35					40					45			
Thr	Ala	Gln	Asn	Ser	Lys	Thr	Lys	Asn	Gln	Ser	Lys	Gly	Tyr	Ile	Trp
	50						55				60				
His	Thr	Thr	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ser	Phe	Lys	Ser	Ala	Thr
	65				70				75					80	
Leu	Ala	Lys	Glu	Leu	Glu	Ser	Val	Ser	Lys	Val	Leu	Phe	Val	Val	Asp
			85						90					95	
Arg	Lys	Asp	Leu	Asp	Tyr	Gln	Thr	Met	Lys	Glu	Tyr	Asp	Lys	Phe	Gln
		100						105					110		
Lys	Asp	Cys	Ala	Asn	Ser	Asn	Thr	Ser	Thr	Lys	Ile	Leu	Lys	Glu	Gln
		115					120					125			
Leu	Glu	Asp	Ser	Asn	Ala	Lys	Ile	Ile	Ile	Thr	Thr	Ile	Gln	Lys	Leu
	130						135					140			

Asp	Lys	Phe	Val	Lys	Ser	His	Lys	Gly	His	Ala	Ile	Phe	Asn	Glu	Glu
145					150					155					160
Val	Val	Met	Ile	Phe	Asp	Glu	Cys	His	Arg	Ser	Gln	Leu	Gly	Ser	Met
				165					170					175	
His	Gln	Ala	Ile	Thr	Lys	Ala	Phe	Lys	Lys	Tyr	His	Leu	Phe	Gly	Phe
			180					185					190		
Thr	Gly	Thr	Pro	Ile	Phe	Ala	Ala	Asn	Cys	Asp	Lys	Asn	Asn	Pro	Leu
		195					200					205			
Gly	Thr	Thr	Glu	Gln	Lys	Phe	Gly	Lys	Cys	Leu	His	Gln	Tyr	Thr	Ile
	210					215					220				
Ile	Asp	Ala	Ile	Arg	Asp	Lys	Asn	Val	Leu	Pro	Phe	Arg	Val	Glu	Tyr
225					230					235					240
His	Asn	Thr	Ile	Lys	Ala	Lys	Glu	Asp	Ile	Lys	Asp	Asn	Lys	Val	Arg
				245					250					255	
Ala	Val	Asp	Glu	Lys	Asn	Ala	Leu	Leu	Asp	Thr	Arg	Arg	Ile	Lys	Glu
			260					265					270		
Ile	Thr	Lys	Cys	Ile	Leu	Glu	Arg	Phe	Asn	Gln	Ala	Thr	Lys	Asn	Lys
		275					280					285			
Lys	Phe	Asn	Ser	Ile	Leu	Ala	Cys	Ser	Ser	Ile	Glu	Ala	Leu	Lys	Lys
	290					295					300				
Tyr	Tyr	Gln	Ala	Phe	Lys	Glu	Glu	Lys	His	Asp	Leu	Lys	Ile	Ala	Ala
305					310					315					320
Ile	Phe	Ser	Tyr	Ser	Ala	Asn	Glu	Glu	Ile	Asp	Thr	Leu	Glu	Asp	Glu
				325					330					335	
Asn	Asn	Glu	Ser	Ala	Cys	Arg	Leu	Asp	Lys	Ser	Ser	Arg	Asp	Phe	Leu
			340					345					350		
Glu	Gly	Ala	Ile	Ala	Asp	Tyr	Asn	Gly	Met	Phe	Gly	Val	Ser	Phe	Asp
		355					360					365			
Thr	Ser	Asp	Gln	Lys	Phe	Gln	Ser	Tyr	Tyr	Lys	Asp	Leu	Ser	Gln	Lys
	370					375					380				
Met	Lys	Glu	Arg	Lys	Ile	Asp	Leu	Leu	Met	Val	Val	Asn	Met	Phe	Leu
385					390					395					400
Thr	Gly	Phe	Asp	Ala	Thr	Arg	Leu	Asn	Thr	Leu	Trp	Val	Asp	Lys	Asn
				405					410					415	
Leu	Lys	Tyr	His	Gly	Leu	Ile	Gln	Ala	Phe	Ser	Arg	Ala	Asn	Arg	Ile
			420					425					430		
Leu	Asp	Ser	Val	Lys	Thr	His	Gly	Asn	Ile	Val	Cys	Phe	Arg	Asp	Leu
		435					440					445			
Glu	Gln	Asp	Leu	Asn	Asp	Ala	Leu	Met	Leu	Phe	Gly	Asn	Lys	Asp	Ala
	450					455					460				
Gln	Ser	Ile	Ala	Leu	Leu	Arg	Lys	Tyr	Glu	Asp	Tyr	Leu	Lys	Gly	Tyr
465					470					475					480
Thr	Asp	Asn	Asn	Lys	Glu	Tyr	Glu	Gly	Tyr	Glu	Gly	Leu	Ile	Lys	Arg
				485					490					495	
Leu	Leu	Thr	Glu	Phe	Pro	Leu	Lys	Glu	Pro	Ile	Val	Ser	Glu	Ser	Gln
		500						505					510		
Lys	Lys	Asp	Phe	Ile	Lys	Leu	Phe	Gly	Lys	Ile	Leu	Lys	Leu	Glu	Asn
		515					520					525			
Ile	Leu	Asn	Ser	Phe	Glu	Asn	Phe	Lys	Lys	Asp	Asp	Tyr	Ile	Asn	Pro
	530					535					540				
Arg	Asp	Phe	Gln	Asp	Tyr	Gln	Ser	Lys	Tyr	Leu	Asp	Phe	Tyr	Asp	Ala
545					550					555					560
Met	Arg	Ser	Glu	Lys	Gly	Lys	Asp	Lys	Glu	Glu	Ile	Asn	Asp	Asp	Leu
				565					570					575	
Ile	Phe	Glu	Ile	Glu	Leu	Ile	Lys	Gln	Val	Glu	Val	Asn	Ile	Asp	Tyr
			580					585				590			
Ile	Leu	Asn	Leu	Ile	Glu	Glu	Phe	Ala	Lys	Glu	His	Gly	Val	Glu	Ile
		595					600					605			

Gln	Gly	Val	Lys	Thr	Lys	Ile	Glu	Pro	Ile	Ile	Asn	Ser	Ser	Ile	Glu
610						615					620				
Leu	Arg	Asn	Lys	Lys	Asp	Leu	Ile	Met	Asp	Phe	Ile	Asp	Lys	Tyr	Asn
625					630					635					640
Lys	Asp	Gln	Glu	Val	His	Ala	His	Phe	Gln	Asp	Tyr	Ile	His	Gln	Lys
				645					650					655	
Arg	Glu	Glu	Glu	Phe	Gln	Asn	Ile	Ile	Glu	Glu	Asn	Arg	Leu	Asn	Glu
			660					665					670		
Glu	Lys	Ala	Tyr	Ser	Phe	Met	Gln	His	Ala	Phe	Lys	Gly	Gly	Glu	Ile
		675					680					685			
Ser	Phe	Ser	Gly	Thr	Glu	Phe	Pro	Lys	Ile	Ile	Glu	Glu	Lys	Pro	Ser
	690					695					700				
Met	Phe	Gly	Lys	Asn	Ser	Arg	Tyr	Gln	Glu	Val	Lys	Glu	Lys	Val	Ala
705				710						715					720
Ala	Ser	Leu	Ser	Arg	Phe	Phe	His	Arg	Phe	Cys	Asp	Leu	Thr	Ser	Ala
				725					730					735	
Ile	Phe	Lys	Lys	Asn	Glu	Val	Lys	Lys	Asp	Glu	Val	Asn	Glu	Lys	
			740					745					750		

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 850 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 68...799
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

ACCACTATTG	TAGAAAAATA	ACAAGAGGGT	TTGCAAAAAC	TCTCATTAAA	AACAAGGAGC	60
AAAAAAG	ATG AAA AAG	GCG GGC TTT	CTT TTT TTA	GCG GTA ATG	GCT ATC	109
Met	Lys Lys Ala	Gly Phe Leu	Phe Leu Ala	Val Met Ala	Ile	
1		5		10		
GTT GTT ATG	AGT TTA AAC	GCT AAA GAT	CCG AAT GTG	TTG CGT AAG	ATT	157
Val Val Met	Ser Leu Asn	Ala Lys Asp	Pro Asn Val	Leu Arg Lys	Ile	
15		20		25	30	
GTT TTT GAG	AAA TGT CTG	CCT AAT TAT	GAG AAA AAT	CAG AAT CCT	TCG	205
Val Phe Glu	Lys Cys Leu	Pro Asn Tyr	Glu Lys Asn	Gln Asn Pro	Ser	
	35		40		45	
CCA TGC ATA	GAA GTC AAA	CCC GAT GCC	GGC TAT GTG	GTT TTA AAA	GAT	253
Pro Cys Ile	Glu Val Lys	Pro Asp Ala	Gly Tyr Val	Val Leu Lys	Asp	
	50		55		60	
ATT AAC GGC	CCG TTG CAA	TAT TTG TTG	ATG CCA ACA	ACT CAC ATT	AGC	301
Ile Asn Gly	Pro Leu Gln	Tyr Leu Leu	Met Pro Thr	Thr His Ile	Ser	
	65		70		75	

GGT ATT GAA AGC CCT TTG TTA CTT GAT CCT TCT ACG CCT AAC TTT TTT	349
Gly Ile Glu Ser Pro Leu Leu Leu Asp Pro Ser Thr Pro Asn Phe Phe	
80 85 90	
TAT TTA TCC TGG CAA GCG CGT GAT TTT ATG AGT AAA AAA TAC GGC CAA	397
Tyr Leu Ser Trp Gln Ala Arg Asp Phe Met Ser Lys Lys Tyr Gly Gln	
95 100 105 110	
CCC ATT CCT GAT TAT GCG ATT TCT TTG ACG ATT AAC TCT AGC AAA GGG	445
Pro Ile Pro Asp Tyr Ala Ile Ser Leu Thr Ile Asn Ser Ser Lys Gly	
115 120 125	
CGA TCG CAA AAC CAT TTT CAT ATC CAT ATC TCT TGC ATT AGT CTT GAA	493
Arg Ser Gln Asn His Phe His Ile His Ile Ser Cys Ile Ser Leu Glu	
130 135 140	
GCA CGC AAA CAG CTG GAT AAT AAC CTA AAA AAA ATC AAC AGC CGT TGG	541
Ala Arg Lys Gln Leu Asp Asn Asn Leu Lys Lys Ile Asn Ser Arg Trp	
145 150 155	
TCG CCA TTA CCG GGC GGT TTG AAT GGG CAT AAA TAC TTG GCG CGT CGG	589
Ser Pro Leu Pro Gly Gly Leu Asn Gly His Lys Tyr Leu Ala Arg Arg	
160 165 170	
GTA ACA GAG AGC GAG TTA GTG CAA AAA AGC CCG TTT GTC ATG CTT AAT	637
Val Thr Glu Ser Glu Leu Val Gln Lys Ser Pro Phe Val Met Leu Asn	
175 180 185 190	
AAA GAA GTG CCT AAT GCG TAC AAA CGC ATG GGG GAC TAT GGC TTA GCG	685
Lys Glu Val Pro Asn Ala Tyr Lys Arg Met Gly Asp Tyr Gly Leu Ala	
195 200 205	
GTG GTG CAA CAA AGC GAT AAC TCC TTT GTC TTA TTA GCG ACA CAA TTT	733
Val Val Gln Gln Ser Asp Asn Ser Phe Val Leu Leu Ala Thr Gln Phe	
210 215 220	
AAC CCA TTG ACT TTA AAT CGC GCT TCA GCC GAA GAG ATT CAA GAT CAT	781
Asn Pro Leu Thr Leu Asn Arg Ala Ser Ala Glu Glu Ile Gln Asp His	
225 230 235	
GAA TGC GCG ATT TTG CAC TAAAGCGAGT TAGATTCTTA AGCTTGAGCG ATAACCTT	837
Glu Cys Ala Ile Leu His	
240	
TAAAAAGCGT TAT	850

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Met	Lys	Lys	Ala	Gly	Phe	Leu	Phe	Leu	Ala	Val	Met	Ala	Ile	Val	Val
1				5					10					15	
Met	Ser	Leu	Asn	Ala	Lys	Asp	Pro	Asn	Val	Leu	Arg	Lys	Ile	Val	Phe
			20					25					30		
Glu	Lys	Cys	Leu	Pro	Asn	Tyr	Glu	Lys	Asn	Gln	Asn	Pro	Ser	Pro	Cys
		35					40					45			
Ile	Glu	Val	Lys	Pro	Asp	Ala	Gly	Tyr	Val	Val	Leu	Lys	Asp	Ile	Asn
	50					55					60				
Gly	Pro	Leu	Gln	Tyr	Leu	Leu	Met	Pro	Thr	Thr	His	Ile	Ser	Gly	Ile
65					70				75					80	
Glu	Ser	Pro	Leu	Leu	Leu	Asp	Pro	Ser	Thr	Pro	Asn	Phe	Phe	Tyr	Leu
			85						90					95	
Ser	Trp	Gln	Ala	Arg	Asp	Phe	Met	Ser	Lys	Lys	Tyr	Gly	Gln	Pro	Ile
			100					105					110		
Pro	Asp	Tyr	Ala	Ile	Ser	Leu	Thr	Ile	Asn	Ser	Ser	Lys	Gly	Arg	Ser
		115					120					125			
Gln	Asn	His	Phe	His	Ile	His	Ile	Ser	Cys	Ile	Ser	Leu	Glu	Ala	Arg
	130					135					140				
Lys	Gln	Leu	Asp	Asn	Asn	Leu	Lys	Lys	Ile	Asn	Ser	Arg	Trp	Ser	Pro
145					150				155					160	
Leu	Pro	Gly	Gly	Leu	Asn	Gly	His	Lys	Tyr	Leu	Ala	Arg	Arg	Val	Thr
			165						170					175	
Glu	Ser	Glu	Leu	Val	Gln	Lys	Ser	Pro	Phe	Val	Met	Leu	Asn	Lys	Glu
			180					185					190		
Val	Pro	Asn	Ala	Tyr	Lys	Arg	Met	Gly	Asp	Tyr	Gly	Leu	Ala	Val	Val
		195					200					205			
Gln	Gln	Ser	Asp	Asn	Ser	Phe	Val	Leu	Leu	Ala	Thr	Gln	Phe	Asn	Pro
	210					215					220				
Leu	Thr	Leu	Asn	Arg	Ala	Ser	Ala	Glu	Glu	Ile	Gln	Asp	His	Glu	Cys
225					230					235				240	
Ala	Ile	Leu	His												

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 57...929
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

GTCCTATTTT TTCATTCATT CAACGAATTT AAAAATTACA ATAAAGAGTT ATAGTT ATG 59
Met
1

AAA CGA AGG GAT TTT ATT AAA ACG ACT ACT TTA GGC GCT ACA GGT GCT 107
Lys Arg Arg Asp Phe Ile Lys Thr Thr Thr Leu Gly Ala Thr Gly Ala

5					10					15						
GTT	TTA	GGA	GCA	CAG	ATT	TTG	CAG	GCA	GAA	GAA	AGT	AAA	GGG	AGT	GTT	155
Val	Leu	Gly	Ala	Gln	Ile	Leu	Gln	Ala	Glu	Glu	Ser	Lys	Gly	Ser	Val	
		20					25					30				
GCA	AAA	TAT	AAA	ATA	GAA	GCT	CAA	TAC	AGC	ATT	GAT	TTT	GAT	TCT	GCA	203
Ala	Lys	Tyr	Lys	Ile	Glu	Ala	Gln	Tyr	Ser	Ile	Asp	Phe	Asp	Ser	Ala	
	35					40					45					
GAA	CAC	ACT	TCA	CTT	TTC	ATT	CCC	ATG	CCG	AGT	GTT	GTA	GCG	AGC	AAT	251
Glu	His	Thr	Ser	Leu	Phe	Ile	Pro	Met	Pro	Ser	Val	Val	Ala	Ser	Asn	
50					55					60					65	
GTG	CAT	TTA	CAA	GGC	AAT	CAT	GCT	AGC	TAT	AAA	AGC	ATG	CTC	AAT	TTT	299
Val	His	Leu	Gln	Gly	Asn	His	Ala	Ser	Tyr	Lys	Ser	Met	Leu	Asn	Phe	
				70					75					80		
GGA	GTG	CCT	TAT	TTG	CAA	GTG	GAT	TTT	TTA	AAA	AGC	ACT	CAA	AAA	AAG	347
Gly	Val	Pro	Tyr	Leu	Gln	Val	Asp	Phe	Leu	Lys	Ser	Thr	Gln	Lys	Lys	
			85					90					95			
CAA	GTC	CAT	TTG	TCT	TAT	GAG	ATC	GCT	AGC	TAT	CAA	TTG	AAT	GAG	CGT	395
Gln	Val	His	Leu	Ser	Tyr	Glu	Ile	Ala	Ser	Tyr	Gln	Leu	Asn	Glu	Arg	
		100					105					110				
TTG	TTT	GAA	ACG	AGC	GAT	TTT	GTA	GCA	ATG	GGG	CGT	TAT	GAA	AGA	GAC	443
Leu	Phe	Glu	Thr	Ser	Asp	Phe	Val	Ala	Met	Gly	Arg	Tyr	Glu	Arg	Asp	
	115					120					125					
GAT	GCG	AGC	GTG	GCT	AAC	ATT	GCC	AAC	CAG	CTT	AAG	GGA	ACA	ACC	CCT	491
Asp	Ala	Ser	Val	Ala	Asn	Ile	Ala	Asn	Gln	Leu	Lys	Gly	Thr	Thr	Pro	
130					135					140					145	
AAA	GAA	AGC	GTT	CGC	AAT	TTT	TAT	GCG	TTC	ATC	AAG	CAT	GAG	ATG	CCT	539
Lys	Glu	Ser	Val	Arg	Asn	Phe	Tyr	Ala	Phe	Ile	Lys	His	Glu	Met	Pro	
				150					155					160		
AAG	AGA	CAG	AAG	GCT	TTA	GAG	GGT	AAA	GAA	AAT	TTA	CCT	AAG	CGT	GAG	587
Lys	Arg	Gln	Lys	Ala	Leu	Glu	Gly	Lys	Glu	Asn	Leu	Pro	Lys	Arg	Glu	
			165					170					175			
AGT	TTG	CCC	TGG	TTT	GCA	ACC	ATT	TCA	AAA	GAG	AGC	ATG	TTT	GTG	TCC	635
Ser	Leu	Pro	Trp	Phe	Ala	Thr	Ile	Ser	Lys	Glu	Ser	Met	Phe	Val	Ser	
		180					185					190				
TTA	TGC	CAT	GCG	TGC	GGG	ATT	AAA	AGC	GCT	GAA	GTG	CAA	GGC	TTG	AAA	683
Leu	Cys	His	Ala	Cys	Gly	Ile	Lys	Ser	Ala	Glu	Val	Gln	Gly	Leu	Lys	
	195					200					205					
CTG	GGT	CAA	AAC	AGC	GTG	GTG	AAA	AAC	GCT	CCT	AGA	GTG	GAA	GTG	TAT	731
Leu	Gly	Gln	Asn	Ser	Val	Val	Lys	Asn	Ala	Pro	Arg	Val	Glu	Val	Tyr	
210					215					220					225	
TTG	AAA	GAT	TCA	TTT	CTA	GCG	TTT	GAT	TTT	CAA	AAT	AAT	CAC	AAG	GAA	779
Leu	Lys	Asp	Ser	Phe	Leu	Ala	Phe	Asp	Phe	Gln	Asn	Asn	His	Lys	Glu	
				230					235					240		

GTT TTT ATC CCG TTG AAT CGT CAT AAA GAC ATG CAG TTA GAT TCT GCC	827
Val Phe Ile Pro Leu Asn Arg His Lys Asp Met Gln Leu Asp Ser Ala	
245 250 255	
TTA TTG GCG ACT TTT GGC GAT GCT TTT GCC CTT GTG GAT GGT AGG GAT	875
Leu Leu Ala Thr Phe Gly Asp Ala Phe Ala Leu Val Asp Gly Arg Asp	
260 265 270	
TTA GGC AAT TAC GAG AGC AAA CTT TTT GAA AAA AGA GTG TCC TAT ACG	923
Leu Gly Asn Tyr Glu Ser Lys Leu Phe Glu Lys Arg Val Ser Tyr Thr	
275 280 285	
ATT GTC TAAAGGCATG AAATCTAGGA ATATTCCTTG ATAGCGGGCT TTCCTTTTTA GG	981
Ile Val	
290	

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Met	Lys	Arg	Arg	Asp	Phe	Ile	Lys	Thr	Thr	Thr	Leu	Gly	Ala	Thr	Gly
1				5					10					15	
Ala	Val	Leu	Gly	Ala	Gln	Ile	Leu	Gln	Ala	Glu	Glu	Ser	Lys	Gly	Ser
		20						25					30		
Val	Ala	Lys	Tyr	Lys	Ile	Glu	Ala	Gln	Tyr	Ser	Ile	Asp	Phe	Asp	Ser
		35					40					45			
Ala	Glu	His	Thr	Ser	Leu	Phe	Ile	Pro	Met	Pro	Ser	Val	Val	Ala	Ser
	50					55				60					
Asn	Val	His	Leu	Gln	Gly	Asn	His	Ala	Ser	Tyr	Lys	Ser	Met	Leu	Asn
65				70					75					80	
Phe	Gly	Val	Pro	Tyr	Leu	Gln	Val	Asp	Phe	Leu	Lys	Ser	Thr	Gln	Lys
			85					90					95		
Lys	Gln	Val	His	Leu	Ser	Tyr	Glu	Ile	Ala	Ser	Tyr	Gln	Leu	Asn	Glu
		100						105					110		
Arg	Leu	Phe	Glu	Thr	Ser	Asp	Phe	Val	Ala	Met	Gly	Arg	Tyr	Glu	Arg
		115				120					125				
Asp	Asp	Ala	Ser	Val	Ala	Asn	Ile	Ala	Asn	Gln	Leu	Lys	Gly	Thr	Thr
	130					135				140					
Pro	Lys	Glu	Ser	Val	Arg	Asn	Phe	Tyr	Ala	Phe	Ile	Lys	His	Glu	Met
145				150					155					160	
Pro	Lys	Arg	Gln	Lys	Ala	Leu	Glu	Gly	Lys	Glu	Asn	Leu	Pro	Lys	Arg
			165					170					175		
Glu	Ser	Leu	Pro	Trp	Phe	Ala	Thr	Ile	Ser	Lys	Glu	Ser	Met	Phe	Val
		180					185					190			
Ser	Leu	Cys	His	Ala	Cys	Gly	Ile	Lys	Ser	Ala	Glu	Val	Gln	Gly	Leu
	195					200					205				
Lys	Leu	Gly	Gln	Asn	Ser	Val	Val	Lys	Asn	Ala	Pro	Arg	Val	Glu	Val
210					215						220				

Tyr Leu Lys Asp Ser Phe Leu Ala Phe Asp Phe Gln Asn Asn His Lys
 225 230 235 240
 Glu Val Phe Ile Pro Leu Asn Arg His Lys Asp Met Gln Leu Asp Ser
 245 250 255
 Ala Leu Leu Ala Thr Phe Gly Asp Ala Phe Ala Leu Val Asp Gly Arg
 260 265 270
 Asp Leu Gly Asn Tyr Glu Ser Lys Leu Phe Glu Lys Arg Val Ser Tyr
 275 280 285
 Thr Ile Val
 290

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 82...633
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

TGTGATTAAA CAAAATCAAA AACTTTTAA CTATAATCAA ACCTAAATTA AAGTTCAAGG 60
 AGTGGCATT TGTTTAAAAG A ATG GTT TTA ATC GCT CTT TTA GGG GTG TTT 111
 Met Val Leu Ile Ala Leu Leu Gly Val Phe
 1 5 10
 TCA AGC GTT TCA TTA AGC GCT AAG AGT CTT TTA AGA GAT GAT GGG ATT 159
 Ser Ser Val Ser Leu Ser Ala Lys Ser Leu Leu Arg Asp Asp Gly Ile
 15 20 25
 TTA GTC TCT GAT TTA AAG GGC ATG AAA TCA GAA CTA TCT GAT GCT CCT 207
 Leu Val Ser Asp Leu Lys Gly Met Lys Ser Glu Leu Ser Asp Ala Pro
 30 35 40
 GCT TGG GTT TTT GAA GAC GCT AAA GCC CCC TAC GAA GAA ATG GGC GTG 255
 Ala Trp Val Phe Glu Asp Ala Lys Ala Pro Tyr Glu Glu Met Gly Val
 45 50 55
 GCG TAT ATC CCT GTT AAT AAT AAA TAT TTA GGG ATT GAG CAA GCG ACC 303
 Ala Tyr Ile Pro Val Asn Asn Lys Tyr Leu Gly Ile Glu Gln Ala Thr
 60 65 70
 TTA AAC GCT AAA TTG AGT CTG ATC GTG GTT TTT CAT GAA ATC ATG ATG 351
 Leu Asn Ala Lys Leu Ser Leu Ile Val Val Phe His Glu Ile Met Met
 75 80 85 90
 AAG TAT AAA AAA CGC TTC ATG GAG CAA TTC CAT GAG TCC GAG CAG ACG 399
 Lys Tyr Lys Lys Arg Phe Met Glu Gln Phe His Glu Ser Glu Gln Thr
 95 100 105

ACT ACG AAT ATC AGT TAC GCT ATC TAT AAT TAT CTA GCG ACT AAG ATC 447
 Thr Thr Asn Ile Ser Tyr Ala Ile Tyr Asn Tyr Leu Ala Thr Lys Ile
 110 115 120

CAG GTA TCC AAC ACC TAC ACG AAT TTA AAA TCG GAG GTG GCG GTG GTG 495
 Gln Val Ser Asn Thr Tyr Thr Asn Leu Lys Ser Glu Val Ala Val Val
 125 130 135

AAA ATC AAG CTA GTG GGT TGT CAG ATT GAG CAA ATC AAA AGG TAT TTA 543
 Lys Ile Lys Leu Val Gly Cys Gln Ile Glu Gln Ile Lys Arg Tyr Leu
 140 145 150

AAA GCG AGC GTT GAA AAC CTT AAC GAT AAT GAA ATC GCT TAC ATC GCT 591
 Lys Ala Ser Val Glu Asn Leu Asn Asp Asn Glu Ile Ala Tyr Ile Ala
 155 160 165 170

AAG GTC GCT CAA AAA GAA TTT GGT AGC GTT TGT GCG TTA AGG TAGTTTTAT 642
 Lys Val Ala Gln Lys Glu Phe Gly Ser Val Cys Ala Leu Arg
 175 180

AGCATTCTAG CGAGCATGTT TAAGGCATGC TCTACGCTTT TATT 686

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

Met Val Leu Ile Ala Leu Leu Gly Val Phe Ser Ser Val Ser Leu Ser
 1 5 10 15
 Ala Lys Ser Leu Leu Arg Asp Asp Gly Ile Leu Val Ser Asp Leu Lys
 20 25 30
 Gly Met Lys Ser Glu Leu Ser Asp Ala Pro Ala Trp Val Phe Glu Asp
 35 40 45
 Ala Lys Ala Pro Tyr Glu Glu Met Gly Val Ala Tyr Ile Pro Val Asn
 50 55 60
 Asn Lys Tyr Leu Gly Ile Glu Gln Ala Thr Leu Asn Ala Lys Leu Ser
 65 70 75 80
 Leu Ile Val Val Phe His Glu Ile Met Met Lys Tyr Lys Lys Arg Phe
 85 90 95
 Met Glu Gln Phe His Glu Ser Glu Gln Thr Thr Thr Asn Ile Ser Tyr
 100 105 110
 Ala Ile Tyr Asn Tyr Leu Ala Thr Lys Ile Gln Val Ser Asn Thr Tyr
 115 120 125
 Thr Asn Leu Lys Ser Glu Val Ala Val Val Lys Ile Lys Leu Val Gly
 130 135 140
 Cys Gln Ile Glu Gln Ile Lys Arg Tyr Leu Lys Ala Ser Val Glu Asn
 145 150 155 160
 Leu Asn Asp Asn Glu Ile Ala Tyr Ile Ala Lys Val Ala Gln Lys Glu
 165 170 175
 Phe Gly Ser Val Cys Ala Leu Arg

180

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 112...252
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

ATGCCTGCCA	TTTCATAGCC	TAAATTTTCT	TTAGAGCCGA	ATTGATAAGC	GGCTTTTAAG	60
ACTTCTTTTT	GCTTAGCGTT	AAAATCTTTA	ATATTGTCGC	AATTGGTCAT	C ATG ACT	117
					Met Thr	
					1	
TTA GTA ACG	GGC GAT TTG	GGC TTG TTT	TTA ACC CCT	TTA GCG	GGC TTA	165
Leu Val Thr	Gly Asp Leu	Gly Leu Phe	Leu Thr Pro	Leu Ala	Gly Leu	
5		10		15		
GGC TCT GTT	TTA GTG GGG	CTT TCT GTT	GCG GCT AAA	CTT AAA	GAT GCA	213
Gly Ser Val	Leu Val Gly	Leu Ser Val	Ala Ala Lys	Leu Lys	Asp Ala	
20		25		30		
CTT AAG GCT	GTG CCT AGC	CAT AAG GCT	TTA AAG ATG	GTG TGAGT	GAGTG GG	264
Leu Lys Ala	Val Pro Ser	His Lys Ala	Leu Lys Met	Val		
35		40		45		
GTAAATGTT	TCAAACGCC	TACCTTTTGT	ATTAAGAAAT	AAACTA		310

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

Met Thr Leu	Val Thr Gly	Asp Leu Gly	Leu Phe Leu	Thr Pro Leu	Ala
1		5		10	15
Gly Leu Gly	Ser Val Leu	Val Gly Leu	Ser Val Ala	Ala Lys Leu	Lys
20		25		30	
Asp Ala Leu	Lys Ala Val	Pro Ser His	Lys Ala Leu	Lys Met	Val

35

40

45

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 145...579
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

CGGTTCAATA GAATGCTTTA GTTAGGAAGC TCCTTGCTTT AGCAAGGNGT GGTTCCTACTG	60
AAAGAGAGTA AGAAATTGTA AGAAAGGGTT TATCTTTTTT TAGATGAATT TGTGCGTTTT	120
GGTAAATTGC CTTTTTTATT AGAA ATG CCA GCA TTA AGT AGG AGC TAT GGT	171
Met Pro Ala Leu Ser Arg Ser Tyr Gly	
1 5	
GTG GTT TTA ATT TTT ATC ACG CAA TCC AAC GCT CTT ATT GAA AAA TAT	219
Val Val Leu Ile Phe Ile Thr Gln Ser Asn Ala Leu Ile Glu Lys Tyr	
10 15 20 25	
TAC GGC AGA GAA GAT GCA AGA ATT GTT AAT AGC ACC GTG GCT TAC AAA	267
Tyr Gly Arg Glu Asp Ala Arg Ile Val Asn Ser Thr Val Ala Tyr Lys	
30 35 40	
ATA ATT TTC AAA ATG GAT GAT TTA GAA TAC GCT AAA CAG GTG AGC GAA	315
Ile Ile Phe Lys Met Asp Asp Leu Glu Tyr Ala Lys Gln Val Ser Glu	
45 50 55	
GAA GTC GGT AAG ATG ACT AGA AAA ACA CGA AGC CAC TCT ACA GAA AAA	363
Glu Val Gly Lys Met Thr Arg Lys Thr Arg Ser His Ser Thr Glu Lys	
60 65 70	
GGA CAA CTC ATT ACC GGA GGG ACT TCT AGT ATA GGT AAA GAG GCG TGG	411
Gly Gln Leu Ile Thr Gly Gly Thr Ser Ser Ile Gly Lys Glu Ala Trp	
75 80 85	
GAC TTA TTG AGC GCG CAA GAT ATT ATG AAT ATT GAT AAA GAT GAA GTG	459
Asp Leu Leu Ser Ala Gln Asp Ile Met Asn Ile Asp Lys Asp Glu Val	
90 95 100 105	
ATC GTT TTA GTA AGC GGT CAT AAG GCT AAA CCC TTA AAA TTA AAA GCG	507
Ile Val Leu Val Ser Gly His Lys Ala Lys Pro Leu Lys Leu Lys Ala	
110 115 120	
AAT TAT TAT TTC AAA AAC AAA GAA TTA CTC TCT CGT ATT AAC TGG GAA	555
Asn Tyr Tyr Phe Lys Asn Lys Glu Leu Leu Ser Arg Ile Asn Trp Glu	
125 130 135	

GTC AAG CCC AAT GAA GAA GTG TTT TGATGGATTA AAAAAGTTTG CATGAGTATT 609
 Val Lys Pro Asn Glu Glu Val Phe
 140 145

TTTTAATTGC TTTTTTAAAA AT 631

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

Met	Pro	Ala	Leu	Ser	Arg	Ser	Tyr	Gly	Val	Val	Leu	Ile	Phe	Ile	Thr
1				5					10					15	
Gln	Ser	Asn	Ala	Leu	Ile	Glu	Lys	Tyr	Tyr	Gly	Arg	Glu	Asp	Ala	Arg
			20					25					30		
Ile	Val	Asn	Ser	Thr	Val	Ala	Tyr	Lys	Ile	Ile	Phe	Lys	Met	Asp	Asp
		35					40					45			
Leu	Glu	Tyr	Ala	Lys	Gln	Val	Ser	Glu	Glu	Val	Gly	Lys	Met	Thr	Arg
	50				55					60					
Lys	Thr	Arg	Ser	His	Ser	Thr	Glu	Lys	Gly	Gln	Leu	Ile	Thr	Gly	Gly
65					70				75					80	
Thr	Ser	Ser	Ile	Gly	Lys	Glu	Ala	Trp	Asp	Leu	Leu	Ser	Ala	Gln	Asp
				85				90					95		
Ile	Met	Asn	Ile	Asp	Lys	Asp	Glu	Val	Ile	Val	Leu	Val	Ser	Gly	His
		100					105					110			
Lys	Ala	Lys	Pro	Leu	Lys	Leu	Lys	Ala	Asn	Tyr	Tyr	Phe	Lys	Asn	Lys
		115				120						125			
Glu	Leu	Leu	Ser	Arg	Ile	Asn	Trp	Glu	Val	Lys	Pro	Asn	Glu	Glu	Val
	130					135					140				
Phe															
145															

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 106...237
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

TAAGGGCTTA CGCATAAAAT CGCATCCGCG CCGATTTTTT GAGCGAACTT TGCTAAAGAA 60
 AGGGAATCGC TCGTGCGGTT ACTGCCACG CCGGCTAACA CTTTC ATG CGC GAA TTT 117
 Met Arg Glu Phe
 1

GAG GGC GTT TTA GTG TTT TTG CAA GTT TCT ATG GCG ATT TCA ATG CAA 165
 Glu Gly Val Leu Val Phe Leu Gln Val Ser Met Ala Ile Ser Met Gln
 5 10 15 20

CGC ATG TGC TCT TTG TGG GTG AGC GTG GCG GAT TCT CCT GTC GTG CCA 213
 Arg Met Cys Ser Leu Trp Val Ser Val Ala Asp Ser Pro Val Val Pro
 25 30 35

ACA GGC ACG CAT GCG TCC ATG CCC TGAAAAATTT GGCGCTTGAT CAAGGTTTCA 267
 Thr Gly Thr His Ala Ser Met Pro
 40

TAAGCGGCCT CATCAACGCT CAA 290

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

Met Arg Glu Phe Glu Gly Val Leu Val Phe Leu Gln Val Ser Met Ala
 1 5 10 15
 Ile Ser Met Gln Arg Met Cys Ser Leu Trp Val Ser Val Ala Asp Ser
 20 25 30
 Pro Val Val Pro Thr Gly Thr His Ala Ser Met Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 58...369
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

AAAGAAGGTT TGAAAAGCTT TTTTAAAAGG CTTTGAAGT ATTTGGGGTA GGCTTGA ATG 60
Met
1

AAA GTG CAA AAT TTT ATC CAT TTT TCT GTT GTG GTA GGG TTT TTT TTG 108
Lys Val Gln Asn Phe Ile His Phe Ser Val Val Val Gly Phe Phe Leu
5 10 15

GGG TTA GTG TTT TCG GTG TTG AAA TTC AAT GAG CCA GAG AGC ATT TTA 156
Gly Leu Val Phe Ser Val Leu Lys Phe Asn Glu Pro Glu Ser Ile Leu
20 25 30

TTA TGG ACG GTG TTA TCC ACG CTT GGG GGG TAC TTG ATT GCG TTG TTG 204
Leu Trp Thr Val Leu Ser Thr Leu Gly Gly Tyr Leu Ile Ala Leu Leu
35 40 45

TTT GCG TCT ATT TTT ATC GCT TGC ACG GAT TTG GAT ATT TGT CTT TTT 252
Phe Ala Ser Ile Phe Ile Ala Cys Thr Asp Leu Asp Ile Cys Leu Phe
50 55 60 65

GAC AAA AAA GGC ACT GAA GAG AGT TTG CTT CGT TTC AAC CAT GAG TTT 300
Asp Lys Lys Gly Thr Glu Glu Ser Leu Leu Arg Phe Asn His Glu Phe
70 75 80

AAA AAC AGA GAA AAA GAA GTG GCT AGT ATT TTA GAA TAC ATT AGA AGT 348
Lys Asn Arg Glu Lys Glu Val Ala Ser Ile Leu Glu Tyr Ile Arg Ser
85 90 95

TAT GAT TTT GAT GAT GGA AAA TAGAATGCCC AAAGGAATTC AAAAACTGA AACA 403
Tyr Asp Phe Asp Asp Gly Lys
100

AGCGAAAAAA ATATAGAA 421

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Met Lys Val Gln Asn Phe Ile His Phe Ser Val Val Val Gly Phe Phe
1 5 10 15
Leu Gly Leu Val Phe Ser Val Leu Lys Phe Asn Glu Pro Glu Ser Ile
20 25 30
Leu Leu Trp Thr Val Leu Ser Thr Leu Gly Gly Tyr Leu Ile Ala Leu
35 40 45
Leu Phe Ala Ser Ile Phe Ile Ala Cys Thr Asp Leu Asp Ile Cys Leu
50 55 60
Phe Asp Lys Lys Gly Thr Glu Glu Ser Leu Leu Arg Phe Asn His Glu
65 70 75 80
Phe Lys Asn Arg Glu Lys Glu Val Ala Ser Ile Leu Glu Tyr Ile Arg

85
Ser Tyr Asp Phe Asp Asp Gly Lys
100

90

95

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...617
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GTTTAGAAAA GCGTTTGAAC GCTATAAAAA ATGCAGAGTG GCTTTAAGGC ATG AAA	56
Met Lys	
1	
AAG ATT GCA TTT TTT ATT TTT GTC ATT TTG TTT TCG GTA GGG ATT TAT	104
Lys Ile Ala Phe Phe Ile Phe Val Ile Leu Phe Ser Val Gly Ile Tyr	
5 10 15	
TTA ATT TGG CAT GTT TTA TTG GAA AAA GCC CTA GAA TTG AAA TTA GCA	152
Leu Ile Trp His Val Leu Leu Glu Lys Ala Leu Glu Leu Lys Leu Ala	
20 25 30	
ACC TCA GCT AAT GAT TTG CTT TTA AAA TTG TTG GCA ATT CTT GGC GTT	200
Thr Ser Ala Asn Asp Leu Leu Leu Lys Leu Leu Ala Ile Leu Gly Val	
35 40 45 50	
TTT TCA ATG TTA GTG CTT TTT CAA GGC ATT ATT TCT TCG TAT AAG AAG	248
Phe Ser Met Leu Val Leu Phe Gln Gly Ile Ile Ser Ser Tyr Lys Lys	
55 60 65	
CGC CAA CTC AAA CGC ATT TTA CAA AAA ATA GAC GCC ATG AAC GGC TTT	296
Arg Gln Leu Lys Arg Ile Leu Gln Lys Ile Asp Ala Met Asn Gly Phe	
70 75 80	
GAA TTT GAA GAA TAT TCC AAA ATC TTT TTC ACT TCA AAG GGT TTT GAA	344
Glu Phe Glu Glu Tyr Ser Lys Ile Phe Phe Thr Ser Lys Gly Phe Glu	
85 90 95	
GTG AGC ATC ACG CAA AAA AGC GGC GAT TAT GGA GCG GAT TTG ATT ATA	392
Val Ser Ile Thr Gln Lys Ser Gly Asp Tyr Gly Ala Asp Leu Ile Ile	
100 105 110	
GAA AAA GAC GGC ATC AAG TGG GCG GTT CAA GTC AAA CGC TAC TCG CAT	440
Glu Lys Asp Gly Ile Lys Trp Ala Val Gln Val Lys Arg Tyr Ser His	
115 120 125 130	

AAA GTT TCG CCC AAA GCC ATT CAA GAG GTG GTC TCT TCT AAA GCT TAT 488
 Lys Val Ser Pro Lys Ala Ile Gln Glu Val Val Ser Ser Lys Ala Tyr
 135 140 145

 TAC GCT TGC GAA AAA GCT TGC GTG ATC ACC AAC AGC TAT TTC ACG CAA 536
 Tyr Ala Cys Glu Lys Ala Cys Val Ile Thr Asn Ser Tyr Phe Thr Gln
 150 155 160

 GCC GCT CAA AAA CTG GCT CAA GCT AAC GAA GTG CTC TTG ATT GAC AGA 584
 Ala Ala Gln Lys Leu Ala Gln Ala Asn Glu Val Leu Leu Ile Asp Arg
 165 170 175

 GAC GAA TGG GTC AGG TTT TTG AAC GAA AAG AGA TGAACCGATC CCATCAGATC 637
 Asp Glu Trp Val Arg Phe Leu Asn Glu Lys Arg
 180 185

 GTTTGTCTC AAGTTCTTTT AAAATTTTGT CGT 670

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Met Lys Lys Ile Ala Phe Phe Ile Phe Val Ile Leu Phe Ser Val Gly
 1 5 10 15
 Ile Tyr Leu Ile Trp His Val Leu Leu Glu Lys Ala Leu Glu Leu Lys
 20 25 30
 Leu Ala Thr Ser Ala Asn Asp Leu Leu Lys Leu Leu Ala Ile Leu
 35 40 45
 Gly Val Phe Ser Met Leu Val Leu Phe Gln Gly Ile Ile Ser Ser Tyr
 50 55 60
 Lys Lys Arg Gln Leu Lys Arg Ile Leu Gln Lys Ile Asp Ala Met Asn
 65 70 75 80
 Gly Phe Glu Phe Glu Glu Tyr Ser Lys Ile Phe Phe Thr Ser Lys Gly
 85 90 95
 Phe Glu Val Ser Ile Thr Gln Lys Ser Gly Asp Tyr Gly Ala Asp Leu
 100 105 110
 Ile Ile Glu Lys Asp Gly Ile Lys Trp Ala Val Gln Val Lys Arg Tyr
 115 120 125
 Ser His Lys Val Ser Pro Lys Ala Ile Gln Glu Val Val Ser Ser Lys
 130 135 140
 Ala Tyr Tyr Ala Cys Glu Lys Ala Cys Val Ile Thr Asn Ser Tyr Phe
 145 150 155 160
 Thr Gln Ala Ala Gln Lys Leu Ala Gln Ala Asn Glu Val Leu Leu Ile
 165 170 175
 Asp Arg Asp Glu Trp Val Arg Phe Leu Asn Glu Lys Arg
 180 185

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 125...538
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

```

CAAAGAGTGG GATAAAATCA CAGAAATTTG TAAGAGAGCG CTAGCTTTAA GATAACAAAA      60
AGATCATGGC ATTTTGTATT TGCTTAATAA CACTATAATA AAATTTTTAA TAAGGAGATA      120
CATC ATG TTA GAA AAT GTC AAA AAG TCC TTT TTT AGG GTT TTG TGC TTG      169
  Met Leu Glu Asn Val Lys Lys Ser Phe Phe Arg Val Leu Cys Leu
    1             5             10             15

GGT GCG TTG TGT TTA GGG GGG CTA ATG GCA GAG CAA GAC CCT AAA GAG      217
Gly Ala Leu Cys Leu Gly Gly Leu Met Ala Glu Gln Asp Pro Lys Glu
           20             25             30

CTT GTG GGT TTG GGG GCA AAG AGC TAC AAA GAG AAA GAT TTC ACT CAA      265
Leu Val Gly Leu Gly Ala Lys Ser Tyr Lys Glu Lys Asp Phe Thr Gln
           35             40             45

GCG AAG AAA TAT TTT GAG AAA GCG TGC GAT TTG AAA GAA AAT AGC GGG      313
Ala Lys Lys Tyr Phe Glu Lys Ala Cys Asp Leu Lys Glu Asn Ser Gly
           50             55             60

TGT TTT AAT TTA GGG GTG CTT TAT TAT CAA GGG CAA GGG GTG GAA AAG      361
Cys Phe Asn Leu Gly Val Leu Tyr Tyr Gln Gly Gln Gly Val Glu Lys
           65             70             75

AAC TTG AAA AAA GCC GCC TCC TTT TAC GCT AAA GCT TGC GAT TTG AAT      409
Asn Leu Lys Lys Ala Ala Ser Phe Tyr Ala Lys Ala Cys Asp Leu Asn
           80             85             90             95

TAC AGC AAT GGG TGT CAT TTG CTA GGG AAT TTA TAT TAC AGC GGG CAA      457
Tyr Ser Asn Gly Cys His Leu Leu Gly Asn Leu Tyr Tyr Ser Gly Gln
           100            105            110

GGC GTG TCC CAA AAC ACC AAT AAA GCC CTA CAA TAC TAC TCT AAA GCG      505
Gly Val Ser Gln Asn Thr Asn Lys Ala Leu Gln Tyr Tyr Ser Lys Ala
           115            120            125

TGC GAT TTG AAA TAC GCT GAA GGG TGC GCG ACT TAGGGGGGAT TTATCATGAT      558
Cys Asp Leu Lys Tyr Ala Glu Gly Cys Ala Thr
           130            135

GGTAAAGTGG TAACTAGGGA TTTTAAAAAA GCGGTGGAAT AT      600

```

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

```

Met Leu Glu Asn Val Lys Lys Ser Phe Phe Arg Val Leu Cys Leu Gly
 1             5             10             15
Ala Leu Cys Leu Gly Gly Leu Met Ala Glu Gln Asp Pro Lys Glu Leu
 20             25             30
Val Gly Leu Gly Ala Lys Ser Tyr Lys Glu Lys Asp Phe Thr Gln Ala
 35             40             45
Lys Lys Tyr Phe Glu Lys Ala Cys Asp Leu Lys Glu Asn Ser Gly Cys
 50             55             60
Phe Asn Leu Gly Val Leu Tyr Tyr Gln Gly Gln Gly Val Glu Lys Asn
 65             70             75             80
Leu Lys Lys Ala Ala Ser Phe Tyr Ala Lys Ala Cys Asp Leu Asn Tyr
 85             90             95
Ser Asn Gly Cys His Leu Leu Gly Asn Leu Tyr Tyr Ser Gly Gln Gly
100             105             110
Val Ser Gln Asn Thr Asn Lys Ala Leu Gln Tyr Tyr Ser Lys Ala Cys
115             120             125
Asp Leu Lys Tyr Ala Glu Gly Cys Ala Thr
130             135

```

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 59...826
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

```

TTTTAAGATT GGTAGCCATT GGCATTATGT TTGATCTTAT TAAAGCAGAG GAGTAACA      58

ATG GGA TAC GCA AGC AAA TTA GCC TTG AAG ATT TGT TTG GCA AGT TTA      106
Met Gly Tyr Ala Ser Lys Leu Ala Leu Lys Ile Cys Leu Ala Ser Leu
 1             5             10             15

TGT TTA TTT AGC GCT CTT GGT GCA GAA CAC CTT GAA CAA AAA AGG AAC      154
Cys Leu Phe Ser Ala Leu Gly Ala Glu His Leu Glu Gln Lys Arg Asn

```

20										25					30					
TAT	ATT	TAT	AAM	GGG	GAG	GAA	GCC	TAT	AAT	AAT	AAG	GAA	TAT	GAG	CGG	202				
Tyr	Ile	Tyr	Xaa	Gly	Glu	Glu	Ala	Tyr	Asn	Asn	Lys	Glu	Tyr	Glu	Arg					
35			40			45														
GCG	GCT	TCT	TTT	TAT	AAG	AGC	GCG	ATT	AAA	AAT	GGC	GAG	CCG	CTT	GCT	250				
Ala	Ala	Ser	Phe	Tyr	Lys	Ser	Ala	Ile	Lys	Asn	Gly	Glu	Pro	Leu	Ala					
50			55			60														
TAT	GTT	CTT	TTA	GGG	ATC	ATG	TAT	GAA	AAT	GGT	AGG	GGT	GTG	CCT	AAA	298				
Tyr	Val	Leu	Leu	Gly	Ile	Met	Tyr	Glu	Asn	Gly	Arg	Gly	Val	Pro	Lys					
65			70			75			80											
GAT	GAA	AAG	AAA	GCG	GCT	GAA	TAT	TTT	CAA	AAA	GCG	GTT	GAT	AAC	GAT	346				
Asp	Glu	Lys	Lys	Ala	Ala	Glu	Tyr	Phe	Gln	Lys	Ala	Val	Asp	Asn	Asp					
85			90			95														
ATA	CCT	AGA	GGG	TAT	AAC	AAT	TTA	GGC	GTG	ATG	TAT	AAA	GAG	GGT	AGA	394				
Ile	Pro	Arg	Gly	Tyr	Asn	Asn	Leu	Gly	Val	Met	Tyr	Lys	Glu	Gly	Arg					
100			105			110														
GGT	GTG	CCT	AAA	GAT	GAA	AAG	AAA	GCC	GTG	GAG	TAT	TTT	AGA	ATA	GCT	442				
Gly	Val	Pro	Lys	Asp	Glu	Lys	Lys	Ala	Val	Glu	Tyr	Phe	Arg	Ile	Ala					
115			120			125														
ACC	GAG	AAG	GGC	TAT	ACT	AAC	GCC	TAT	ATA	AAC	TTA	GGC	ATC	ATG	TAT	490				
Thr	Glu	Lys	Gly	Tyr	Thr	Asn	Ala	Tyr	Ile	Asn	Leu	Gly	Ile	Met	Tyr					
130			135			140														
ATG	GAG	GGT	AGG	GGA	GTT	CCA	AGC	AAC	TAT	GTG	AAA	GCG	ACA	GAG	TGC	538				
Met	Glu	Gly	Arg	Gly	Val	Pro	Ser	Asn	Tyr	Val	Lys	Ala	Thr	Glu	Cys					
145			150			155			160											
TTT	AGA	AAA	GCG	ATG	CAT	AAG	GGT	AAT	GTA	GAA	GCT	TAT	ATC	CTT	TTA	586				
Phe	Arg	Lys	Ala	Met	His	Lys	Gly	Asn	Val	Glu	Ala	Tyr	Ile	Leu	Leu					
165			170			175														
GGG	GAT	ATT	TAT	TAT	AGT	GGG	AAT	GAT	CAA	TTG	GGT	ATT	GAG	CCA	GAC	634				
Gly	Asp	Ile	Tyr	Tyr	Ser	Gly	Asn	Asp	Gln	Leu	Gly	Ile	Glu	Pro	Asp					
180			185			190														
AAA	GAT	AAG	GCG	ATT	GTC	TAT	TAT	AAA	ATG	GCG	GCT	GAT	ATG	AGC	TCT	682				
Lys	Asp	Lys	Ala	Ile	Val	Tyr	Tyr	Lys	Met	Ala	Ala	Asp	Met	Ser	Ser					
195			200			205														
TCT	AGA	GCT	TAT	GAA	GGG	TTA	GCA	GAG	TCT	TAT	CAG	TAT	GGG	TTA	GGC	730				
Ser	Arg	Ala	Tyr	Glu	Gly	Leu	Ala	Glu	Ser	Tyr	Gln	Tyr	Gly	Leu	Gly					
210			215			220														
GTG	GAA	AAA	GAT	AAG	AAA	AAG	GCT	GAA	GAA	TAC	ATG	CAA	AAA	GCA	TGC	778				
Val	Glu	Lys	Asp	Lys	Lys	Lys	Ala	Glu	Glu	Tyr	Met	Gln	Lys	Ala	Cys					
225			230			235			240											
GAT	TTT	GAC	ATT	GAT	AAA	AAT	TGT	AAG	AAA	AAG	AAC	ACT	TCA	AGC	CGA	826				
Asp	Phe	Asp	Ile	Asp	Lys	Asn	Cys	Lys	Lys	Lys	Asn	Thr	Ser	Ser	Arg					
245			250			255														

TAACTCTCAA ACTTGGGCTT GATTAGGATT TTTGTTTTAT TTTAAGTAGC ATG

879

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Met	Gly	Tyr	Ala	Ser	Lys	Leu	Ala	Leu	Lys	Ile	Cys	Leu	Ala	Ser	Leu	1	5	10	15
Cys	Leu	Phe	Ser	Ala	Leu	Gly	Ala	Glu	His	Leu	Glu	Gln	Lys	Arg	Asn	20	25	30	
Tyr	Ile	Tyr	Xaa	Gly	Glu	Glu	Ala	Tyr	Asn	Asn	Lys	Glu	Tyr	Glu	Arg	35	40	45	
Ala	Ala	Ser	Phe	Tyr	Lys	Ser	Ala	Ile	Lys	Asn	Gly	Glu	Pro	Leu	Ala	50	55	60	
Tyr	Val	Leu	Leu	Gly	Ile	Met	Tyr	Glu	Asn	Gly	Arg	Gly	Val	Pro	Lys	65	70	75	80
Asp	Glu	Lys	Lys	Ala	Glu	Tyr	Phe	Gln	Lys	Ala	Val	Asp	Asn	Asp		85	90	95	
Ile	Pro	Arg	Gly	Tyr	Asn	Asn	Leu	Gly	Val	Met	Tyr	Lys	Glu	Gly	Arg	100	105	110	
Gly	Val	Pro	Lys	Asp	Glu	Lys	Lys	Ala	Val	Glu	Tyr	Phe	Arg	Ile	Ala	115	120	125	
Thr	Glu	Lys	Gly	Tyr	Thr	Asn	Ala	Tyr	Ile	Asn	Leu	Gly	Ile	Met	Tyr	130	135	140	
Met	Glu	Gly	Arg	Gly	Val	Pro	Ser	Asn	Tyr	Val	Lys	Ala	Thr	Glu	Cys	145	150	155	160
Phe	Arg	Lys	Ala	Met	His	Lys	Gly	Asn	Val	Glu	Ala	Tyr	Ile	Leu	Leu	165	170	175	
Gly	Asp	Ile	Tyr	Tyr	Ser	Gly	Asn	Asp	Gln	Leu	Gly	Ile	Glu	Pro	Asp	180	185	190	
Lys	Asp	Lys	Ala	Ile	Val	Tyr	Tyr	Lys	Met	Ala	Ala	Asp	Met	Ser	Ser	195	200	205	
Ser	Arg	Ala	Tyr	Glu	Gly	Leu	Ala	Glu	Ser	Tyr	Gln	Tyr	Gly	Leu	Gly	210	215	220	
Val	Glu	Lys	Asp	Lys	Lys	Lys	Ala	Glu	Glu	Tyr	Met	Gln	Lys	Ala	Cys	225	230	235	240
Asp	Phe	Asp	Ile	Asp	Lys	Asn	Cys	Lys	Lys	Lys	Asn	Thr	Ser	Ser	Arg	245	250	255	

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 66...269
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

```

TGGGGGTTGT GGTGCTCAT GTTCGCATGG GTAGTAAGGT ATAGGAGTAT TTAAAAGGCA    60
AGGTC ATG AAT AGT TCT AAT CTC AAA AAT TGG CTA TTC CCT ACC ATT TGC    110
  Met Asn Ser Ser Asn Leu Lys Asn Trp Leu Phe Pro Thr Ile Cys
    1              5              10              15

TTT TTT TTA TTT TGT TAT ATT TTA ATT TTT TTA ATG TTC TTT ATG TTT    158
Phe Phe Leu Phe Cys Tyr Ile Leu Ile Phe Leu Met Phe Phe Met Phe
          20              25              30

AAA AGT TTG CAA TCG CAA TCG TTT GGC TCT GTG GCA GAA ACC GGA AAA    206
Lys Ser Leu Gln Ser Gln Ser Phe Gly Ser Val Ala Glu Thr Gly Lys
          35              40              45

AAA CCC ATC ACC ACC ACC AAG AAA TTT GGT AAG GAA TTG CAA AAA CAG    254
Lys Pro Ile Thr Thr Thr Lys Lys Phe Gly Lys Glu Leu Gln Lys Gln
          50              55              60

ATT TCA AAA ATC CAT TAACTTTTTT TCTTTTTTGC CGATACTTGC TGTAATGGAA T    310
Ile Ser Lys Ile His
    65

GAATATCAA    319
  
```

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

```

Met Asn Ser Ser Asn Leu Lys Asn Trp Leu Phe Pro Thr Ile Cys Phe
  1              5              10              15
Phe Leu Phe Cys Tyr Ile Leu Ile Phe Leu Met Phe Phe Met Phe Lys
          20              25              30
Ser Leu Gln Ser Gln Ser Phe Gly Ser Val Ala Glu Thr Gly Lys Lys
          35              40              45
Pro Ile Thr Thr Thr Lys Lys Phe Gly Lys Glu Leu Gln Lys Gln Ile
          50              55              60
Ser Lys Ile His
    65
  
```

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 66...1058
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

AAAACTAGA GAGTGTATA AAGAAAACAG AAGAGTGGAT GTCAAATTAA TGAAGTAATT	60
CTAGG ATG AAA AGG CTT TTT TTT ATC CCT TTT ATC GCT CCC TTT TTT CTC	110
Met Lys Arg Leu Phe Phe Ile Pro Phe Ile Ala Pro Phe Phe Leu	
1 5 10 15	
AAT GGG GAG CCT TCA GCG TTT GAT TTG CAA AGT GGG GCT ACC AAA AAA	158
Asn Gly Glu Pro Ser Ala Phe Asp Leu Gln Ser Gly Ala Thr Lys Lys	
20 25 30	
GAA CTC AAG CAG TTG CAA ATC AAT AGT AAG AAT TTT TCT AAT ATT TTG	206
Glu Leu Lys Gln Leu Gln Ile Asn Ser Lys Asn Phe Ser Asn Ile Leu	
35 40 45	
ACC AAA ATC CAT TCG CAA GTA GAG GCT AAC ACT CAA GCT CAA GAG GGT	254
Thr Lys Ile His Ser Gln Val Glu Ala Asn Thr Gln Ala Gln Glu Gly	
50 55 60	
TTG AGA AGC GTT TAT GAG GGG CAG GCT AAT AAG ATT AAA GAT CTC AAT	302
Leu Arg Ser Val Tyr Glu Gly Gln Ala Asn Lys Ile Lys Asp Leu Asn	
65 70 75	
AAC GCT ATC CTT TCC CAA GAA GAA TCC TTA CGA GCC TTA AAA GCT TCG	350
Asn Ala Ile Leu Ser Gln Glu Glu Ser Leu Arg Ala Leu Lys Ala Ser	
80 85 90 95	
CAA GAA GTG CAG GCT AAC ACG CTT AAG CAG CAA TCG CAA ACT TTA GAG	398
Gln Glu Val Gln Ala Asn Thr Leu Lys Gln Gln Ser Gln Thr Leu Glu	
100 105 110	
GAT TTG AGG AAT GAG ATT CAC GCT AAC CAG CAA GCT ATC CAG CAG TTA	446
Asp Leu Arg Asn Glu Ile His Ala Asn Gln Gln Ala Ile Gln Gln Leu	
115 120 125	
GAC AAG CAA AAT AAA GAG ATG AGT GAA TTA TTG ACC AAG TTA AGC CAG	494
Asp Lys Gln Asn Lys Glu Met Ser Glu Leu Leu Thr Lys Leu Ser Gln	
130 135 140	
GAT TTG GTT TCA CAA ATC GCC TTA ATC CAA AAA GCT CTC AAA GAA CAA	542
Asp Leu Val Ser Gln Ile Ala Leu Ile Gln Lys Ala Leu Lys Glu Gln	
145 150 155	
GAG GAA AAA GCT GAA AAG CCG CTC AAA TCA AAC GCT CCG GCT AAT AAA	590

Glu	Glu	Lys	Ala	Glu	Lys	Pro	Leu	Lys	Ser	Asn	Ala	Pro	Ala	Asn	Lys	
160					165					170					175	
ACC	CCC	TCT	TTG	AAA	GCC	GAA	TCC	CCA	AAA	AAT	CAA	GAG	GGA	AAA	ACT	638
Thr	Pro	Ser	Leu	Lys	Ala	Glu	Ser	Pro	Lys	Asn	Gln	Glu	Gly	Lys	Thr	
				180					185					190		
CAA	GAA	AAG	GCG	AAA	ATT	GAG	TTT	GAT	AAA	GAC	TTG	TCT	AAG	CAA	AAA	686
Gln	Glu	Lys	Ala	Lys	Ile	Glu	Phe	Asp	Lys	Asp	Leu	Ser	Lys	Gln	Lys	
			195					200					205			
GAG	ATC	TTT	CAA	GAA	GCT	CTG	TCT	TTT	TTT	AAA	AAT	AAA	TCC	TAT	GCA	734
Glu	Ile	Phe	Gln	Glu	Ala	Leu	Ser	Phe	Phe	Lys	Asn	Lys	Ser	Tyr	Ala	
		210					215					220				
GAA	GCC	AAA	GAG	CGT	TTG	TTG	TGG	TTA	GAA	GCC	AAT	AGT	TAC	AGA	CTT	782
Glu	Ala	Lys	Glu	Arg	Leu	Leu	Trp	Leu	Glu	Ala	Asn	Ser	Tyr	Arg	Leu	
	225					230					235					
TAT	TAT	GTG	CGT	TAT	GTT	CTT	GGA	GAA	GTG	GCT	TAT	GGG	GAA	AAG	AGA	830
Tyr	Tyr	Val	Arg	Tyr	Val	Leu	Gly	Glu	Val	Ala	Tyr	Gly	Glu	Lys	Arg	
240					245				250						255	
TAC	AGA	GAA	GCG	ATC	AAG	TAT	TAC	AAA	GAG	AGC	GCT	CTT	TTA	AAC	AAA	878
Tyr	Arg	Glu	Ala	Ile	Lys	Tyr	Tyr	Lys	Glu	Ser	Ala	Leu	Leu	Asn	Lys	
				260					265					270		
AAA	GCG	TCT	TAC	ATG	CCT	GTG	CTT	TTG	TGG	CAT	ACG	GCA	TGG	TCG	TTT	926
Lys	Ala	Ser	Tyr	Met	Pro	Val	Leu	Leu	Trp	His	Thr	Ala	Trp	Ser	Phe	
			275					280					285			
AAA	AAA	ATC	AAA	GAC	GAT	CAA	AAC	TAT	TAT	AAA	TTT	TTA	AAC	ACT	TTG	974
Lys	Lys	Ile	Lys	Asp	Asp	Gln	Asn	Tyr	Tyr	Lys	Phe	Leu	Asn	Thr	Leu	
		290					295					300				
CAA	CAC	TTG	TAT	CCT	TCA	AGC	GAA	CAA	GCT	AAA	ATG	GCG	CAA	AAA	ATC	1022
Gln	His	Leu	Tyr	Pro	Ser	Ser	Glu	Gln	Ala	Lys	Met	Ala	Gln	Lys	Ile	
	305					310					315					
TTA	GAA	AAC	AAG	GAG	AAA	CAC	CAC	CAT	GCA	AAA	CCA	TGATT	TAGAG	TCAATC		1074
Leu	Glu	Asn	Lys	Glu	Lys	His	His	His	Ala	Lys	Pro					
320					325				330							
AAACAAGCCG	CTTTGATTGA	ATATGAAGTG	AGAGAACA													1112

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

Met	Lys	Arg	Leu	Phe	Phe	Ile	Pro	Phe	Ile	Ala	Pro	Phe	Phe	Leu	Asn	
1				5					10					15		
Gly	Glu	Pro	Ser	Ala	Phe	Asp	Leu	Gln	Ser	Gly	Ala	Thr	Lys	Lys	Glu	
			20					25					30			
Leu	Lys	Gln	Leu	Gln	Ile	Asn	Ser	Lys	Asn	Phe	Ser	Asn	Ile	Leu	Thr	
		35				40					45					
Lys	Ile	His	Ser	Gln	Val	Glu	Ala	Asn	Thr	Gln	Ala	Gln	Glu	Gly	Leu	
	50					55				60						
Arg	Ser	Val	Tyr	Glu	Gly	Gln	Ala	Asn	Lys	Ile	Lys	Asp	Leu	Asn	Asn	
65				70						75				80		
Ala	Ile	Leu	Ser	Gln	Glu	Glu	Ser	Leu	Arg	Ala	Leu	Lys	Ala	Ser	Gln	
				85					90					95		
Glu	Val	Gln	Ala	Asn	Thr	Leu	Lys	Gln	Gln	Ser	Gln	Thr	Leu	Glu	Asp	
			100					105					110			
Leu	Arg	Asn	Glu	Ile	His	Ala	Asn	Gln	Gln	Ala	Ile	Gln	Gln	Leu	Asp	
		115					120					125				
Lys	Gln	Asn	Lys	Glu	Met	Ser	Glu	Leu	Leu	Thr	Lys	Leu	Ser	Gln	Asp	
	130					135					140					
Leu	Val	Ser	Gln	Ile	Ala	Leu	Ile	Gln	Lys	Ala	Leu	Lys	Glu	Gln	Glu	
145				150					155					160		
Glu	Lys	Ala	Glu	Lys	Pro	Leu	Lys	Ser	Asn	Ala	Pro	Ala	Asn	Lys	Thr	
				165					170					175		
Pro	Ser	Leu	Lys	Ala	Glu	Ser	Pro	Lys	Asn	Gln	Glu	Gly	Lys	Thr	Gln	
			180					185					190			
Glu	Lys	Ala	Lys	Ile	Glu	Phe	Asp	Lys	Asp	Leu	Ser	Lys	Gln	Lys	Glu	
		195					200					205				
Ile	Phe	Gln	Glu	Ala	Leu	Ser	Phe	Phe	Lys	Asn	Lys	Ser	Tyr	Ala	Glu	
	210					215					220					
Ala	Lys	Glu	Arg	Leu	Leu	Trp	Leu	Glu	Ala	Asn	Ser	Tyr	Arg	Leu	Tyr	
225				230					235					240		
Tyr	Val	Arg	Tyr	Val	Leu	Gly	Glu	Val	Ala	Tyr	Gly	Glu	Lys	Arg	Tyr	
				245					250					255		
Arg	Glu	Ala	Ile	Lys	Tyr	Tyr	Lys	Glu	Ser	Ala	Leu	Leu	Asn	Lys	Lys	
			260					265					270			
Ala	Ser	Tyr	Met	Pro	Val	Leu	Leu	Trp	His	Thr	Ala	Trp	Ser	Phe	Lys	
		275					280					285				
Lys	Ile	Lys	Asp	Asp	Gln	Asn	Tyr	Tyr	Lys	Phe	Leu	Asn	Thr	Leu	Gln	
	290					295					300					
His	Leu	Tyr	Pro	Ser	Ser	Glu	Gln	Ala	Lys	Met	Ala	Gln	Lys	Ile	Leu	
305				310					315					320		
Glu	Asn	Lys	Glu	Lys	His	His	His	Ala	Lys	Pro						
				325					330							

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...483
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

AACAAATGCG AGTTTCAAAT ATTTTGTAGG ATTTTAGGAA AGAAATAGGT T ATG AAT	57
Met Asn	
1	
ATA TCG GTT AAC CCC TAT TTA ATG GCG GTC GTT TTT GTG GTG TTT GTG	105
Ile Ser Val Asn Pro Tyr Leu Met Ala Val Val Phe Val Val Phe Val	
5 10 15	
TTA TTG TTA TGG GCG ATG AAT GTT TGG GTG TAT AGG CCT TTG TTG GCT	153
Leu Leu Leu Trp Ala Met Asn Val Trp Val Tyr Arg Pro Leu Leu Ala	
20 25 30	
TTT ATG GAT AAC AGA CAG GCA GAG ATA AAG GAT AGC TTG GCT AAA ATC	201
Phe Met Asp Asn Arg Gln Ala Glu Ile Lys Asp Ser Leu Ala Lys Ile	
35 40 45 50	
AAA ACG GAT AAT GCC CAA AGT GTG GAG ATT GGC CAT CAA ATT GAG GCT	249
Lys Thr Asp Asn Ala Gln Ser Val Glu Ile Gly His Gln Ile Glu Ala	
55 60 65	
CTT CTT AAA GAA GCG GCT GAA AAA CGC AGA GAA ATA ATA GCA GAA GCG	297
Leu Leu Lys Glu Ala Ala Glu Lys Arg Arg Glu Ile Ile Ala Glu Ala	
70 75 80	
ATT CAA AAA GCC ACA GAG TCC TAT GAC GCT GTG ATC AAG CAA AAA GAG	345
Ile Gln Lys Ala Thr Glu Ser Tyr Asp Ala Val Ile Lys Gln Lys Glu	
85 90 95	
AAC GAA CTC AAT CAA GAG TTT GAA GCG TTT GCG AAG CAA TTA CAA AAT	393
Asn Glu Leu Asn Gln Glu Phe Glu Ala Phe Ala Lys Gln Leu Gln Asn	
100 105 110	
GAA AAG CAA GCG CTA AAA GAG CAG TTG CAA GCG CAA ATG CCG GTA TTT	441
Glu Lys Gln Ala Leu Lys Glu Gln Leu Gln Ala Gln Met Pro Val Phe	
115 120 125 130	
GAA GAC GAG TTA AAC AAG CGT GTG GCT ATG GGT TTA GGG AGT TGATGAATG	492
Glu Asp Glu Leu Asn Lys Arg Val Ala Met Gly Leu Gly Ser	
135 140	
TTTGTAGTTA AAATGGTGTG AGGGTTTTTG ATCCTTTTA	531

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

```

Met Asn Ile Ser Val Asn Pro Tyr Leu Met Ala Val Val Phe Val Val
 1           5           10           15
Phe Val Leu Leu Leu Trp Ala Met Asn Val Trp Val Tyr Arg Pro Leu
           20           25           30
Leu Ala Phe Met Asp Asn Arg Gln Ala Glu Ile Lys Asp Ser Leu Ala
 35           40           45
Lys Ile Lys Thr Asp Asn Ala Gln Ser Val Glu Ile Gly His Gln Ile
 50           55           60
Glu Ala Leu Leu Lys Glu Ala Ala Glu Lys Arg Arg Glu Ile Ile Ala
 65           70           75           80
Glu Ala Ile Gln Lys Ala Thr Glu Ser Tyr Asp Ala Val Ile Lys Gln
           85           90           95
Lys Glu Asn Glu Leu Asn Gln Glu Phe Glu Ala Phe Ala Lys Gln Leu
 100          105          110
Gln Asn Glu Lys Gln Ala Leu Lys Glu Gln Leu Gln Ala Gln Met Pro
 115          120          125
Val Phe Glu Asp Glu Leu Asn Lys Arg Val Ala Met Gly Leu Gly Ser
 130          135          140

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(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5832 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 387...5777
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

```

AAGCTTGATA TGGAGCATT T GATCGCTTG ACCATGCTCA ATAGAGAAGA ATTGTTGCGC      60
GTTACTCGCT CCTTTCTCAA GCGATTTTAG AAGAGCCTTT CAGCCATAAC GGCAAGGATT      120
ATAAAGAAGG CGATCAAATC CCTAAAGAAG AAATCGCTTC AATCAACCGC TTCACTTTGG      180
CTAGTTTGGT CAAAAAGTAT TCTAAAGAAG TGCAAAACCA CTATGAAATC ACTAAAAACA      240
ATTTCTTAGA GCAAAAGAAA GTTTTGGGCG AAGAGCATGA AGAAAAGCTT TCTATTTTAG      300
AAAAAGATGA TATTTGCGCT AATGGCGTGA TCAAAAAAGT CAAGCTCTAT ATCGCTACAA      360
AACGAAAGCT TAAAGTGGGC GATAAA ATG GCA GGA AGG CAT GGG AAT AAA GGG      413
                               Met Ala Gly Arg His Gly Asn Lys Gly
                               1           5

ATT GTG TCT AAT ATC GTG CCG GTT GCG GAT ATG CCT TAT ACC GCT GAT      461
Ile Val Ser Asn Ile Val Pro Val Ala Asp Met Pro Tyr Thr Ala Asp
10           15           20           25

GGC GAG CCT GTA GAT ATT GTT TTA AAC CCT TTA GGC GTG CCA AGC CGC      509
Gly Glu Pro Val Asp Ile Val Leu Asn Pro Leu Gly Val Pro Ser Arg
           30           35           40

ATG AAT ATC GGG CAG ATT TTA GAA ATG CAT TTA GGC TTA GTG GGG AAA      557
Met Asn Ile Gly Gln Ile Leu Glu Met His Leu Gly Leu Val Gly Lys

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45					50					55						
GAA	TTT	GGG	AAG	CAA	ATC	GCT	CGC	ATG	CTA	GAG	GAT	AAA	ACC	AAA	GAT	605
Glu	Phe	Gly	Lys	Gln	Ile	Ala	Arg	Met	Leu	Glu	Asp	Lys	Thr	Lys	Asp	
60					65					70						
TTT	GCC	AAA	GAA	TTG	CGT	GCT	AAA	ATG	CTA	GAA	AWC	GCT	AAC	GCT	ATT	653
Phe	Ala	Lys	Glu	Leu	Arg	Ala	Lys	Met	Leu	Glu	Xaa	Ala	Asn	Ala	Ile	
75					80					85						
AAT	GAA	AAA	GAC	CCC	TTG	ACA	ATC	CAT	GCG	CTT	GAG	AAT	TGT	TCT	GAT	701
Asn	Glu	Lys	Asp	Pro	Leu	Thr	Ile	His	Ala	Leu	Glu	Asn	Cys	Ser	Asp	
90					95					100					105	
GAA	GAG	CTT	TTG	GAA	TAC	GCA	AAA	GAT	TGG	AGC	AAG	GGC	GTT	AAG	ATG	749
Glu	Glu	Leu	Leu	Glu	Tyr	Ala	Lys	Asp	Trp	Ser	Lys	Gly	Val	Lys	Met	
110					115					120						
GCT	ATC	CCT	GTG	TTT	GAA	GGC	ATC	TCG	CAA	GAA	AAA	TTT	TAT	AAG	CTA	797
Ala	Ile	Pro	Val	Phe	Glu	Gly	Ile	Ser	Gln	Glu	Lys	Phe	Tyr	Lys	Leu	
125					130					135						
TTT	GAA	TTA	GCT	AAG	ATC	GCT	ATG	GAT	GGC	AAA	ATG	GAT	CTG	TAT	GAC	845
Phe	Glu	Leu	Ala	Lys	Ile	Ala	Met	Asp	Gly	Lys	Met	Asp	Leu	Tyr	Asp	
140					145					150						
GGA	CGC	ACA	GGC	GAG	AAA	ATG	AGG	GAG	CGC	GTG	AAT	GTG	GGC	TAC	ATG	893
Gly	Arg	Thr	Gly	Glu	Lys	Met	Arg	Glu	Arg	Val	Asn	Val	Gly	Tyr	Met	
155					160					165						
TAT	ATG	ATC	AAA	CTC	CAC	CAT	TTA	GTG	GAT	GAA	AAA	GTC	CAT	GCC	AGA	941
Tyr	Met	Ile	Lys	Leu	His	His	Leu	Val	Asp	Glu	Lys	Val	His	Ala	Arg	
170					175					180					185	
AGC	ACA	GGC	CCT	TAT	AGC	TTA	GTA	ACG	CAC	CAG	CCC	GTG	GGG	GGT	AAA	989
Ser	Thr	Gly	Pro	Tyr	Ser	Leu	Val	Thr	His	Gln	Pro	Val	Gly	Gly	Lys	
190					195					200						
GCG	CTC	TTT	GGG	GGT	CAA	AGG	TTT	GGG	GAA	ATG	GAA	GTG	TGG	GCC	TTG	1037
Ala	Leu	Phe	Gly	Gly	Gln	Arg	Phe	Gly	Glu	Met	Glu	Val	Trp	Ala	Leu	
205					210					215						
GAA	GCT	TAT	GGC	GCA	GCG	CAC	ACT	CTA	AAA	GAA	ATG	CTC	ACC	ATT	AAA	1085
Glu	Ala	Tyr	Gly	Ala	Ala	His	Thr	Leu	Lys	Glu	Met	Leu	Thr	Ile	Lys	
220					225					230						
TCC	GAT	GAT	ATT	AGA	GGC	AGA	GAG	AAC	GCT	TAT	AGG	GCT	ATC	GCT	AAA	1133
Ser	Asp	Asp	Ile	Arg	Gly	Arg	Glu	Asn	Ala	Tyr	Arg	Ala	Ile	Ala	Lys	
235					240					245						
GGT	GAG	CAA	GTG	GGC	GAG	AGT	GAA	ATC	CCT	GAG	ACT	TTC	TAT	GTT	TTG	1181
Gly	Glu	Gln	Val	Gly	Glu	Ser	Glu	Ile	Pro	Glu	Thr	Phe	Tyr	Val	Leu	
250					255					260					265	
ACT	AAA	GAA	TTG	CAA	TCG	CTC	GCT	TTG	GAT	ATT	AAT	ATT	TTT	GGG	GAC	1229
Thr	Lys	Glu	Leu	Gln	Ser	Leu	Ala	Leu	Asp	Ile	Asn	Ile	Phe	Gly	Asp	
270					275					280						

GAT GTG GAT GAG GAT GGA GCA CCT AAA CCC ATT GTC ATT AAA GAA GAT	1277
Asp Val Asp Glu Asp Gly Ala Pro Lys Pro Ile Val Ile Lys Glu Asp	
285 290 295	
GAC AGG CCT AAA GAC TTT AGC TCT TTC CAG CTC ACA CTA GCT AGC CCT	1325
Asp Arg Pro Lys Asp Phe Ser Ser Phe Gln Leu Thr Leu Ala Ser Pro	
300 305 310	
GAA AAA ATC CAT TCT TGG AGT TAT GGG GAA GTT AAA AAG CCA GAA ACG	1373
Glu Lys Ile His Ser Trp Ser Tyr Gly Glu Val Lys Lys Pro Glu Thr	
315 320 325	
ATC AAT TAT CGC ACC CTA AAA CCT GAA CGA GAC GGC TTG TTT TGC ATG	1421
Ile Asn Tyr Arg Thr Leu Lys Pro Glu Arg Asp Gly Leu Phe Cys Met	
330 335 340 345	
AAA ATC TTT GGC CCC ACT AAA GAT TAT GAA TGC TTG TGC GGC AAA TAC	1469
Lys Ile Phe Gly Pro Thr Lys Asp Tyr Glu Cys Leu Cys Gly Lys Tyr	
350 355 360	
AAA AAG CCT CGC TTC AAA GAC ATT GGC ACA TGC GAA AAA TGC GGC GTG	1517
Lys Lys Pro Arg Phe Lys Asp Ile Gly Thr Cys Glu Lys Cys Gly Val	
365 370 375	
GCG ATC ACG CAC TCC AAA GTC AGG CGT TTT AGA ATG GGC CAT ATT GAA	1565
Ala Ile Thr His Ser Lys Val Arg Arg Phe Arg Met Gly His Ile Glu	
380 385 390	
TTG GCC ACT CCT GTA GCG CAT ATC TGG TAT GTT AAT TCC TTG CCT AGC	1613
Leu Ala Thr Pro Val Ala His Ile Trp Tyr Val Asn Ser Leu Pro Ser	
395 400 405	
CGT ATC GGC ACG CTT TTA GGC GTT AAG ATG AAA GAC TTA GAG CGC GTG	1661
Arg Ile Gly Thr Leu Leu Gly Val Lys Met Lys Asp Leu Glu Arg Val	
410 415 420 425	
TTG TAT TAT GAA GCT TAT ATC GTT AAA GAA CCA GGC GAA GCC GCT TAT	1709
Leu Tyr Tyr Glu Ala Tyr Ile Val Lys Glu Pro Gly Glu Ala Ala Tyr	
430 435 440	
GAC AAT GAA GGC ACT AAG CTT GTG ATG AAA TAC GAT ATT TTG AAT GAA	1757
Asp Asn Glu Gly Thr Lys Leu Val Met Lys Tyr Asp Ile Leu Asn Glu	
445 450 455	
GAG CAG TAT CAA AAT ATC TCA CGA AGA TAC GAA GAC AGG GGC TTT GTA	1805
Glu Gln Tyr Gln Asn Ile Ser Arg Arg Tyr Glu Asp Arg Gly Phe Val	
460 465 470	
GCG CAA ATG GGC GGT GAA GCG ATC AAG GAT TTG TTA GAA GAA ATT GAT	1853
Ala Gln Met Gly Gly Glu Ala Ile Lys Asp Leu Leu Glu Glu Ile Asp	
475 480 485	
TTG ATC ACC TTA TTG CAG AGT TTG AAA GAA GAA GTG AAA GAC ACC AAT	1901
Leu Ile Thr Leu Leu Gln Ser Leu Lys Glu Glu Val Lys Asp Thr Asn	
490 495 500 505	
TCT GAT GCG AAA AAG AAA AAA CTC ATT AAG CGT TTG AAA GTG GTA GAA	1949
Ser Asp Ala Lys Lys Lys Lys Leu Ile Lys Arg Leu Lys Val Val Glu	

510										515					520					
AGC	TTT	TTA	AAT	TCT	GGT	AAT	AGG	CCT	GAA	TGG	ATG	ATG	CTC	ACG	GTT	1997				
Ser	Phe	Leu	Asn	Ser	Gly	Asn	Arg	Pro	Glu	Trp	Met	Met	Leu	Thr	Val					
			525					530					535							
TTA	CCG	GTA	TTG	CCA	CCG	GAT	TTA	AGG	CCT	TTA	GTC	GCG	CTA	GAT	GGC	2045				
Leu	Pro	Val	Leu	Pro	Pro	Asp	Leu	Arg	Pro	Leu	Val	Ala	Leu	Asp	Gly					
		540					545					550								
GGG	AAG	TTT	GCA	GTC	AGC	GAT	GTG	AAT	GAA	TTG	TAT	CGT	CGT	GTC	ATC	2093				
Gly	Lys	Phe	Ala	Val	Ser	Asp	Val	Asn	Glu	Leu	Tyr	Arg	Arg	Val	Ile					
	555					560					565									
AAT	CGT	AAC	CAA	CGC	TTG	AAA	CGC	TTA	ATG	GAG	CTT	GGA	GCG	CCA	GAA	2141				
Asn	Arg	Asn	Gln	Arg	Leu	Lys	Arg	Leu	Met	Glu	Leu	Gly	Ala	Pro	Glu					
570					575					580					585					
ATC	ATT	GTG	CGC	AAT	GAA	AAA	AGG	ATG	TTG	CAA	GAA	GCC	GTG	GAT	GTG	2189				
Ile	Ile	Val	Arg	Asn	Glu	Lys	Arg	Met	Leu	Gln	Glu	Ala	Val	Asp	Val					
				590					595					600						
CTT	TTT	GAT	AAC	GGC	CGC	AGC	ACT	AAT	GCG	GTT	AAA	GGG	GCT	AAC	AAA	2237				
Leu	Phe	Asp	Asn	Gly	Arg	Ser	Thr	Asn	Ala	Val	Lys	Gly	Ala	Asn	Lys					
			605					610					615							
CGC	CCT	TTA	AAA	TCG	CTC	AGT	GAA	ATC	ATT	AAA	GGC	AAG	CAG	GGG	CGT	2285				
Arg	Pro	Leu	Lys	Ser	Leu	Ser	Glu	Ile	Ile	Lys	Gly	Lys	Gln	Gly	Arg					
		620					625					630								
TTC	AGG	CAA	AAC	CTT	TTA	GGT	AAG	CGC	GTG	GAT	TTT	TCA	GGC	AGA	AGC	2333				
Phe	Arg	Gln	Asn	Leu	Leu	Gly	Lys	Arg	Val	Asp	Phe	Ser	Gly	Arg	Ser					
	635					640					645									
GTG	ATT	GTG	GTT	GGG	CCT	AAT	CTC	AAA	ATG	GAT	GAA	TGC	GGG	TTG	CCT	2381				
Val	Ile	Val	Val	Gly	Pro	Asn	Leu	Lys	Met	Asp	Glu	Cys	Gly	Leu	Pro					
650					655					660					665					
AAA	AAC	ATG	GCG	TTA	GAA	CTC	TTC	AAA	CCG	CAT	TTG	TTA	TCC	AAG	CTT	2429				
Lys	Asn	Met	Ala	Leu	Glu	Leu	Phe	Lys	Pro	His	Leu	Leu	Ser	Lys	Leu					
				670				675						680						
GAA	GAG	AGA	GGC	TAT	GCC	ACC	ACG	CTC	AAA	CAG	GCT	AAA	CGC	ATG	ATT	2477				
Glu	Glu	Arg	Gly	Tyr	Ala	Thr	Thr	Leu	Lys	Gln	Ala	Lys	Arg	Met	Ile					
			685					690					695							
GAG	CAA	AAA	AGC	AAT	GAA	GTA	TGG	GAG	TGC	TTG	CAA	GAA	ATC	ACA	GAG	2525				
Glu	Gln	Lys	Ser	Asn	Glu	Val	Trp	Glu	Cys	Leu	Gln	Glu	Ile	Thr	Glu					
		700					705					710								
GGG	TAT	CCG	GTG	CTA	CTC	AAC	CGC	GCT	CCT	ACC	TTG	CAC	AAG	CAA	TCC	2573				
Gly	Tyr	Pro	Val	Leu	Leu	Asn	Arg	Ala	Pro	Thr	Leu	His	Lys	Gln	Ser					
	715					720					725									
ATT	CAA	GCG	TTC	CAT	CCA	AAG	CTG	ATT	GAC	GGC	AAA	GCG	ATC	CAA	TTG	2621				
Ile	Gln	Ala	Phe	His	Pro	Lys	Leu	Ile	Asp	Gly	Lys	Ala	Ile	Gln	Leu					
730					735					740					745					

CAC	CCG	TTA	GTG	TGT	TCA	GCG	TTC	AAC	GCC	GAT	TTT	GAC	GGG	GAC	CAA	2669
His	Pro	Leu	Val	Cys	Ser	Ala	Phe	Asn	Ala	Asp	Phe	Asp	Gly	Asp	Gln	
				750					755					760		
ATG	GCG	GTG	CAT	GTG	CCT	TTA	AGC	CAG	GAA	GCG	ATC	GCT	GAA	TGC	AAG	2717
Met	Ala	Val	His	Val	Pro	Leu	Ser	Gln	Glu	Ala	Ile	Ala	Glu	Cys	Lys	
				765				770					775			
GTG	CTG	ATG	CTA	AGC	TCT	ATG	AAT	ATC	CTT	TTG	CCT	GCT	AGC	GGT	AAG	2765
Val	Leu	Met	Leu	Ser	Ser	Met	Asn	Ile	Leu	Leu	Pro	Ala	Ser	Gly	Lys	
				780				785					790			
GCC	GTA	GCC	ATT	CCT	AGC	CAA	GAT	ATG	GTT	TTA	GGG	CTT	TAT	TAT	CTT	2813
Ala	Val	Ala	Ile	Pro	Ser	Gln	Asp	Met	Val	Leu	Gly	Leu	Tyr	Tyr	Leu	
				795			800				805					
TCT	TTA	GAA	AAG	AGC	GGG	GTC	AAG	GGC	GAG	CAT	AAG	CTT	TTT	TCT	AGC	2861
Ser	Leu	Glu	Lys	Ser	Gly	Val	Lys	Gly	Glu	His	Lys	Leu	Phe	Ser	Ser	
810					815					820					825	
GTG	AAT	GAA	ATC	ATC	ACC	GCC	ATT	GAC	ACG	AAA	GAA	TTA	GAC	ATC	CAC	2909
Val	Asn	Glu	Ile	Ile	Thr	Ala	Ile	Asp	Thr	Lys	Glu	Leu	Asp	Ile	His	
					830				835					840		
GCA	AAG	ATT	AGG	GTT	TTA	GAT	CAA	GGG	AAT	ATT	ATC	GCT	ACG	AGT	GCA	2957
Ala	Lys	Ile	Arg	Val	Leu	Asp	Gln	Gly	Asn	Ile	Ile	Ala	Thr	Ser	Ala	
					845			850					855			
GGG	CGC	ATG	ATC	ATT	AAG	TCC	ATT	TTG	CCT	GAT	TTT	ATC	CCT	ACG	GAT	3005
Gly	Arg	Met	Ile	Ile	Lys	Ser	Ile	Leu	Pro	Asp	Phe	Ile	Pro	Thr	Asp	
					860			865				870				
TTG	TGG	AAC	AGA	CCC	ATG	AAG	AAA	AAA	GAT	ATT	GGC	GTG	CTT	GTG	GAT	3053
Leu	Trp	Asn	Arg	Pro	Met	Lys	Lys	Lys	Asp	Ile	Gly	Val	Leu	Val	Asp	
					875			880			885					
TAT	GTG	CAT	AAA	GTT	GGC	GGT	ATC	GGT	ATT	ACT	GCA	ACC	TTT	TTG	GAT	3101
Tyr	Val	His	Lys	Val	Gly	Gly	Ile	Gly	Ile	Thr	Ala	Thr	Phe	Leu	Asp	
890					895					900					905	
AAT	TTA	AAA	ACG	CTT	GGC	TTT	AGG	TAT	GCG	ACT	AAG	GCT	GGT	ATT	TCT	3149
Asn	Leu	Lys	Thr	Leu	Gly	Phe	Arg	Tyr	Ala	Thr	Lys	Ala	Gly	Ile	Ser	
					910				915					920		
ATC	TCT	ATG	GAG	GAT	ATT	ATC	ACG	CCA	AAA	GAC	AAG	CAA	AAA	ATG	GTG	3197
Ile	Ser	Met	Glu	Asp	Ile	Ile	Thr	Pro	Lys	Asp	Lys	Gln	Lys	Met	Val	
				925				930					935			
GAA	AAA	GCC	AAA	GTA	GAG	GTT	AAA	AAA	ATC	CAG	CAA	CAA	TAC	GAT	CAA	3245
Glu	Lys	Ala	Lys	Val	Glu	Val	Lys	Lys	Ile	Gln	Gln	Gln	Tyr	Asp	Gln	
				940				945				950				
GGG	CTG	CTC	ACT	GAC	CAA	GAG	CGT	TAC	AAT	AAG	ATC	ATT	GAC	ACT	TGG	3293
Gly	Leu	Leu	Thr	Asp	Gln	Glu	Arg	Tyr	Asn	Lys	Ile	Ile	Asp	Thr	Trp	
				955			960				965					
ACT	GAA	GTC	AAT	GAC	AAA	ATG	AGT	AAA	GAA	ATG	ATG	ACC	GCT	ATC	GCG	3341
Thr	Glu	Val	Asn	Asp	Lys	Met	Ser	Lys	Glu	Met	Met	Thr	Ala	Ile	Ala	

970	975	980	985	
CAA GAT AAA GAG GGC TTT AAC TCT ATT TAT ATG ATG GCA GAT AGC GGC				3389
Gln Asp Lys Glu Gly Phe Asn Ser Ile Tyr Met Met Ala Asp Ser Gly	990	995	1000	
GCA AGG GGT AGC GCG GCG CAA ATC CGT CAG CTT TCA GCG ATG AGG GGT				3437
Ala Arg Gly Ser Ala Ala Gln Ile Arg Gln Leu Ser Ala Met Arg Gly	1005	1010	1015	
CTT ATG ACA AAG CCG GAC GGC AGT ATC ATT GAA ACG CCC ATT ATT TCT				3485
Leu Met Thr Lys Pro Asp Gly Ser Ile Ile Glu Thr Pro Ile Ile Ser	1020	1025	1030	
AAC TTT AAA GAG GGG TTG AAT GTC TTA GAA TAC TTC AAT TCC ACG CAT				3533
Asn Phe Lys Glu Gly Leu Asn Val Leu Glu Tyr Phe Asn Ser Thr His	1035	1040	1045	
GGC GCT AGA AAG GGC TTA GCG GAT ACA GCG CTA AAA ACA GCC AAT GCG				3581
Gly Ala Arg Lys Gly Leu Ala Asp Thr Ala Leu Lys Thr Ala Asn Ala	1050	1055	1060	1065
GGG TAT TTG ACC AGA AAG CTC ATT GAT GTT TCG CAA AAT GTC AAG GTG				3629
Gly Tyr Leu Thr Arg Lys Leu Ile Asp Val Ser Gln Asn Val Lys Val	1070	1075	1080	
GTG TCT GAT GAT TGC GGC ACG CAT GAA GGG ATT GAA ATC ACG GAT ATT				3677
Val Ser Asp Asp Cys Gly Thr His Glu Gly Ile Glu Ile Thr Asp Ile	1085	1090	1095	
GCG GTG GGG AGT GAG CTG ATT GAA CCT TTA GAA GAG CGT ATT TTT GGG				3725
Ala Val Gly Ser Glu Leu Ile Glu Pro Leu Glu Glu Arg Ile Phe Gly	1100	1105	1110	
CGC GTT TTA TTA GAA GAT GTG ATC GAT CCC ATT ACG AAT GAA ATC TTG				3773
Arg Val Leu Leu Glu Asp Val Ile Asp Pro Ile Thr Asn Glu Ile Leu	1115	1120	1125	
CTT TAT GCG GAC ACT TTG ATT GAT GAA GAG GGT GCT AAA AAG GTG GTT				3821
Leu Tyr Ala Asp Thr Leu Ile Asp Glu Glu Gly Ala Lys Lys Val Val	1130	1135	1140	1145
GAA GCC GGG ATT AAA TCC ATT ACG ATC CGC ACC CCA GTA ACT TGT AAA				3869
Glu Ala Gly Ile Lys Ser Ile Thr Ile Arg Thr Pro Val Thr Cys Lys	1150	1155	1160	
GCG CCA AAG GGC GTG TGC GCG AAA TGC TAT GGC TTG AAT TTG GGC GAA				3917
Ala Pro Lys Gly Val Cys Ala Lys Cys Tyr Gly Leu Asn Leu Gly Glu	1165	1170	1175	
GGC AAG ATG AGT TAT CCG GGT GAA GCG GTG GGC GTG GTA GCC GCG CAA				3965
Gly Lys Met Ser Tyr Pro Gly Glu Ala Val Gly Val Val Ala Ala Gln	1180	1185	1190	
TCT ATT GGG GAG CCT GGA ACG CAG CTC ACT TTA AGG ACT TTC CAT GTG				4013
Ser Ile Gly Glu Pro Gly Thr Gln Leu Thr Leu Arg Thr Phe His Val	1195	1200	1205	

GGC GGG ACA GCG AGC AGG AGT CAG GAT GAG CGC GAA ATC GTA GCG AGC Gly Gly Thr Ala Ser Arg Ser Gln Asp Glu Arg Glu Ile Val Ala Ser 1210 1215 1220 1225	4061
AAA GAA GGT TTT GTG CGT TTT TAC AAC CTT AGG ACT TAC ACG AAT AAA Lys Glu Gly Phe Val Arg Phe Tyr Asn Leu Arg Thr Tyr Thr Asn Lys 1230 1235 1240	4109
GAG GGT AAA AAC ATT ATC GCT AAC CGC CGT AAC GCT TCT ATT TTA GTG Glu Gly Lys Asn Ile Ile Ala Asn Arg Arg Asn Ala Ser Ile Leu Val 1245 1250 1255	4157
GTA GAG CCT AAG ATT AAA GCG CCT TTT GAT GGG GAA TTA CGC ATT GAA Val Glu Pro Lys Ile Lys Ala Pro Phe Asp Gly Glu Leu Arg Ile Glu 1260 1265 1270	4205
ACG GTT TAT GAA GAA GTC GTT GTG AGC GTG AAA AAT GGC GAT CAA GAA Thr Val Tyr Glu Glu Val Val Val Ser Val Lys Asn Gly Asp Gln Glu 1275 1280 1285	4253
GCT AAA TTT GTT TTA AGG AGA AGC GAT ATT GTC AAG CCA AGC GAA TTA Ala Lys Phe Val Leu Arg Arg Ser Asp Ile Val Lys Pro Ser Glu Leu 1290 1295 1300 1305	4301
GCC GGC GTT GGC GGT AAG ATT GAG GGG AAA GTG TAT TTG CCT TAT GCT Ala Gly Val Gly Gly Lys Ile Glu Gly Lys Val Tyr Leu Pro Tyr Ala 1310 1315 1320	4349
AGT GGG CAT AAG GTG CAT AAG GGG GGA AGT ATC GCT GAT ATT ATC CAA Ser Gly His Lys Val His Lys Gly Gly Ser Ile Ala Asp Ile Ile Gln 1325 1330 1335	4397
GAG GGC TGG AAT GTG CCT AAT CGC ATC CCT TAT GCG AGC GAA TTG CTA Glu Gly Trp Asn Val Pro Asn Arg Ile Pro Tyr Ala Ser Glu Leu Leu 1340 1345 1350	4445
GTC AAG GAT AAT GAC CCT ATT GCG CAA GAT GTG TAT GCC AAA GAA AAA Val Lys Asp Asn Asp Pro Ile Ala Gln Asp Val Tyr Ala Lys Glu Lys 1355 1360 1365	4493
GGC GTA ATC AAA TAC TAT GTT TTA GAG GCT AAC CAT TTA GAG CGC ACC Gly Val Ile Lys Tyr Tyr Val Leu Glu Ala Asn His Leu Glu Arg Thr 1370 1375 1380 1385	4541
CAT GGG ATC AAA AAG GGC GAT ATG GTG AGT GAA AAA GGC TTG TTT GCG His Gly Ile Lys Lys Gly Asp Met Val Ser Glu Lys Gly Leu Phe Ala 1390 1395 1400	4589
GTG ATA GCT GAT GAT AAT GGT AGG GAA GCC GCT CGC CAT TAT ATC GCT Val Ile Ala Asp Asp Asn Gly Arg Glu Ala Ala Arg His Tyr Ile Ala 1405 1410 1415	4637
AGG GGT TCT GAG ATC TTG ATT GAT GAT AAT AGT GAA GTG AGC ACT AAT Arg Gly Ser Glu Ile Leu Ile Asp Asp Asn Ser Glu Val Ser Thr Asn 1420 1425 1430	4685
AGC GTG ATT TCT AAA CCC ACG ACT AAC ACT TTC AAA ACG ATT GCC ACA Ser Val Ile Ser Lys Pro Thr Thr Asn Thr Phe Lys Thr Ile Ala Thr	4733

1435	1440	1445	
TGG GAT CCT TAC AAC ACC CCT ATC ATT GCG GAC TTT AAA GGT AAG GTG			4781
Trp Asp Pro Tyr Asn Thr Pro Ile Ile Ala Asp Phe Lys Gly Lys Val			
1450	1455	1460 1465	
GGT TTT GTG GAT GTT ATC GCA GGG GTT ACG GTC GCT GAA AAA GAA GAC			4829
Gly Phe Val Asp Val Ile Ala Gly Val Thr Val Ala Glu Lys Glu Asp			
	1470	1475 1480	
GAA AAT ACC GGT ATC ACA AGC TTA GTG GTG AAT GAT TAC ATT CCA AGC			4877
Glu Asn Thr Gly Ile Thr Ser Leu Val Val Asn Asp Tyr Ile Pro Ser			
	1485	1490 1495	
GGA TAC AAA CCA AGC TTG TTT TTA GAG GGG GCT AAT GGC GAA GAG ATG			4925
Gly Tyr Lys Pro Ser Leu Phe Leu Glu Gly Ala Asn Gly Glu Glu Met			
	1500	1505 1510	
CGT TAT TTC CTA GAG CCA AAA ACC TCT ATC GCC ATT AGC GAT GGC TCT			4973
Arg Tyr Phe Leu Glu Pro Lys Thr Ser Ile Ala Ile Ser Asp Gly Ser			
	1515	1520 1525	
AGC GTG GAG CAA GCT GAA GTG TTA GCG AAA ATC CCT AAA GCG ACC GTT			5021
Ser Val Glu Gln Ala Glu Val Leu Ala Lys Ile Pro Lys Ala Thr Val			
1530	1535	1540 1545	
AAA TCT AGG GAT ATT ACC GGG GGT CTC CCA AGG GTT TCG GAA CTC TTT			5069
Lys Ser Arg Asp Ile Thr Gly Gly Leu Pro Arg Val Ser Glu Leu Phe			
	1550	1555 1560	
GAA GCG AGA AAA CCC AAG CCT AAA GAT GTG GCG ATC CTT TCT GAA GTT			5117
Glu Ala Arg Lys Pro Lys Pro Lys Asp Val Ala Ile Leu Ser Glu Val			
	1565	1570 1575	
GAT GGG ATT GTG AGT TTT GGC AAA CCC ATT CGC AAT AAA GAA CAC ATC			5165
Asp Gly Ile Val Ser Phe Gly Lys Pro Ile Arg Asn Lys Glu His Ile			
	1580	1585 1590	
ATC GTA ACT TCT AAA GAT GGC CGT TCC ATG GAT TAT TTT GTG GAT AAA			5213
Ile Val Thr Ser Lys Asp Gly Arg Ser Met Asp Tyr Phe Val Asp Lys			
	1595	1600 1605	
GGC AAG CAA ATT TTA GTG CAT GCC GAT GAA TTT GTG CAT GCG GGA GAA			5261
Gly Lys Gln Ile Leu Val His Ala Asp Glu Phe Val His Ala Gly Glu			
1610	1615	1620 1625	
GCG ATG ACG GAC GGA GTA ATT TCA AGC CAT GAT ATT TTA AGG ATC AGT			5309
Ala Met Thr Asp Gly Val Ile Ser Ser His Asp Ile Leu Arg Ile Ser			
	1630	1635 1640	
GGC GAA AAA GAG CTT TAT AAA TAC ATT GTG AGC GAA GTC CAG CAA GTG			5357
Gly Glu Lys Glu Leu Tyr Lys Tyr Ile Val Ser Glu Val Gln Gln Val			
	1645	1650 1655	
TAT CGC AGG CAG GGG GTG AGC ATT GCG GAC AAG CAC ATT GAA ATC ATT			5405
Tyr Arg Arg Gln Gly Val Ser Ile Ala Asp Lys His Ile Glu Ile Ile			
	1660	1665 1670	

GTT TCT CAA ATG CTA AGA CAG GTG CGT ATT TTA GAC AGC GGG GAT AGC 5453
 Val Ser Gln Met Leu Arg Gln Val Arg Ile Leu Asp Ser Gly Asp Ser
 1675 1680 1685

AAG TTT ATT GAA GGG GAT TTA GTC AGT AAA AAA CTT TTC AAA GAA GAA 5501
 Lys Phe Ile Glu Gly Asp Leu Val Ser Lys Lys Leu Phe Lys Glu Glu
 1690 1695 1700 1705

AAC GCT CGT GTG ATC GCT TTA AAA GGC GAG CCA GCG ATT GCT GAA CCG 5549
 Asn Ala Arg Val Ile Ala Leu Lys Gly Glu Pro Ala Ile Ala Glu Pro
 1710 1715 1720

GTG CTT TTA GGG ATC ACT AGA GCG GCT ATT GGG AGC GAT AGC ATC ATC 5597
 Val Leu Leu Gly Ile Thr Arg Ala Ala Ile Gly Ser Asp Ser Ile Ile
 1725 1730 1735

TCA GCG GCC TCT TTC CAA GAA ACG ACT AAA GTT TTA ACA GAA GCC AGT 5645
 Ser Ala Ala Ser Phe Gln Glu Thr Thr Lys Val Leu Thr Glu Ala Ser
 1740 1745 1750

ATC GCT ATG AAA AAA GAC TTT TTA GAG GAT TTG AAA GAG AAT GTG GTG 5693
 Ile Ala Met Lys Lys Asp Phe Leu Glu Asp Leu Lys Glu Asn Val Val
 1755 1760 1765

TTG GGG AGG ATG ATC CCT GTG GGA ACA GGC ATG TAT AAG AAT AAA AAA 5741
 Leu Gly Arg Met Ile Pro Val Gly Thr Gly Met Tyr Lys Asn Lys Lys
 1770 1775 1780 1785

ATC GTG TTA AGA GCG CTT GAG GAT AAC TCT AAA TTT TGATATGAAA AATCGG 5793
 Ile Val Leu Arg Ala Leu Glu Asp Asn Ser Lys Phe
 1790 1795

TTAAGATTTT TAAAAGAAAA ATTAGGGTAA AATGGGGGA 5832

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1797 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Met Ala Gly Arg His Gly Asn Lys Gly Ile Val Ser Asn Ile Val Pro
 1 5 10 15
 Val Ala Asp Met Pro Tyr Thr Ala Asp Gly Glu Pro Val Asp Ile Val
 20 25 30
 Leu Asn Pro Leu Gly Val Pro Ser Arg Met Asn Ile Gly Gln Ile Leu
 35 40 45
 Glu Met His Leu Gly Leu Val Gly Lys Glu Phe Gly Lys Gln Ile Ala
 50 55 60
 Arg Met Leu Glu Asp Lys Thr Lys Asp Phe Ala Lys Glu Leu Arg Ala
 65 70 75 80
 Lys Met Leu Glu Xaa Ala Asn Ala Ile Asn Glu Lys Asp Pro Leu Thr

				85					90					95			
Ile	His	Ala	Leu	Glu	Asn	Cys	Ser	Asp	Glu	Glu	Leu	Leu	Glu	Tyr	Ala		
			100					105					110				
Lys	Asp	Trp	Ser	Lys	Gly	Val	Lys	Met	Ala	Ile	Pro	Val	Phe	Glu	Gly		
		115						120					125				
Ile	Ser	Gln	Glu	Lys	Phe	Tyr	Lys	Leu	Phe	Glu	Leu	Ala	Lys	Ile	Ala		
		130				135					140						
Met	Asp	Gly	Lys	Met	Asp	Leu	Tyr	Asp	Gly	Arg	Thr	Gly	Glu	Lys	Met		
145					150					155					160		
Arg	Glu	Arg	Val	Asn	Val	Gly	Tyr	Met	Tyr	Met	Ile	Lys	Leu	His	His		
				165					170					175			
Leu	Val	Asp	Glu	Lys	Val	His	Ala	Arg	Ser	Thr	Gly	Pro	Tyr	Ser	Leu		
		180						185					190				
Val	Thr	His	Gln	Pro	Val	Gly	Gly	Lys	Ala	Leu	Phe	Gly	Gly	Gln	Arg		
		195					200					205					
Phe	Gly	Glu	Met	Glu	Val	Trp	Ala	Leu	Glu	Ala	Tyr	Gly	Ala	Ala	His		
		210				215					220						
Thr	Leu	Lys	Glu	Met	Leu	Thr	Ile	Lys	Ser	Asp	Asp	Ile	Arg	Gly	Arg		
225					230					235					240		
Glu	Asn	Ala	Tyr	Arg	Ala	Ile	Ala	Lys	Gly	Glu	Gln	Val	Gly	Glu	Ser		
				245					250					255			
Glu	Ile	Pro	Glu	Thr	Phe	Tyr	Val	Leu	Thr	Lys	Glu	Leu	Gln	Ser	Leu		
		260						265					270				
Ala	Leu	Asp	Ile	Asn	Ile	Phe	Gly	Asp	Asp	Val	Asp	Glu	Asp	Gly	Ala		
		275					280					285					
Pro	Lys	Pro	Ile	Val	Ile	Lys	Glu	Asp	Asp	Arg	Pro	Lys	Asp	Phe	Ser		
		290				295					300						
Ser	Phe	Gln	Leu	Thr	Leu	Ala	Ser	Pro	Glu	Lys	Ile	His	Ser	Trp	Ser		
305					310					315					320		
Tyr	Gly	Glu	Val	Lys	Lys	Pro	Glu	Thr	Ile	Asn	Tyr	Arg	Thr	Leu	Lys		
				325					330					335			
Pro	Glu	Arg	Asp	Gly	Leu	Phe	Cys	Met	Lys	Ile	Phe	Gly	Pro	Thr	Lys		
			340					345					350				
Asp	Tyr	Glu	Cys	Leu	Cys	Gly	Lys	Tyr	Lys	Lys	Pro	Arg	Phe	Lys	Asp		
		355					360					365					
Ile	Gly	Thr	Cys	Glu	Lys	Cys	Gly	Val	Ala	Ile	Thr	His	Ser	Lys	Val		
		370				375					380						
Arg	Arg	Phe	Arg	Met	Gly	His	Ile	Glu	Leu	Ala	Thr	Pro	Val	Ala	His		
385					390					395					400		
Ile	Trp	Tyr	Val	Asn	Ser	Leu	Pro	Ser	Arg	Ile	Gly	Thr	Leu	Leu	Gly		
				405					410					415			
Val	Lys	Met	Lys	Asp	Leu	Glu	Arg	Val	Leu	Tyr	Tyr	Glu	Ala	Tyr	Ile		
			420					425					430				
Val	Lys	Glu	Pro	Gly	Glu	Ala	Ala	Tyr	Asp	Asn	Glu	Gly	Thr	Lys	Leu		
		435					440					445					
Val	Met	Lys	Tyr	Asp	Ile	Leu	Asn	Glu	Glu	Gln	Tyr	Gln	Asn	Ile	Ser		
		450				455					460						
Arg	Arg	Tyr	Glu	Asp	Arg	Gly	Phe	Val	Ala	Gln	Met	Gly	Gly	Glu	Ala		
465					470					475					480		
Ile	Lys	Asp	Leu	Leu	Glu	Glu	Ile	Asp	Leu	Ile	Thr	Leu	Leu	Gln	Ser		
				485				490						495			
Leu	Lys	Glu	Glu	Val	Lys	Asp	Thr	Asn	Ser	Asp	Ala	Lys	Lys	Lys	Lys		
			500					505					510				
Leu	Ile	Lys	Arg	Leu	Lys	Val	Val	Glu	Ser	Phe	Leu	Asn	Ser	Gly	Asn		
		515					520					525					
Arg	Pro	Glu	Trp	Met	Met	Leu	Thr	Val	Leu	Pro	Val	Leu	Pro	Pro	Asp		
		530				535					540						
Leu	Arg	Pro	Leu	Val	Ala	Leu	Asp	Gly	Gly	Lys	Phe	Ala	Val	Ser	Asp		

545		550		555		560
Val Asn Glu Leu Tyr Arg Arg Val Ile Asn Arg Asn Gln Arg Leu Lys						
	565		570			575
Arg Leu Met Glu Leu Gly Ala Pro Glu Ile Ile Val Arg Asn Glu Lys						
	580		585			590
Arg Met Leu Gln Glu Ala Val Asp Val Leu Phe Asp Asn Gly Arg Ser						
	595		600			605
Thr Asn Ala Val Lys Gly Ala Asn Lys Arg Pro Leu Lys Ser Leu Ser						
	610		615			620
Glu Ile Ile Lys Gly Lys Gln Gly Arg Phe Arg Gln Asn Leu Leu Gly						
	625		630			635
Lys Arg Val Asp Phe Ser Gly Arg Ser Val Ile Val Val Gly Pro Asn						
	645		650			655
Leu Lys Met Asp Glu Cys Gly Leu Pro Lys Asn Met Ala Leu Glu Leu						
	660		665			670
Phe Lys Pro His Leu Leu Ser Lys Leu Glu Glu Arg Gly Tyr Ala Thr						
	675		680			685
Thr Leu Lys Gln Ala Lys Arg Met Ile Glu Gln Lys Ser Asn Glu Val						
	690		695			700
Trp Glu Cys Leu Gln Glu Ile Thr Glu Gly Tyr Pro Val Leu Leu Asn						
	705		710			715
Arg Ala Pro Thr Leu His Lys Gln Ser Ile Gln Ala Phe His Pro Lys						
	725		730			735
Leu Ile Asp Gly Lys Ala Ile Gln Leu His Pro Leu Val Cys Ser Ala						
	740		745			750
Phe Asn Ala Asp Phe Asp Gly Asp Gln Met Ala Val His Val Pro Leu						
	755		760			765
Ser Gln Glu Ala Ile Ala Glu Cys Lys Val Leu Met Leu Ser Ser Met						
	770		775			780
Asn Ile Leu Leu Pro Ala Ser Gly Lys Ala Val Ala Ile Pro Ser Gln						
	785		790			795
Asp Met Val Leu Gly Leu Tyr Tyr Leu Ser Leu Glu Lys Ser Gly Val						
	805		810			815
Lys Gly Glu His Lys Leu Phe Ser Ser Val Asn Glu Ile Ile Thr Ala						
	820		825			830
Ile Asp Thr Lys Glu Leu Asp Ile His Ala Lys Ile Arg Val Leu Asp						
	835		840			845
Gln Gly Asn Ile Ile Ala Thr Ser Ala Gly Arg Met Ile Ile Lys Ser						
	850		855			860
Ile Leu Pro Asp Phe Ile Pro Thr Asp Leu Trp Asn Arg Pro Met Lys						
	865		870			875
Lys Lys Asp Ile Gly Val Leu Val Asp Tyr Val His Lys Val Gly Gly						
	885		890			895
Ile Gly Ile Thr Ala Thr Phe Leu Asp Asn Leu Lys Thr Leu Gly Phe						
	900		905			910
Arg Tyr Ala Thr Lys Ala Gly Ile Ser Ile Ser Met Glu Asp Ile Ile						
	915		920			925
Thr Pro Lys Asp Lys Gln Lys Met Val Glu Lys Ala Lys Val Glu Val						
	930		935			940
Lys Lys Ile Gln Gln Gln Tyr Asp Gln Gly Leu Leu Thr Asp Gln Glu						
	945		950			955
Arg Tyr Asn Lys Ile Ile Asp Thr Trp Thr Glu Val Asn Asp Lys Met						
	965		970			975
Ser Lys Glu Met Met Thr Ala Ile Ala Gln Asp Lys Glu Gly Phe Asn						
	980		985			990
Ser Ile Tyr Met Met Ala Asp Ser Gly Ala Arg Gly Ser Ala Ala Gln						
	995		1000			1005
Ile Arg Gln Leu Ser Ala Met Arg Gly Leu Met Thr Lys Pro Asp Gly						

1010 1015 1020
 Ser Ile Ile Glu Thr Pro Ile Ile Ser Asn Phe Lys Glu Gly Leu Asn
 025 1030 1035 1040
 Val Leu Glu Tyr Phe Asn Ser Thr His Gly Ala Arg Lys Gly Leu Ala
 1045 1050 1055
 Asp Thr Ala Leu Lys Thr Ala Asn Ala Gly Tyr Leu Thr Arg Lys Leu
 1060 1065 1070
 Ile Asp Val Ser Gln Asn Val Lys Val Val Ser Asp Asp Cys Gly Thr
 1075 1080 1085
 His Glu Gly Ile Glu Ile Thr Asp Ile Ala Val Gly Ser Glu Leu Ile
 1090 1095 1100
 Glu Pro Leu Glu Glu Arg Ile Phe Gly Arg Val Leu Leu Glu Asp Val
 105 1110 1115 1120
 Ile Asp Pro Ile Thr Asn Glu Ile Leu Leu Tyr Ala Asp Thr Leu Ile
 1125 1130 1135
 Asp Glu Glu Gly Ala Lys Lys Val Val Glu Ala Gly Ile Lys Ser Ile
 1140 1145 1150
 Thr Ile Arg Thr Pro Val Thr Cys Lys Ala Pro Lys Gly Val Cys Ala
 1155 1160 1165
 Lys Cys Tyr Gly Leu Asn Leu Gly Glu Gly Lys Met Ser Tyr Pro Gly
 1170 1175 1180
 Glu Ala Val Gly Val Val Ala Ala Gln Ser Ile Gly Glu Pro Gly Thr
 185 1190 1195 1200
 Gln Leu Thr Leu Arg Thr Phe His Val Gly Gly Thr Ala Ser Arg Ser
 1205 1210 1215
 Gln Asp Glu Arg Glu Ile Val Ala Ser Lys Glu Gly Phe Val Arg Phe
 1220 1225 1230
 Tyr Asn Leu Arg Thr Tyr Thr Asn Lys Glu Gly Lys Asn Ile Ile Ala
 1235 1240 1245
 Asn Arg Arg Asn Ala Ser Ile Leu Val Val Glu Pro Lys Ile Lys Ala
 1250 1255 1260
 Pro Phe Asp Gly Glu Leu Arg Ile Glu Thr Val Tyr Glu Glu Val Val
 265 1270 1275 1280
 Val Ser Val Lys Asn Gly Asp Gln Glu Ala Lys Phe Val Leu Arg Arg
 1285 1290 1295
 Ser Asp Ile Val Lys Pro Ser Glu Leu Ala Gly Val Gly Gly Lys Ile
 1300 1305 1310
 Glu Gly Lys Val Tyr Leu Pro Tyr Ala Ser Gly His Lys Val His Lys
 1315 1320 1325
 Gly Gly Ser Ile Ala Asp Ile Ile Gln Glu Gly Trp Asn Val Pro Asn
 1330 1335 1340
 Arg Ile Pro Tyr Ala Ser Glu Leu Leu Val Lys Asp Asn Asp Pro Ile
 345 1350 1355 1360
 Ala Gln Asp Val Tyr Ala Lys Glu Lys Gly Val Ile Lys Tyr Tyr Val
 1365 1370 1375
 Leu Glu Ala Asn His Leu Glu Arg Thr His Gly Ile Lys Lys Gly Asp
 1380 1385 1390
 Met Val Ser Glu Lys Gly Leu Phe Ala Val Ile Ala Asp Asp Asn Gly
 1395 1400 1405
 Arg Glu Ala Ala Arg His Tyr Ile Ala Arg Gly Ser Glu Ile Leu Ile
 1410 1415 1420
 Asp Asp Asn Ser Glu Val Ser Thr Asn Ser Val Ile Ser Lys Pro Thr
 425 1430 1435 1440
 Thr Asn Thr Phe Lys Thr Ile Ala Thr Trp Asp Pro Tyr Asn Thr Pro
 1445 1450 1455
 Ile Ile Ala Asp Phe Lys Gly Lys Val Gly Phe Val Asp Val Ile Ala
 1460 1465 1470
 Gly Val Thr Val Ala Glu Lys Glu Asp Glu Asn Thr Gly Ile Thr Ser

1475 1480 1485
 Leu Val Val Asn Asp Tyr Ile Pro Ser Gly Tyr Lys Pro Ser Leu Phe
 1490 1495 1500
 Leu Glu Gly Ala Asn Gly Glu Glu Met Arg Tyr Phe Leu Glu Pro Lys
 505 1510 1515 1520
 Thr Ser Ile Ala Ile Ser Asp Gly Ser Ser Val Glu Gln Ala Glu Val
 1525 1530 1535
 Leu Ala Lys Ile Pro Lys Ala Thr Val Lys Ser Arg Asp Ile Thr Gly
 1540 1545 1550
 Gly Leu Pro Arg Val Ser Glu Leu Phe Glu Ala Arg Lys Pro Lys Pro
 1555 1560 1565
 Lys Asp Val Ala Ile Leu Ser Glu Val Asp Gly Ile Val Ser Phe Gly
 1570 1575 1580
 Lys Pro Ile Arg Asn Lys Glu His Ile Ile Val Thr Ser Lys Asp Gly
 585 1590 1595 1600
 Arg Ser Met Asp Tyr Phe Val Asp Lys Gly Lys Gln Ile Leu Val His
 1605 1610 1615
 Ala Asp Glu Phe Val His Ala Gly Glu Ala Met Thr Asp Gly Val Ile
 1620 1625 1630
 Ser Ser His Asp Ile Leu Arg Ile Ser Gly Glu Lys Glu Leu Tyr Lys
 1635 1640 1645
 Tyr Ile Val Ser Glu Val Gln Gln Val Tyr Arg Arg Gln Gly Val Ser
 1650 1655 1660
 Ile Ala Asp Lys His Ile Glu Ile Ile Val Ser Gln Met Leu Arg Gln
 665 1670 1675 1680
 Val Arg Ile Leu Asp Ser Gly Asp Ser Lys Phe Ile Glu Gly Asp Leu
 1685 1690 1695
 Val Ser Lys Lys Leu Phe Lys Glu Glu Asn Ala Arg Val Ile Ala Leu
 1700 1705 1710
 Lys Gly Glu Pro Ala Ile Ala Glu Pro Val Leu Leu Gly Ile Thr Arg
 1715 1720 1725
 Ala Ala Ile Gly Ser Asp Ser Ile Ile Ser Ala Ala Ser Phe Gln Glu
 1730 1735 1740
 Thr Thr Lys Val Leu Thr Glu Ala Ser Ile Ala Met Lys Lys Asp Phe
 745 1750 1755 1760
 Leu Glu Asp Leu Lys Glu Asn Val Val Leu Gly Arg Met Ile Pro Val
 1765 1770 1775
 Gly Thr Gly Met Tyr Lys Asn Lys Lys Ile Val Leu Arg Ala Leu Glu
 1780 1785 1790
 Asp Asn Ser Lys Phe
 1795

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 65...640
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

TAAGCGATTT	GCTCTGTGTG	GTGATTGACC	CTAGGATTGA	TTTTGAAAAG	CGTTGAGGGT	60
AGGA	ATG	AAA	ACT	GAG	ATG	109
Met	Lys	Thr	Glu	Met	Lys	
1		5			10	15
TTG	TTG	GTG	GTT	TTA	GCG	157
Leu	Leu	Val	Val	Leu	Ala	
				20		30
GCG	CTT	GGT	TTT	TAT	GTA	205
Ala	Leu	Gly	Phe	Tyr	Val	
		35			40	45
GTA	GAA	AAA	ACC	GAG	ACA	253
Val	Glu	Lys	Thr	Glu	Thr	
		50			55	60
CAA	GAA	GAA	GCC	AAC	GCA	301
Gln	Glu	Glu	Ala	Asn	Ala	
		65			70	75
AAA	GAC	ACA	GCG	CCG	CCT	349
Lys	Asp	Thr	Ala	Pro	Pro	
80				85		90
AAA	CAA	GAG	CAA	GAA	AAA	397
Lys	Gln	Glu	Gln	Glu	Lys	
		100			105	110
CCC	GTT	CAA	AAC	AAT	CAA	445
Pro	Val	Gln	Asn	Asn	Gln	
		115			120	125
AAA	CCT	TTA	GAG	TAT	AAA	493
Lys	Pro	Leu	Glu	Tyr	Lys	
		130			135	140
TTT	CCC	AGC	ACA	AAA	GGT	541
Phe	Pro	Ser	Thr	Lys	Gly	
		145			150	155
AGC	GTG	AAA	GTT	TTA	GAA	589
Ser	Val	Lys	Val	Leu	Glu	
160				165		170
TCT	CAC	GAA	ACA	AAG	GGC	637
Ser	His	Glu	Thr	Lys	Gly	
		180			185	190
GAA	TGAAAGAATA	ATGAAATTAA	AATCTTTTGG	GGTTTTTGGGA	AATCCCATTA	690
Glu						

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

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Met Lys Thr Glu Met Lys Ser Ser Leu Lys Leu Phe Met Arg Pro Leu
 1           5           10           15
Leu Val Val Leu Ala Phe Met Leu Leu Tyr Ala Leu Val His Ala Ala
 20           25           30
Leu Gly Phe Tyr Val Lys Lys Asp Ser Ala Pro Ile Ser Pro Asn Val
 35           40           45
Glu Lys Thr Glu Thr Glu Arg Gln Asn Gly Val Leu Ser Pro Lys Gln
 50           55           60
Glu Glu Ala Asn Ala Thr Thr Thr Ala Thr Glu Glu Ser Pro Thr Lys
 65           70           75           80
Asp Thr Ala Pro Pro Leu Asp Thr Ala Ala Gln Lys Gln Glu Thr Lys
 85           90           95
Gln Glu Gln Glu Lys Glu Asn Glu Pro Lys Gln Asp Ser Val Pro Pro
100           105           110
Val Gln Asn Asn Gln Lys Thr Pro Thr Thr Pro Leu Met Gly Lys Lys
115           120           125
Pro Leu Glu Tyr Lys Val Ala Val Ser Gly Val Asn Val Arg Ala Phe
130           135           140
Pro Ser Thr Lys Gly Lys Ile Leu Gly Leu Leu Leu Lys Asn Lys Ser
145           150           155           160
Val Lys Val Leu Glu Ile Gln Asn Asp Trp Ala Glu Ile Glu Phe Ser
165           170           175
His Glu Thr Lys Gly Tyr Val Phe Leu Lys Leu Leu Lys Lys Ala Glu
180           185           190

```

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 66...1502
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

```

TTATGACTTT TACTAAACCT TTTTTTAAGC TATAATCCAA AAATCTAAAA TAAAAAGGAA      60
TAAGC ATG AAA AAA TCC CTT TGT CTG TCT TTC TTT CTG ACT TTC TCT AAC      110
Met Lys Lys Ser Leu Cys Leu Ser Phe Phe Leu Thr Phe Ser Asn

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1				5				10				15				
CCT	CTT	CAA	GCC	CTT	GTG	ATC	GAG	CTT	TTA	GAA	GAA	ATC	AAA	ACT	TCG	158
Pro	Leu	Gln	Ala	Leu	Val	Ile	Glu	Leu	Leu	Glu	Glu	Ile	Lys	Thr	Ser	
				20					25					30		
CCG	CAT	AAA	GGC	ACT	TTT	AAG	GCT	AAA	GTC	CTT	GAT	TCT	AAA	AAA	CCA	206
Pro	His	Lys	Gly	Thr	Phe	Lys	Ala	Lys	Val	Leu	Asp	Ser	Lys	Lys	Pro	
			35					40					45			
AGA	CAA	GTT	TTA	GGC	GTT	TAT	AAT	ATC	TCC	CCA	CAC	AAA	AAA	CTC	ACG	254
Arg	Gln	Val	Leu	Gly	Val	Tyr	Asn	Ile	Ser	Pro	His	Lys	Lys	Leu	Thr	
		50					55					60				
CTC	ACT	ATC	ACC	CAC	ATA	TCC	ACT	GCA	ATC	GTC	TAT	CAA	CCC	CTT	GAT	302
Leu	Thr	Ile	Thr	His	Ile	Ser	Thr	Ala	Ile	Val	Tyr	Gln	Pro	Leu	Asp	
	65					70					75					
GAA	AAA	CTT	TCT	TTA	GAA	ACA	ACC	TTA	AAC	CCT	AAC	CGC	CCT	ACT	ATC	350
Glu	Lys	Leu	Ser	Leu	Glu	Thr	Thr	Leu	Asn	Pro	Asn	Arg	Pro	Thr	Ile	
	80				85				90					95		
CCT	AGA	AAC	ACC	CAG	ATT	GTT	TTT	TCT	TCA	AAA	GAA	TTG	AAA	GAG	TCG	398
Pro	Arg	Asn	Thr	Gln	Ile	Val	Phe	Ser	Ser	Lys	Glu	Leu	Lys	Glu	Ser	
				100					105					110		
CAC	CCG	CAC	CAA	ATG	CCT	TCT	TTA	AAC	GCG	CCC	ATG	CAA	AAA	CCA	CAA	446
His	Pro	His	Gln	Met	Pro	Ser	Leu	Asn	Ala	Pro	Met	Gln	Lys	Pro	Gln	
			115					120					125			
AAC	AAA	CCC	CAT	TCA	TCG	CAA	CAA	CCT	TCT	CAA	AAC	TTT	TCT	TAC	CCA	494
Asn	Lys	Pro	His	Ser	Ser	Gln	Gln	Pro	Ser	Gln	Asn	Phe	Ser	Tyr	Pro	
		130					135					140				
GAG	CCC	AAA	CTA	GGC	TCT	AAA	AAC	TCT	AAA	AAC	AGC	CTT	TTA	CAG	CCT	542
Glu	Pro	Lys	Leu	Gly	Ser	Lys	Asn	Ser	Lys	Asn	Ser	Leu	Leu	Gln	Pro	
	145					150					155					
TTA	GCA	ATT	CCT	AGC	AAA	ATA	AGT	CCC	ACT	AAC	GAA	ACT	CAA	ACG	CCA	590
Leu	Ala	Ile	Pro	Ser	Lys	Ile	Ser	Pro	Thr	Asn	Glu	Thr	Gln	Thr	Pro	
	160				165				170						175	
ACA	AAC	GAC	ACT	AAA	CCC	CCT	TTA	AAG	CAT	TCT	TCA	GAA	GAT	CAA	GAA	638
Thr	Asn	Asp	Thr	Lys	Pro	Pro	Leu	Lys	His	Ser	Ser	Glu	Asp	Gln	Glu	
				180					185					190		
AGC	AAC	CTC	TTT	ATA	ACG	CCA	CCC	ACT	GAA	AAA	ACG	CTC	CCT	AAC	AAC	686
Ser	Asn	Leu	Phe	Ile	Thr	Pro	Pro	Thr	Glu	Lys	Thr	Leu	Pro	Asn	Asn	
			195					200					205			
ACC	TCT	AAC	GCT	GAT	ATT	AGT	GAA	AAC	AAT	GAA	AGC	AAT	GAG	AAT	AAA	734
Thr	Ser	Asn	Ala	Asp	Ile	Ser	Glu	Asn	Asn	Glu	Ser	Asn	Glu	Asn	Lys	
		210					215					220				
GAT	AAT	GTG	GAA	AAA	CAA	GCC	ATT	AGA	GAT	GCT	AAT	ATT	AAA	GAA	TTT	782
Asp	Asn	Val	Glu	Lys	Gln	Ala	Ile	Arg	Asp	Ala	Asn	Ile	Lys	Glu	Phe	
	225					230					235					

GCA TGC GGG AAG TGG GTC TAT GAC GAT GAA AAT TTA CAA GCC TAC CGC	830
Ala Cys Gly Lys Trp Val Tyr Asp Asp Glu Asn Leu Gln Ala Tyr Arg	
240 245 250 255	
CCA AGC ATT TTA AAA CGC GTT GAT GAA GAC AAA CAA ACT GCA ACA GAT	878
Pro Ser Ile Leu Lys Arg Val Asp Glu Asp Lys Gln Thr Ala Thr Asp	
260 265 270	
ATT ACC CCT TGC GAT TAC AGC ACC GCT GAA AAT AAA AGC GGT AAA ATC	926
Ile Thr Pro Cys Asp Tyr Ser Thr Ala Glu Asn Lys Ser Gly Lys Ile	
275 280 285	
ATT ACC CCC TAT ACT AAA ATC TCC GTT CAT AAA ACA GAG CCT TTA GAA	974
Ile Thr Pro Tyr Thr Lys Ile Ser Val His Lys Thr Glu Pro Leu Glu	
290 295 300	
GAG CCA CAA ACT TTT GAA GCT AAA AAT AAT TTC GCC ATT CTT CAA GCC	1022
Glu Pro Gln Thr Phe Glu Ala Lys Asn Asn Phe Ala Ile Leu Gln Ala	
305 310 315	
AGA AGC TCT ACA GAA AAA TGC AAA AGG GCT AGA GCA AGA AAA GAC GGC	1070
Arg Ser Ser Thr Glu Lys Cys Lys Arg Ala Arg Ala Arg Lys Asp Gly	
320 325 330 335	
ACG ACT AGG CAA TGC TAT CTA ATA GAA GAG CCT TTA AAA CAA GCA TGG	1118
Thr Thr Arg Gln Cys Tyr Leu Ile Glu Glu Pro Leu Lys Gln Ala Trp	
340 345 350	
GAG AGT GAG TAT GAA ATC ACC ACG CAA TTA GTG AAA GCC ATT TAT GAG	1166
Glu Ser Glu Tyr Glu Ile Thr Thr Gln Leu Val Lys Ala Ile Tyr Glu	
355 360 365	
CGC CCC AAA CAA GAC GAT CAA GTA GAG CCG ACT TTT TAT GAA ACC AGC	1214
Arg Pro Lys Gln Asp Asp Gln Val Glu Pro Thr Phe Tyr Glu Thr Ser	
370 375 380	
GAA TTG GCT TAT TCT TCC ACA CGA AAA AGC GAA ATA ACG CAC AAT GAA	1262
Glu Leu Ala Tyr Ser Ser Thr Arg Lys Ser Glu Ile Thr His Asn Glu	
385 390 395	
TTG AAT TTG AAT GAA AAA TTC ATG GAA TTT GTG GAA GTG TAT GAG GGG	1310
Leu Asn Leu Asn Glu Lys Phe Met Glu Phe Val Glu Val Tyr Glu Gly	
400 405 410 415	
CAT TAT TTA AAC GAT ATA ATT AAA GAG AGC AGT GAA TAT AAA GAA TGG	1358
His Tyr Leu Asn Asp Ile Ile Lys Glu Ser Ser Glu Tyr Lys Glu Trp	
420 425 430	
GTT AAA AAC CAT GTG CGC TTT AAA GAA GGG GTG TGC ATG GCT TTA GAA	1406
Val Lys Asn His Val Arg Phe Lys Glu Gly Val Cys Met Ala Leu Glu	
435 440 445	
ATA GAA GAA CAG CCA CGA GCT AAA AGC ACG CCT TTG AGT ATT GAA AAC	1454
Ile Glu Glu Gln Pro Arg Ala Lys Ser Thr Pro Leu Ser Ile Glu Asn	
450 455 460	
TCT CGT GTG GTA TGT GTC AAA AAG GGG AAT TAT TTA TTC AAC GAA GTT T	1503
Ser Arg Val Val Cys Val Lys Lys Gly Asn Tyr Leu Phe Asn Glu Val	

				325						330					335				
Thr	Arg	Gln	Cys	Tyr	Leu	Ile	Glu	Glu	Pro	Leu	Lys	Gln	Ala	Trp	Glu				
			340					345					350						
Ser	Glu	Tyr	Glu	Ile	Thr	Thr	Gln	Leu	Val	Lys	Ala	Ile	Tyr	Glu	Arg				
		355					360					365							
Pro	Lys	Gln	Asp	Asp	Gln	Val	Glu	Pro	Thr	Phe	Tyr	Glu	Thr	Ser	Glu				
	370					375					380								
Leu	Ala	Tyr	Ser	Ser	Thr	Arg	Lys	Ser	Glu	Ile	Thr	His	Asn	Glu	Leu				
385					390					395					400				
Asn	Leu	Asn	Glu	Lys	Phe	Met	Glu	Phe	Val	Glu	Val	Tyr	Glu	Gly	His				
			405					410					415						
Tyr	Leu	Asn	Asp	Ile	Ile	Lys	Glu	Ser	Ser	Glu	Tyr	Lys	Glu	Trp	Val				
		420					425						430						
Lys	Asn	His	Val	Arg	Phe	Lys	Glu	Gly	Val	Cys	Met	Ala	Leu	Glu	Ile				
		435					440					445							
Glu	Glu	Gln	Pro	Arg	Ala	Lys	Ser	Thr	Pro	Leu	Ser	Ile	Glu	Asn	Ser				
	450					455				460									
Arg	Val	Val	Cys	Val	Lys	Lys	Gly	Asn	Tyr	Leu	Phe	Asn	Glu	Val					
465					470					475									

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 68...568
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

TGTA	AAATAG	GGATTTGCTA	GGCCTTTAGT	CGTTAAAGG	TAATTATCAT	TAAGGAGTTT	60
TTTA	ATC	ATG GCA GAT ATT CAA AGG CGT GAT TTT TTA GGA ATG AGC CTT	109				
	Met	Ala	Asp	Ile	Gln	Arg	Arg
	1			5			10
GCT	AGT	GTT	ACA	GCT	ATA	GGG	GCT
Ala	Ser	Val	Thr	Ala	Ile	Gly	Ala
15				20			25
							30
AAG	ACT	TGG	GAT	CCG	CTT	CCA	AGC
Lys	Thr	Trp	Asp	Pro	Leu	Pro	Ser
			35				40
							45
ATA	GAT	GTG	GCG	AAT	ATG	CAA	GAA
Ile	Asp	Val	Ala	Asn	Met	Gln	Glu
		50				55	
							60
CGT	GGG	AAA	CCG	GTC	TAT	ATC	CTC
Arg	Gly	Lys	Pro	Val	Tyr	Ile	Leu
							Lys
							Arg
							Ser
							Lys
							Lys
							Glu
							Gly
							Phe

65										70					75					
AAT	GAA	AAG	CGC	GAT	TTT	AAA	GTT	GGC	GAG	AGC	GTT	TTT	ACC	ACA	GCC	349				
Asn	Glu	Lys	Arg	Asp	Phe	Lys	Val	Gly	Glu	Ser	Val	Phe	Thr	Thr	Ala					
80						85					90									
ATT	CAA	ATT	TGC	ACG	CAT	TTA	GGG	TGT	ATC	CCC	ACT	TAT	CAA	GAT	GAA	397				
Ile	Gln	Ile	Cys	Thr	His	Leu	Gly	Cys	Ile	Pro	Thr	Tyr	Gln	Asp	Glu					
95					100					105					110					
GAA	AAA	GGC	TTT	TTA	TGC	CCA	TGC	CAT	GGG	GGG	CGT	TTC	ACT	TCT	GAT	445				
Glu	Lys	Gly	Phe	Leu	Cys	Pro	Cys	His	Gly	Gly	Arg	Phe	Thr	Ser	Asp					
			115						120					125						
GGC	GTG	AAT	ATT	GCC	GGC	ACT	CCC	CCT	CCA	CGC	CCT	TTT	GAT	ATC	CCG	493				
Gly	Val	Asn	Ile	Ala	Gly	Thr	Pro	Pro	Pro	Arg	Pro	Phe	Asp	Ile	Pro					
			130					135					140							
CCT	TTT	AAA	ATT	GAA	GGC	ACT	AAG	ATC	ACT	TTT	GGT	GAA	GCC	GGG	GCT	541				
Pro	Phe	Lys	Ile	Glu	Gly	Thr	Lys	Ile	Thr	Phe	Gly	Glu	Ala	Gly	Ala					
		145					150					155								
GAA	TAC	AAG	AAA	ATG	ATG	GCT	AAA	GCG	TAAGGAGAGT	TTAATGGCAG	AGATAAAA	595								
Glu	Tyr	Lys	Lys	Met	Met	Ala	Lys	Ala												
160						165														
AAAAGCGAAA	AATTTAGGCG	AATGG														620				

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

Met	Ala	Asp	Ile	Gln	Arg	Arg	Asp	Phe	Leu	Gly	Met	Ser	Leu	Ala	Ser
1				5					10					15	
Val	Thr	Ala	Ile	Gly	Ala	Ile	Ala	Ser	Leu	Val	Ala	Met	Lys	Lys	Thr
		20						25					30		
Trp	Asp	Pro	Leu	Pro	Ser	Val	Val	Ser	Ala	Gly	Phe	Thr	Thr	Ile	Asp
		35					40					45			
Val	Ala	Asn	Met	Gln	Glu	Gly	Gln	Phe	Ser	Thr	Val	Glu	Trp	Arg	Gly
		50				55					60				
Lys	Pro	Val	Tyr	Ile	Leu	Lys	Arg	Ser	Lys	Lys	Glu	Gly	Phe	Asn	Glu
65					70					75					80
Lys	Arg	Asp	Phe	Lys	Val	Gly	Glu	Ser	Val	Phe	Thr	Thr	Ala	Ile	Gln
			85						90					95	
Ile	Cys	Thr	His	Leu	Gly	Cys	Ile	Pro	Thr	Tyr	Gln	Asp	Glu	Glu	Lys
			100					105					110		
Gly	Phe	Leu	Cys	Pro	Cys	His	Gly	Gly	Arg	Phe	Thr	Ser	Asp	Gly	Val
		115					120					125			
Asn	Ile	Ala	Gly	Thr	Pro	Pro	Pro	Arg	Pro	Phe	Asp	Ile	Pro	Pro	Phe

130		135		140											
Lys	Ile	Glu	Gly	Thr	Lys	Ile	Thr	Phe	Gly	Glu	Ala	Gly	Ala	Glu	Tyr
145					150					155					160
Lys	Lys	Met	Met	Ala	Lys	Ala									
				165											

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1221 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 52...1167
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

TTATAATCAA AGCTATTTTA AAAGCTGAAT AGCTATAGTT ATTAGGATGC G ATG TCA	57
Met Ser	
1	
AAA AGA ATG AAG TGT TTT AGT CAA AAA TGG TTG GTT TTT TTT GTT ACC	105
Lys Arg Met Lys Cys Phe Ser Gln Lys Trp Leu Val Phe Phe Val Thr	
5 10 15	
CTT TTA TTG GCT TCT TTA GGC CAT GCG AAA ATG GCT TTT GAA TCC GAT	153
Leu Leu Leu Ala Ser Leu Gly His Ala Lys Met Ala Phe Glu Ser Asp	
20 25 30	
ATT GAC ACC AAA GCG CTA GAG GCT TTT GGG GTT AAT GCG GGC TTT TTA	201
Ile Asp Thr Lys Ala Leu Glu Ala Phe Gly Val Asn Ala Gly Phe Leu	
35 40 45 50	
TCC CAA ATG CCC AAC GCT TTA AAA AAA ATG AAT AAA GAA GAA GAA TGG	249
Ser Gln Met Pro Asn Ala Leu Lys Lys Met Asn Lys Glu Glu Glu Trp	
55 60 65	
AAG AGA CTT GTC AAA AGA TTT GAT GTG AAT TAC CAG TTC ATC CCC ATC	297
Lys Arg Leu Val Lys Arg Phe Asp Val Asn Tyr Gln Phe Ile Pro Ile	
70 75 80	
ATT AAA AAC ATG CTC ATA GAA GCG AGC GTG CCG CAA GAA TTT TTA TTT	345
Ile Lys Asn Met Leu Ile Glu Ala Ser Val Pro Gln Glu Phe Leu Phe	
85 90 95	
TTA GCC ATG GCC GAG TCT AAA TTT TCA TCA AGG GCT TAT AGC AGG AAA	393
Leu Ala Met Ala Glu Ser Lys Phe Ser Ser Arg Ala Tyr Ser Arg Lys	
100 105 110	
AAA GCG GTA GGG ATT TGG CAA TTC ATG CCA AGC ACG GCT AAA GAA TTA	441

Lys	Ala	Val	Gly	Ile	Trp	Gln	Phe	Met	Pro	Ser	Thr	Ala	Lys	Glu	Leu	
115					120					125					130	
GGG	CTT	AAG	GTC	AAT	CAT	TAC	ATT	GAT	GAA	AGA	AGA	GAT	CCC	ATT	AAA	489
Gly	Leu	Lys	Val	Asn	His	Tyr	Ile	Asp	Glu	Arg	Arg	Asp	Pro	Ile	Lys	
				135					140					145		
AGC	ACT	CAA	GCG	GCG	ATC	ACT	TAT	TTG	AAA	CGG	CTC	TAC	AAG	CAA	ACC	537
Ser	Thr	Gln	Ala	Ala	Ile	Thr	Tyr	Leu	Lys	Arg	Leu	Tyr	Lys	Gln	Thr	
			150					155					160			
GGA	GAG	TGG	TAT	TTG	GTC	GCT	ATG	GCG	TAT	AAT	TAC	GGC	TTA	CGC	AAG	585
Gly	Glu	Trp	Tyr	Leu	Val	Ala	Met	Ala	Tyr	Asn	Tyr	Gly	Leu	Arg	Lys	
		165					170					175				
GTT	CAA	AAC	GCT	ATT	AAA	GCC	GCC	GGC	ACT	TCG	GAC	ATT	AAA	ATT	TTG	633
Val	Gln	Asn	Ala	Ile	Lys	Ala	Ala	Gly	Thr	Ser	Asp	Ile	Lys	Ile	Leu	
	180					185					190					
TTG	GAT	GAA	GAT	AAG	AAA	TAC	CTC	CCT	AAA	GAA	ACA	CGA	GAG	TAT	ATC	681
Leu	Asp	Glu	Asp	Lys	Lys	Tyr	Leu	Pro	Lys	Glu	Thr	Arg	Glu	Tyr	Ile	
195					200					205					210	
CGC	TCC	ATT	CTA	AGC	CTA	GCG	TTA	AAA	TTC	AAC	AGC	CTA	GAC	AAC	CTC	729
Arg	Ser	Ile	Leu	Ser	Leu	Ala	Leu	Lys	Phe	Asn	Ser	Leu	Asp	Asn	Leu	
				215					220					225		
AAA	GAT	AAA	GAA	TAT	CTG	CTC	AAT	CGT	GGG	GCG	AGG	GTG	AGT	TTA	GTG	777
Lys	Asp	Lys	Glu	Tyr	Leu	Leu	Asn	Arg	Gly	Ala	Arg	Val	Ser	Leu	Val	
			230					235					240			
GGC	GTC	CCG	TTT	AAA	AGG	CGT	GCT	TCT	TTA	GTC	CAA	GTA	GCC	AAA	AAT	825
Gly	Val	Pro	Phe	Lys	Arg	Arg	Ala	Ser	Leu	Val	Gln	Val	Ala	Lys	Asn	
		245					250					255				
TTG	AAT	TTG	AGT	TTG	GAA	ACC	TTA	AAA	TCC	TAC	AAC	CAC	CAA	TTC	CGT	873
Leu	Asn	Leu	Ser	Leu	Glu	Thr	Leu	Lys	Ser	Tyr	Asn	His	Gln	Phe	Arg	
	260					265					270					
TAT	AAC	ATT	CTG	CCT	TCT	AAA	GAC	CCC	ACT	TAT	ACC	ATT	TAT	ATC	CCT	921
Tyr	Asn	Ile	Leu	Pro	Ser	Lys	Asp	Pro	Thr	Tyr	Thr	Ile	Tyr	Ile	Pro	
275					280					285					290	
TAT	GAA	AAA	CTC	GCT	CTT	TTC	AAA	CAA	CGC	CAG	ATC	AAA	CAA	AAT	AAA	969
Tyr	Glu	Lys	Leu	Ala	Leu	Phe	Lys	Gln	Arg	Gln	Ile	Lys	Gln	Asn	Lys	
				295					300					305		
AAC	ATT	CAA	GCC	AGT	TCA	AAA	AGC	CCT	TTT	ATC	ACC	CAT	GTG	GTC	TTA	1017
Asn	Ile	Gln	Ala	Ser	Ser	Lys	Ser	Pro	Phe	Ile	Thr	His	Val	Val	Leu	
			310					315					320			
CCT	AAA	GAA	ACC	CTA	TCT	TCT	ATC	GCT	AAA	CGC	TAT	CAA	GTC	AGT	ATT	1065
Pro	Lys	Glu	Thr	Leu	Ser	Ser	Ile	Ala	Lys	Arg	Tyr	Gln	Val	Ser	Ile	
		325					330					335				
TCC	AAT	ATC	CAA	TTA	GCC	AAT	GAT	CTC	AAA	GAT	TCT	AAT	ATT	TTT	ATC	1113
Ser	Asn	Ile	Gln	Leu	Ala	Asn	Asp	Leu	Lys	Asp	Ser	Asn	Ile	Phe	Ile	
	340					345					350					

[illegible]

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 46...510
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

AAATGAGCTA AAATGAGCGT TTCA'TTTGAC AAATAAAGGG ATTGA ATG GCT TTT AAG															57	
Met Ala Phe Lys																
1																
GTG	GTG	CAA	ATT	TGC	GGA	GGG	CTT	GGG	AAT	CAA	ATG	TTT	CAA	TAC	GCT	105
Val	Val	Gln	Ile	Cys	Gly	Gly	Leu	Gly	Asn	Gln	Met	Phe	Gln	Tyr	Ala	
5				10						15				20		
TTC	GCT	AAA	AGT	TTG	CAA	AAA	CAC	TCT	AAT	ACG	CCT	GTG	CTG	TTA	GAT	153
Phe	Ala	Lys	Ser	Leu	Gln	Lys	His	Ser	Asn	Thr	Pro	Val	Leu	Leu	Asp	
				25				30						35		
ATC	ACT	TCT	TTT	GAT	TGG	AGC	GAT	AGG	AAA	ATG	CAA	TTA	GAA	CTT	TTC	201
Ile	Thr	Ser	Phe	Asp	Trp	Ser	Asp	Arg	Lys	Met	Gln	Leu	Glu	Leu	Phe	
		40						45				50				
CCT	ATT	GAT	TTG	CCC	TAT	GCG	AGC	GCG	AAA	GAA	ATC	GCT	ATA	GCT	AAA	249
Pro	Ile	Asp	Leu	Pro	Tyr	Ala	Ser	Ala	Lys	Glu	Ile	Ala	Ile	Ala	Lys	
		55				60						65				
ATG	CAA	CAC	CTC	CCC	AAG	CTA	GTA	AGA	GAC	GCG	CTC	AAA	TGC	ATG	GGA	297
Met	Gln	His	Leu	Pro	Lys	Leu	Val	Arg	Asp	Ala	Leu	Lys	Cys	Met	Gly	
70						75				80						
TTT	GAT	AGG	GTG	AGT	CAA	GAA	ATC	GTT	TTT	GAA	TAC	GAG	CCT	AAA	TTG	345

Phe	Asp	Arg	Val	Ser	Gln	Glu	Ile	Val	Phe	Glu	Tyr	Glu	Pro	Lys	Leu	
85					90				95						100	
CTA	AAG	CCA	AGC	CGC	TTG	ACT	TAT	TTT	TTT	GGC	TAT	TTC	CAA	GAT	CCA	393
Leu	Lys	Pro	Ser	Arg	Leu	Thr	Tyr	Phe	Phe	Gly	Tyr	Phe	Gln	Asp	Pro	
				105					110					115		
CGA	TAC	TTT	GAT	GCT	ATA	TCC	CCT	TTA	ATC	AAG	CAA	ACC	TTC	ACT	CTA	441
Arg	Tyr	Phe	Asp	Ala	Ile	Ser	Pro	Leu	Ile	Lys	Gln	Thr	Phe	Thr	Leu	
			120					125					130			
CCC	CCC	CCC	CCC	CCG	AAA	ATA	ATA	AGA	ATA	ATA	ATA	AAA	AAG	AGG	AAG	489
Pro	Pro	Pro	Pro	Pro	Lys	Ile	Ile	Arg	Ile	Ile	Ile	Lys	Lys	Arg	Lys	
			135				140					145				
AAT	ATC	AGT	GCA	AGC	TTT	CTT	TGATTTTAGC	CGCTAAAAAC	AGCGTGTTTG	TGCA						544
Asn	Ile	Ser	Ala	Ser	Phe	Leu										
	150					155										
TATAAGAAGA	GGGGATT															561

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Met	Ala	Phe	Lys	Val	Val	Gln	Ile	Cys	Gly	Gly	Leu	Gly	Asn	Gln	Met	
1				5					10					15		
Phe	Gln	Tyr	Ala	Phe	Ala	Lys	Ser	Leu	Gln	Lys	His	Ser	Asn	Thr	Pro	
			20					25					30			
Val	Leu	Leu	Asp	Ile	Thr	Ser	Phe	Asp	Trp	Ser	Asp	Arg	Lys	Met	Gln	
		35					40					45				
Leu	Glu	Leu	Phe	Pro	Ile	Asp	Leu	Pro	Tyr	Ala	Ser	Ala	Lys	Glu	Ile	
	50					55					60					
Ala	Ile	Ala	Lys	Met	Gln	His	Leu	Pro	Lys	Leu	Val	Arg	Asp	Ala	Leu	
65					70					75					80	
Lys	Cys	Met	Gly	Phe	Asp	Arg	Val	Ser	Gln	Glu	Ile	Val	Phe	Glu	Tyr	
				85					90					95		
Glu	Pro	Lys	Leu	Leu	Lys	Pro	Ser	Arg	Leu	Thr	Tyr	Phe	Phe	Gly	Tyr	
			100					105					110			
Phe	Gln	Asp	Pro	Arg	Tyr	Phe	Asp	Ala	Ile	Ser	Pro	Leu	Ile	Lys	Gln	
		115					120					125				
Thr	Phe	Thr	Leu	Pro	Pro	Pro	Pro	Lys	Ile	Ile	Arg	Ile	Ile	Ile		
	130					135				140						
Lys	Lys	Arg	Lys	Asn	Ile	Ser	Ala	Ser	Phe	Leu						
145					150					155						

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 86...1201
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

GGTTATTATA GTATAATATT GTCAAAAAAT AAATTCAACT TTGGATTAAA TTGATTAAAA	60
ACCTATTTTA GGGAAACCGC TTAAA ATG AGT ATT ATT ATT CCT ATT GTC ATC	112
Met Ser Ile Ile Ile Pro Ile Val Ile	
1 5	
GCT TTT GAT AAT CAC TAT GCC ATG CCG GCT GGC GTG AGC TTG TAT TCC	160
Ala Phe Asp Asn His Tyr Ala Met Pro Ala Gly Val Ser Leu Tyr Ser	
10 15 20 25	
ATG CTA GCT TGC GCT AAA ACA GAA CAC CCC CAA TCA CAA AAT GAT AGT	208
Met Leu Ala Cys Ala Lys Thr Glu His Pro Gln Ser Gln Asn Asp Ser	
30 35 40	
GAA AAA CTT TTT TAT AAG ATC CAC TGC CTG GTG GAT AAC TTA AGC CTT	256
Glu Lys Leu Phe Tyr Lys Ile His Cys Leu Val Asp Asn Leu Ser Leu	
45 50 55	
GAA AAC CAG AGC AAA CTA AAA GAG ACT CTA GCC CCC TTT AGC GCT TTT	304
Glu Asn Gln Ser Lys Leu Lys Glu Thr Leu Ala Pro Phe Ser Ala Phe	
60 65 70	
TCG AGC CTA GAA TTT TTA GAC ATT TCA ACC CCC AAT CTT CAC GCC ACT	352
Ser Ser Leu Glu Phe Leu Asp Ile Ser Thr Pro Asn Leu His Ala Thr	
75 80 85	
CCA ATA GAA CCC TCT GCG ATT GAT AAA ATC AAT GAA GCT TTT TTG CAA	400
Pro Ile Glu Pro Ser Ala Ile Asp Lys Ile Asn Glu Ala Phe Leu Gln	
90 95 100 105	
CTC AAT ATT TAC GCT AAG ACT CGC TTT TCT AAA ATG GTC ATG TGC CGC	448
Leu Asn Ile Tyr Ala Lys Thr Arg Phe Ser Lys Met Val Met Cys Arg	
110 115 120	
TTG TTT TTG GCT TCT TTA TTC CCA CAA TAC GAC AAA ATC ATC ATG TTT	496
Leu Phe Leu Ala Ser Leu Phe Pro Gln Tyr Asp Lys Ile Ile Met Phe	
125 130 135	
GAT GCA GAC ACT TTG TTT TTA AAC GAT GTG AGC GAG AGC TTT TTC ATC	544
Asp Ala Asp Thr Leu Phe Leu Asn Asp Val Ser Glu Ser Phe Phe Ile	
140 145 150	
CCA CTA GAT GGC TAT TAT TTT GGA GCG GCT AAA GAT TTT GCT TCC GAT	592

Pro	Leu	Asp	Gly	Tyr	Tyr	Phe	Gly	Ala	Ala	Lys	Asp	Phe	Ala	Ser	Asp	
155						160					165					
AAA	AGC	CCT	AAA	CAT	TTT	CAA	ATA	GTG	CGA	GAA	AAA	GAC	CCT	CGT	CAA	640
Lys	Ser	Pro	Lys	His	Phe	Gln	Ile	Val	Arg	Glu	Lys	Asp	Pro	Arg	Gln	
170					175					180					185	
GCC	TTT	TCC	CTT	TAT	GAG	CAT	TAC	CTT	AAT	GAA	AGC	GAT	ATG	CAA	ATC	688
Ala	Phe	Ser	Leu	Tyr	Glu	His	Tyr	Leu	Asn	Glu	Ser	Asp	Met	Gln	Ile	
				190					195					200		
ATC	TAT	GAA	AGC	AAT	TAT	AAC	GCC	GGG	TTT	TTA	GTC	GTG	AAT	TTA	AAG	736
Ile	Tyr	Glu	Ser	Asn	Tyr	Asn	Ala	Gly	Phe	Leu	Val	Val	Asn	Leu	Lys	
			205					210					215			
CTG	TGG	CGT	GCT	GAT	CAT	TTA	GAA	GAG	CGC	TTA	CTC	AAT	TTA	ACC	CAT	784
Leu	Trp	Arg	Ala	Asp	His	Leu	Glu	Glu	Arg	Leu	Leu	Asn	Leu	Thr	His	
		220					225					230				
CAA	AAA	GGC	CAG	TGC	GTG	TTT	TAC	CCT	GAA	CAG	GAC	CTT	TTA	ACG	CTC	832
Gln	Lys	Gly	Gln	Cys	Val	Phe	Tyr	Pro	Glu	Gln	Asp	Leu	Leu	Thr	Leu	
	235					240					245					
GCA	TGC	TAT	CAA	AAA	GTT	TTA	ATC	TTG	CCT	TAT	ATT	TAT	AAC	ACC	CAC	880
Ala	Cys	Tyr	Gln	Lys	Val	Leu	Ile	Leu	Pro	Tyr	Ile	Tyr	Asn	Thr	His	
250					255					260					265	
CCT	TTC	ATG	GCC	AAT	CAA	AAA	CGC	TTC	ATC	CCT	GAC	AAA	AAA	GAA	ATC	928
Pro	Phe	Met	Ala	Asn	Gln	Lys	Arg	Phe	Ile	Pro	Asp	Lys	Lys	Glu	Ile	
				270					275					280		
GTC	ATG	CTG	CAT	TTT	TAT	TTT	GTA	GGA	AAA	CCT	TGG	GTT	TTA	CCT	ACT	976
Val	Met	Leu	His	Phe	Tyr	Phe	Val	Gly	Lys	Pro	Trp	Val	Leu	Pro	Thr	
			285					290					295			
TTT	TCA	TAT	TCT	AAA	GAA	TGG	CAT	GAG	ACT	CTT	TTA	AAA	ACC	CCT	TTT	1024
Phe	Ser	Tyr	Ser	Lys	Glu	Trp	His	Glu	Thr	Leu	Leu	Lys	Thr	Pro	Phe	
		300					305					310				
TAT	GCT	GAA	TAT	TCC	GTG	AAA	TTC	CTT	AAA	CAA	ATG	ACA	GAA	TGT	TTA	1072
Tyr	Ala	Glu	Tyr	Ser	Val	Lys	Phe	Leu	Lys	Gln	Met	Thr	Glu	Cys	Leu	
	315					320					325					
AGC	CTT	AAA	GAC	AAA	CAA	AAA	ACC	TTT	GAA	TTT	CTT	GCC	CCC	CTA	CTC	1120
Ser	Leu	Lys	Asp	Lys	Gln	Lys	Thr	Phe	Glu	Phe	Leu	Ala	Pro	Leu	Leu	
330					335					340					345	
AAT	AAA	AAA	ACC	CTT	TTA	GAA	TAC	GTC	TTT	TTT	AGA	TTG	AAT	AGG	ATT	1168
Asn	Lys	Lys	Thr	Leu	Leu	Glu	Tyr	Val	Phe	Phe	Arg	Leu	Asn	Arg	Ile	
			350						355					360		
TTC	AAA	CGC	TTA	AAA	GAA	AAA	TTT	TTT	AAC	TCT	TAGCGTTCTC	GTTTGGGCAA				1221
Phe	Lys	Arg	Leu	Lys	Glu	Lys	Phe		Asn	Ser						
			365					370								
CACGCTATAG	GCGAATTTGA	CATAAATCGC														1251

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

Met	Ser	Ile	Ile	Ile	Pro	Ile	Val	Ile	Ala	Phe	Asp	Asn	His	Tyr	Ala	1	5	10	15
Met	Pro	Ala	Gly	Val	Ser	Leu	Tyr	Ser	Met	Leu	Ala	Cys	Ala	Lys	Thr	20	25	30	
Glu	His	Pro	Gln	Ser	Gln	Asn	Asp	Ser	Glu	Lys	Leu	Phe	Tyr	Lys	Ile	35	40	45	
His	Cys	Leu	Val	Asp	Asn	Leu	Ser	Leu	Glu	Asn	Gln	Ser	Lys	Leu	Lys	50	55	60	
Glu	Thr	Leu	Ala	Pro	Phe	Ser	Ala	Phe	Ser	Ser	Leu	Glu	Phe	Leu	Asp	65	70	75	80
Ile	Ser	Thr	Pro	Asn	Leu	His	Ala	Thr	Pro	Ile	Glu	Pro	Ser	Ala	Ile	85	90	95	
Asp	Lys	Ile	Asn	Glu	Ala	Phe	Leu	Gln	Leu	Asn	Ile	Tyr	Ala	Lys	Thr	100	105	110	
Arg	Phe	Ser	Lys	Met	Val	Met	Cys	Arg	Leu	Phe	Leu	Ala	Ser	Leu	Phe	115	120	125	
Pro	Gln	Tyr	Asp	Lys	Ile	Ile	Met	Phe	Asp	Ala	Asp	Thr	Leu	Phe	Leu	130	135	140	
Asn	Asp	Val	Ser	Glu	Ser	Phe	Phe	Ile	Pro	Leu	Asp	Gly	Tyr	Tyr	Phe	145	150	155	160
Gly	Ala	Ala	Lys	Asp	Phe	Ala	Ser	Asp	Lys	Ser	Pro	Lys	His	Phe	Gln	165	170	175	
Ile	Val	Arg	Glu	Lys	Asp	Pro	Arg	Gln	Ala	Phe	Ser	Leu	Tyr	Glu	His	180	185	190	
Tyr	Leu	Asn	Glu	Ser	Asp	Met	Gln	Ile	Ile	Tyr	Glu	Ser	Asn	Tyr	Asn	195	200	205	
Ala	Gly	Phe	Leu	Val	Val	Asn	Leu	Lys	Leu	Trp	Arg	Ala	Asp	His	Leu	210	215	220	
Glu	Glu	Arg	Leu	Leu	Asn	Leu	Thr	His	Gln	Lys	Gly	Gln	Cys	Val	Phe	225	230	235	240
Tyr	Pro	Glu	Gln	Asp	Leu	Leu	Thr	Leu	Ala	Cys	Tyr	Gln	Lys	Val	Leu	245	250	255	
Ile	Leu	Pro	Tyr	Ile	Tyr	Asn	Thr	His	Pro	Phe	Met	Ala	Asn	Gln	Lys	260	265	270	
Arg	Phe	Ile	Pro	Asp	Lys	Lys	Glu	Ile	Val	Met	Leu	His	Phe	Tyr	Phe	275	280	285	
Val	Gly	Lys	Pro	Trp	Val	Leu	Pro	Thr	Phe	Ser	Tyr	Ser	Lys	Glu	Trp	290	295	300	
His	Glu	Thr	Leu	Leu	Lys	Thr	Pro	Phe	Tyr	Ala	Glu	Tyr	Ser	Val	Lys	305	310	315	320
Phe	Leu	Lys	Gln	Met	Thr	Glu	Cys	Leu	Ser	Leu	Lys	Asp	Lys	Gln	Lys	325	330	335	
Thr	Phe	Glu	Phe	Leu	Ala	Pro	Leu	Leu	Asn	Lys	Lys	Thr	Leu	Leu	Glu	340	345	350	
Tyr	Val	Phe	Phe	Arg	Leu	Asn	Arg	Ile	Phe	Lys	Arg	Leu	Lys	Glu	Lys	355	360	365	
Phe	Phe	Asn	Ser																

370

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...2193
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

CAAGAAGCCA TAGAAGCTGA TGGGAAATTC CACAAAGAAT AAGGGTAGAA A ATG AAA	57
Met Lys	
1	
ATA ACA TAT TGT GAT GCG CTA ATT ATT GGA GGC GGA CTA GCT GGG TTA	105
Ile Thr Tyr Cys Asp Ala Leu Ile Ile Gly Gly Gly Leu Ala Gly Leu	
5 10 15	
AGG GCT AGT ATC GCA TGC AAA CAA AAG GGT TTA AAC ACC ATC GTT TTA	153
Arg Ala Ser Ile Ala Cys Lys Gln Lys Gly Leu Asn Thr Ile Val Leu	
20 25 30	
AGC CTA GTG CCT GTC AGG CGT TCG CAC TCT GCA GCC GCT CAA GGG GGC	201
Ser Leu Val Pro Val Arg Ser His Ser Ala Ala Ala Gln Gly Gly	
35 40 45 50	
ATG CAA GCG AGC CTT GCG AAC GCT AAA AAA AGC GAG GGC GAT AAT GAA	249
Met Gln Ala Ser Leu Ala Asn Ala Lys Lys Ser Glu Gly Asp Asn Glu	
55 60 65	
GAT TTA CAC TTT TTA GAC ACG GTT AAG GGG AGC GAT TGG GGG TGC GAT	297
Asp Leu His Phe Leu Asp Thr Val Lys Gly Ser Asp Trp Gly Cys Asp	
70 75 80	
CAG CAA GTG GCT AGG ATG TTT GTA ACC ACT GCT CCT AAA GCC ATT AGG	345
Gln Gln Val Ala Arg Met Phe Val Thr Thr Ala Pro Lys Ala Ile Arg	
85 90 95	
GAA TTG GCC AGT TGG GGG GTG CCT TGG ACT AGG ATT AAA AAG GGC GAT	393
Glu Leu Ala Ser Trp Gly Val Pro Trp Thr Arg Ile Lys Lys Gly Asp	
100 105 110	
AGG CCT GCG GTC GTC AAT GGT GAG CAT GTA ACT ATC ACT GAA AGA GAC	441
Arg Pro Ala Val Val Asn Gly Glu His Val Thr Ile Thr Glu Arg Asp	
115 120 125 130	
GAC AGG CAT GGT TAT ATC TTA AGC CGT GAT TTT GGC GGC ACT AAA AAA	489

Asp	Arg	His	Gly	Tyr	Ile	Leu	Ser	Arg	Asp	Phe	Gly	Gly	Thr	Lys	Lys	
				135					140					145		
TGG	CGC	ACA	TGC	TTT	ACG	GCT	GAT	GCC	ACA	GGG	CAT	ACC	ATG	CTT	TAT	537
Trp	Arg	Thr	Cys	Phe	Thr	Ala	Asp	Ala	Thr	Gly	His	Thr	Met	Leu	Tyr	
			150					155					160			
GCG	GTC	GCT	AAT	GAA	GCC	TTA	CAC	CAC	AAA	GTG	GAT	ATT	CAA	GAC	AGA	585
Ala	Val	Ala	Asn	Glu	Ala	Leu	His	His	Lys	Val	Asp	Ile	Gln	Asp	Arg	
			165				170					175				
AAG	GAC	ATG	CTC	GCT	TTC	ATT	CAT	CAT	GAT	AAT	AAA	TGC	TAT	GGG	GCG	633
Lys	Asp	Met	Leu	Ala	Phe	Ile	His	His	Asp	Asn	Lys	Cys	Tyr	Gly	Ala	
	180					185					190					
GTG	GTA	AGG	GAT	TTG	ATC	ACA	GGC	GAA	ATT	TCA	GCG	TAT	GTT	TCT	AAA	681
Val	Val	Arg	Asp	Leu	Ile	Thr	Gly	Glu	Ile	Ser	Ala	Tyr	Val	Ser	Lys	
195				200					205						210	
GGC	ACG	CTT	TTA	GCT	ACC	GGA	GGT	TAT	GGG	CGC	GTG	TAT	AAA	CAC	ACC	729
Gly	Thr	Leu	Leu	Ala	Thr	Gly	Gly	Tyr	Gly	Arg	Val	Tyr	Lys	His	Thr	
				215				220						225		
ACT	AAC	GCT	GTG	ATT	TGC	GAT	GGA	GCC	GGG	GCT	GCA	AGC	GCC	TTA	GAA	777
Thr	Asn	Ala	Val	Ile	Cys	Asp	Gly	Ala	Gly	Ala	Ala	Ser	Ala	Leu	Glu	
			230					235					240			
ACC	GGC	GTG	GCT	AAA	TTG	GGC	AAC	ATG	GAA	GCG	GTG	CAA	TTC	CAC	CCT	825
Thr	Gly	Val	Ala	Lys	Leu	Gly	Asn	Met	Glu	Ala	Val	Gln	Phe	His	Pro	
			245				250					255				
ACC	GCT	TTA	GTG	CCA	AGC	GGG	ATT	TTA	ATG	ACC	GAA	GGT	TGC	AGG	GGC	873
Thr	Ala	Leu	Val	Pro	Ser	Gly	Ile	Leu	Met	Thr	Glu	Gly	Cys	Arg	Gly	
			260			265					270					
GAT	GGC	GGT	GTT	TTA	AGA	GAC	AAG	TTT	GGC	AGA	CGC	TTC	ATG	CCC	GCT	921
Asp	Gly	Gly	Val	Leu	Arg	Asp	Lys	Phe	Gly	Arg	Arg	Phe	Met	Pro	Ala	
275				280					285					290		
TAT	GAG	CCG	GAG	AAA	AAA	GAG	CTT	GCA	AGC	AGA	GAT	GTG	GTC	TCA	AGG	969
Tyr	Glu	Pro	Glu	Lys	Lys	Glu	Leu	Ala	Ser	Arg	Asp	Val	Val	Ser	Arg	
				295				300						305		
CGG	ATT	TTA	GAG	CAT	ATC	CAA	AAA	GGC	TAT	GGA	GCC	AAA	TCG	CCT	TAT	1017
Arg	Ile	Leu	Glu	His	Ile	Gln	Lys	Gly	Tyr	Gly	Ala	Lys	Ser	Pro	Tyr	
			310					315					320			
GGG	GAT	CAT	GTG	TGG	CTG	GAT	ATT	GCT	ATT	TTA	GGG	CGT	AAC	CAT	GTG	1065
Gly	Asp	His	Val	Trp	Leu	Asp	Ile	Ala	Ile	Leu	Gly	Arg	Asn	His	Val	
			325				330					335				
GAA	AAA	AAC	TTA	AGG	GAT	GTG	CGC	GAT	ATA	GCC	ATG	ACT	TTT	GCG	GGC	1113
Glu	Lys	Asn	Leu	Arg	Asp	Val	Arg	Asp	Ile	Ala	Met	Thr	Phe	Ala	Gly	
	340					345					350					
ATT	GAT	CCG	GCT	GAT	AGC	AAG	GAA	CAA	ACC	AAA	GAC	AAC	ATG	CAA	GGA	1161
Ile	Asp	Pro	Ala	Asp	Ser	Lys	Glu	Gln	Thr	Lys	Asp	Asn	Met	Gln	Gly	
355					360					365					370	

GTG	CCC	GCA	AAT	GAG	CCT	GAA	TAC	GGG	CAA	GCG	ATG	GCC	AAG	CAA	AAA	1209
Val	Pro	Ala	Asn	Glu	Pro	Glu	Tyr	Gly	Gln	Ala	Met	Ala	Lys	Gln	Lys	
			375						380						385	
GGC	TGG	ATC	CCC	ATA	AAA	CCC	ATG	CAA	CAC	TAT	TCT	ATG	GGT	GGG	GTT	1257
Gly	Trp	Ile	Pro	Ile	Lys	Pro	Met	Gln	His	Tyr	Ser	Met	Gly	Gly	Val	
			390					395					400			
AGG	ACA	AAC	CCT	AAA	GGC	GAA	ACC	CAT	TTA	AAA	GGC	TTG	TTT	TGC	GCG	1305
Arg	Thr	Asn	Pro	Lys	Gly	Glu	Thr	His	Leu	Lys	Gly	Leu	Phe	Cys	Ala	
		405					410					415				
GGT	GAA	GCG	GCA	TGC	TGG	GAT	TTG	CAT	GGG	TTT	AAC	CGC	TTG	GGG	GGT	1353
Gly	Glu	Ala	Ala	Cys	Trp	Asp	Leu	His	Gly	Phe	Asn	Arg	Leu	Gly	Gly	
	420					425					430					
AAT	TCT	GTG	AGT	GAA	GCG	GTG	GTC	GCT	GGC	ATG	ATC	ATT	GGG	GAT	TAT	1401
Asn	Ser	Val	Ser	Glu	Ala	Val	Val	Ala	Gly	Met	Ile	Ile	Gly	Asp	Tyr	
435					440					445					450	
TTT	GCC	TCG	CAT	TGT	TTA	GAA	GCG	CAA	ATT	GAA	ATC	AAC	ACG	CAA	AAA	1449
Phe	Ala	Ser	His	Cys	Leu	Glu	Ala	Gln	Ile	Glu	Ile	Asn	Thr	Gln	Lys	
				455					460					465		
GTT	GAA	GCT	TTC	ATT	AAA	GAA	AGC	CAA	GAC	TAT	ATG	CAT	TTT	TTA	TTG	1497
Val	Glu	Ala	Phe	Ile	Lys	Glu	Ser	Gln	Asp	Tyr	Met	His	Phe	Leu	Leu	
			470					475					480			
CAT	AAT	GAA	GGC	AAA	GAA	GAT	GTG	TAT	GAA	ATT	AGA	GAG	CGC	ATG	AAA	1545
His	Asn	Glu	Gly	Lys	Glu	Asp	Val	Tyr	Glu	Ile	Arg	Glu	Arg	Met	Lys	
		485					490					495				
GAA	GTC	ATG	GAT	GAA	AAA	GTG	GGC	GTT	TTT	AGA	GAA	GGC	AAA	AGG	CTA	1593
Glu	Val	Met	Asp	Glu	Lys	Val	Gly	Val	Phe	Arg	Glu	Gly	Lys	Arg	Leu	
	500					505					510					
GAA	GAA	GCC	CTT	AAA	GAA	TTG	CAA	GAG	CTT	TAT	GCA	CGC	TCC	AAA	AAC	1641
Glu	Glu	Ala	Leu	Lys	Glu	Leu	Gln	Glu	Leu	Tyr	Ala	Arg	Ser	Lys	Asn	
515					520				525						530	
ATT	TGC	GTG	AAA	AAC	AAG	GTT	TTA	CAC	AAT	AAC	CCT	GAA	TTA	GAA	GAC	1689
Ile	Cys	Val	Lys	Asn	Lys	Val	Leu	His	Asn	Asn	Pro	Glu	Leu	Glu	Asp	
				535					540					545		
GCT	TAC	CGC	ACC	AAA	AAA	ATG	CTC	AAA	CTC	GCG	CTT	TGT	ATC	ACT	CAA	1737
Ala	Tyr	Arg	Thr	Lys	Lys	Met	Leu	Lys	Leu	Ala	Leu	Cys	Ile	Thr	Gln	
			550					555					560			
GGA	GCG	TTA	CTG	CGC	ACT	GAA	AGC	AGA	GGG	GCT	CAC	ACA	AGG	ATT	GAC	1785
Gly	Ala	Leu	Leu	Arg	Thr	Glu	Ser	Arg	Gly	Ala	His	Thr	Arg	Ile	Asp	
		565					570					575				
TAC	CCT	AAA	AGA	GAC	GAT	GAA	AAA	TGG	CTT	AAT	CGG	ACT	CTA	GCG	AGC	1833
Tyr	Pro	Lys	Arg	Asp	Asp	Glu	Lys	Trp	Leu	Asn	Arg	Thr	Leu	Ala	Ser	
	580						585				590					
TGG	CCT	AGC	GCT	GAG	CAA	GAC	ATG	CCC	ACG	ATT	GAA	TAC	GAA	GAA	TTA	1881
Trp	Pro	Ser	Ala	Glu	Gln	Asp	Met	Pro	Thr	Ile	Glu	Tyr	Glu	Glu	Leu	

595	600	605	610	
GAT GTG ATG AAA ATG GAA ATC AGC CCT GAT TTT AGG GGC TAT GGC AAA				1929
Asp Val Met Lys Met Glu Ile Ser Pro Asp Phe Arg Gly Tyr Gly Lys	615	620	625	
AAG GGT AAT TTC ATC CCC CAC CCC AAA AAA GAA GAG CGC GAC GCT GAG				1977
Lys Gly Asn Phe Ile Pro His Pro Lys Lys Glu Glu Arg Asp Ala Glu	630	635	640	
ATT TTG AAA ACG ATT TTA GAA CTA GAA AAG CTT GGA AAA GAC AGA ATA				2025
Ile Leu Lys Thr Ile Leu Glu Leu Glu Lys Leu Gly Lys Asp Arg Ile	645	650	655	
GAA GTC CAA CAT GCG CTC ATG CCT TTT GAA TTG CAA GAA AAA TAC AAG				2073
Glu Val Gln His Ala Leu Met Pro Phe Glu Leu Gln Glu Lys Tyr Lys	660	665	670	
GCT AGG AAT ATG CGT TTA GAA GAT GAG GAA GTC AGG GCT AGG GGG GAA				2121
Ala Arg Asn Met Arg Leu Glu Asp Glu Glu Val Arg Ala Arg Gly Glu	675	680	685	690
CAT TTG TAT TCT TTC AAT GTC CAT GAG TTA TTG GAC CAA CAC AAC GCT				2169
His Leu Tyr Ser Phe Asn Val His Glu Leu Leu Asp Gln His Asn Ala	695	700	705	
AAC CTA AAA GGA GAA CAC CAT GAG TGATAATGAA CGAACGATTG TAGTTAGAGT				2223
Asn Leu Lys Gly Glu His His Glu	710			
GCTAAAATTT GACCTCA				2241

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

Met	Lys	Ile	Thr	Tyr	Cys	Asp	Ala	Leu	Ile	Ile	Gly	Gly	Gly	Leu	Ala
1				5					10					15	
Gly	Leu	Arg	Ala	Ser	Ile	Ala	Cys	Lys	Gln	Lys	Gly	Leu	Asn	Thr	Ile
			20					25					30		
Val	Leu	Ser	Leu	Val	Pro	Val	Arg	Arg	Ser	His	Ser	Ala	Ala	Ala	Gln
			35				40					45			
Gly	Gly	Met	Gln	Ala	Ser	Leu	Ala	Asn	Ala	Lys	Lys	Ser	Glu	Gly	Asp
			50			55					60				
Asn	Glu	Asp	Leu	His	Phe	Leu	Asp	Thr	Val	Lys	Gly	Ser	Asp	Trp	Gly
65					70					75				80	
Cys	Asp	Gln	Gln	Val	Ala	Arg	Met	Phe	Val	Thr	Thr	Ala	Pro	Lys	Ala
				85					90					95	
Ile	Arg	Glu	Leu	Ala	Ser	Trp	Gly	Val	Pro	Trp	Thr	Arg	Ile	Lys	Lys

			100					105					110				
Gly	Asp	Arg	Pro	Ala	Val	Val	Asn	Gly	Glu	His	Val	Thr	Ile	Thr	Glu		
	115						120					125					
Arg	Asp	Asp	Arg	His	Gly	Tyr	Ile	Leu	Ser	Arg	Asp	Phe	Gly	Gly	Thr		
	130					135					140						
Lys	Lys	Trp	Arg	Thr	Cys	Phe	Thr	Ala	Asp	Ala	Thr	Gly	His	Thr	Met		
145					150					155					160		
Leu	Tyr	Ala	Val	Ala	Asn	Glu	Ala	Leu	His	His	Lys	Val	Asp	Ile	Gln		
			165				170							175			
Asp	Arg	Lys	Asp	Met	Leu	Ala	Phe	Ile	His	His	Asp	Asn	Lys	Cys	Tyr		
			180				185					190					
Gly	Ala	Val	Val	Arg	Asp	Leu	Ile	Thr	Gly	Glu	Ile	Ser	Ala	Tyr	Val		
	195					200						205					
Ser	Lys	Gly	Thr	Leu	Leu	Ala	Thr	Gly	Gly	Tyr	Gly	Arg	Val	Tyr	Lys		
	210				215						220						
His	Thr	Thr	Asn	Ala	Val	Ile	Cys	Asp	Gly	Ala	Gly	Ala	Ala	Ser	Ala		
225					230					235					240		
Leu	Glu	Thr	Gly	Val	Ala	Lys	Leu	Gly	Asn	Met	Glu	Ala	Val	Gln	Phe		
			245				250							255			
His	Pro	Thr	Ala	Leu	Val	Pro	Ser	Gly	Ile	Leu	Met	Thr	Glu	Gly	Cys		
			260				265					270					
Arg	Gly	Asp	Gly	Gly	Val	Leu	Arg	Asp	Lys	Phe	Gly	Arg	Arg	Phe	Met		
	275						280					285					
Pro	Ala	Tyr	Glu	Pro	Glu	Lys	Lys	Glu	Leu	Ala	Ser	Arg	Asp	Val	Val		
	290					295					300						
Ser	Arg	Arg	Ile	Leu	Glu	His	Ile	Gln	Lys	Gly	Tyr	Gly	Ala	Lys	Ser		
305				310						315					320		
Pro	Tyr	Gly	Asp	His	Val	Trp	Leu	Asp	Ile	Ala	Ile	Leu	Gly	Arg	Asn		
			325				330							335			
His	Val	Glu	Lys	Asn	Leu	Arg	Asp	Val	Arg	Asp	Ile	Ala	Met	Thr	Phe		
			340				345					350					
Ala	Gly	Ile	Asp	Pro	Ala	Asp	Ser	Lys	Glu	Gln	Thr	Lys	Asp	Asn	Met		
	355						360					365					
Gln	Gly	Val	Pro	Ala	Asn	Glu	Pro	Glu	Tyr	Gly	Gln	Ala	Met	Ala	Lys		
	370				375						380						
Gln	Lys	Gly	Trp	Ile	Pro	Ile	Lys	Pro	Met	Gln	His	Tyr	Ser	Met	Gly		
385				390						395					400		
Gly	Val	Arg	Thr	Asn	Pro	Lys	Gly	Glu	Thr	His	Leu	Lys	Gly	Leu	Phe		
			405				410							415			
Cys	Ala	Gly	Glu	Ala	Ala	Cys	Trp	Asp	Leu	His	Gly	Phe	Asn	Arg	Leu		
			420				425					430					
Gly	Gly	Asn	Ser	Val	Ser	Glu	Ala	Val	Val	Ala	Gly	Met	Ile	Ile	Gly		
	435						440					445					
Asp	Tyr	Phe	Ala	Ser	His	Cys	Leu	Glu	Ala	Gln	Ile	Glu	Ile	Asn	Thr		
	450					455					460						
Gln	Lys	Val	Glu	Ala	Phe	Ile	Lys	Glu	Ser	Gln	Asp	Tyr	Met	His	Phe		
465					470					475					480		
Leu	Leu	His	Asn	Glu	Gly	Lys	Glu	Asp	Val	Tyr	Glu	Ile	Arg	Glu	Arg		
			485				490							495			
Met	Lys	Glu	Val	Met	Asp	Glu	Lys	Val	Gly	Val	Phe	Arg	Glu	Gly	Lys		
			500				505					510					
Arg	Leu	Glu	Glu	Ala	Leu	Lys	Glu	Leu	Gln	Glu	Leu	Tyr	Ala	Arg	Ser		
	515						520					525					
Lys	Asn	Ile	Cys	Val	Lys	Asn	Lys	Val	Leu	His	Asn	Asn	Pro	Glu	Leu		
	530					535					540						
Glu	Asp	Ala	Tyr	Arg	Thr	Lys	Lys	Met	Leu	Lys	Leu	Ala	Leu	Cys	Ile		
545					550					555					560		
Thr	Gln	Gly	Ala	Leu	Leu	Arg	Thr	Glu	Ser	Arg	Gly	Ala	His	Thr	Arg		

				565					570					575					
Ile	Asp	Tyr	Pro	Lys	Arg	Asp	Asp	Glu	Lys	Trp	Leu	Asn	Arg	Thr	Leu				
			580					585					590						
Ala	Ser	Trp	Pro	Ser	Ala	Glu	Gln	Asp	Met	Pro	Thr	Ile	Glu	Tyr	Glu				
		595					600					605							
Glu	Leu	Asp	Val	Met	Lys	Met	Glu	Ile	Ser	Pro	Asp	Phe	Arg	Gly	Tyr				
	610					615					620								
Gly	Lys	Lys	Gly	Asn	Phe	Ile	Pro	His	Pro	Lys	Lys	Glu	Glu	Arg	Asp				
625				630						635					640				
Ala	Glu	Ile	Leu	Lys	Thr	Ile	Leu	Glu	Leu	Glu	Lys	Leu	Gly	Lys	Asp				
			645					650						655					
Arg	Ile	Glu	Val	Gln	His	Ala	Leu	Met	Pro	Phe	Glu	Leu	Gln	Glu	Lys				
		660						665					670						
Tyr	Lys	Ala	Arg	Asn	Met	Arg	Leu	Glu	Asp	Glu	Glu	Val	Arg	Ala	Arg				
	675					680						685							
Gly	Glu	His	Leu	Tyr	Ser	Phe	Asn	Val	His	Glu	Leu	Leu	Asp	Gln	His				
	690				695						700								
Asn	Ala	Asn	Leu	Lys	Gly	Glu	His	His	Glu										
705				710															

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 77...445
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

ATTAGTTCA AGAGCTTTTA GAAGAATTTT TGCAAAGCGG GGCTAAAGAG ATTTTAGAAA	60
AGGCGCAGTT GTTTTA ATG CGT TTG TTT ATC GCG CTA GTT TTG TTT TGG TGG	112
Met Arg Leu Phe Ile Ala Leu Val Leu Phe Trp Trp	
1 5 10	
TGG TTA AGC TTG AAC GCT AAA GAA GCG GAT TTT ATC TCT GAT TTA GAA	160
Trp Leu Ser Leu Asn Ala Lys Glu Ala Asp Phe Ile Ser Asp Leu Glu	
15 20 25	
TAC GGG ATG GCT CTT TAT AAA AAC CCT AGG GGT GTT GCG TGC GCG AAA	208
Tyr Gly Met Ala Leu Tyr Lys Asn Pro Arg Gly Val Ala Cys Ala Lys	
30 35 40	
TGC CAT GGC ATT AAA GGC GAA CAA CAA GAA ATC ACC TTT TAT TAT GAA	256
Cys His Gly Ile Lys Gly Glu Gln Gln Glu Ile Thr Phe Tyr Tyr Glu	
45 50 55 60	
AAA GGC GAG AAA AAA ATC CTC TAC GCC CCT AAA ATC AAC CAT TTG GAT	304
Lys Gly Glu Lys Lys Ile Leu Tyr Ala Pro Lys Ile Asn His Leu Asp	

65															70					75					
TTT	AAA	ACC	TTT	AAA	GAC	GCC	TTG	AGT	TTA	GGC	AAA	GGC	ATG	ATG	CCT	352									
Phe	Lys	Thr	Phe	Lys	Asp	Ala	Leu	Ser	Leu	Gly	Lys	Gly	Met	Met	Pro										
			80					85					90												
AAA	TAC	AAT	CTC	AAT	TTA	GAA	GAA	ATC	CAA	GCG	ATT	TAT	CTT	TAT	ATC	400									
Lys	Tyr	Asn	Leu	Asn	Leu	Glu	Glu	Ile	Gln	Ala	Ile	Tyr	Leu	Tyr	Ile										
		95					100					105													
ATC	TCT	TTA	GAG	CAT	AAA	GAA	GAG	CGT	AAG	GAT	TCT	CCT	AAG	CCT	TAATC	450									
Ile	Ser	Leu	Glu	His	Lys	Glu	Glu	Arg	Lys	Asp	Ser	Pro	Lys	Pro											
	110					115					120														
AAAGCGCTTG	ATTTATGCTA	AAATGGAGCG	TTGCATTTTT	GTTTTG												496									

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Met	Arg	Leu	Phe	Ile	Ala	Leu	Val	Leu	Phe	Trp	Trp	Trp	Leu	Ser	Leu
1				5					10					15	
Asn	Ala	Lys	Glu	Ala	Asp	Phe	Ile	Ser	Asp	Leu	Glu	Tyr	Gly	Met	Ala
		20						25					30		
Leu	Tyr	Lys	Asn	Pro	Arg	Gly	Val	Ala	Cys	Ala	Lys	Cys	His	Gly	Ile
	35					40						45			
Lys	Gly	Glu	Gln	Gln	Glu	Ile	Thr	Phe	Tyr	Tyr	Glu	Lys	Gly	Glu	Lys
	50					55					60				
Lys	Ile	Leu	Tyr	Ala	Pro	Lys	Ile	Asn	His	Leu	Asp	Phe	Lys	Thr	Phe
65					70				75					80	
Lys	Asp	Ala	Leu	Ser	Leu	Gly	Lys	Gly	Met	Met	Pro	Lys	Tyr	Asn	Leu
			85						90					95	
Asn	Leu	Glu	Glu	Ile	Gln	Ala	Ile	Tyr	Leu	Tyr	Ile	Ile	Ser	Leu	Glu
		100						105					110		
His	Lys	Glu	Glu	Arg	Lys	Asp	Ser	Pro	Lys	Pro					
	115					120									

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

(B) LOCATION: 72...464
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

GTTGCAACAA AAAATAGAGA GCAGGAAAAC AGACATTGTG ATCCAATCCA TGGCGAATAT	60
TCTCAGCGGG A ATG AAT GAG CTT ATC CGC TAT GGC TTG ATA TTT CTC TTT	110
Met Asn Glu Leu Ile Arg Tyr Gly Leu Ile Phe Leu Phe	
1 5 10	
TTT TTA AAG GCG TTT GGG CTT GAT TAT GGG ATA GAT AAA ACG CTA GAA	158
Phe Leu Lys Ala Phe Gly Leu Asp Tyr Gly Ile Asp Lys Thr Leu Glu	
15 20 25	
TTA AAA AAA GAT GAA GTG TTT AAA GCG ATC ATC AAA GAC ACT TCA AAT	206
Leu Lys Lys Asp Glu Val Phe Lys Ala Ile Ile Lys Asp Thr Ser Asn	
30 35 40 45	
GAA CAA ACC AAA GAA ATC ACG CTC TAT TGG ACG CTA TAT GCA AAT AAA	254
Glu Gln Thr Lys Glu Ile Thr Leu Tyr Trp Thr Leu Tyr Ala Asn Lys	
50 55 60	
GGT TTA GTC ATC AAC ATG CGT TTT AAC CAT TTC CCT TAC CAG TTT ATT	302
Gly Leu Val Ile Asn Met Arg Phe Asn His Phe Pro Tyr Gln Phe Ile	
65 70 75	
TTA TAC ACC GAT CAT GCG AGA AAC ACC TAT AAT CTC AAA GTT TTT GAA	350
Leu Tyr Thr Asp His Ala Arg Asn Thr Tyr Asn Leu Lys Val Phe Glu	
80 85 90	
GAA AAA TTT TCT TCT AAC AGC ACT CTG TCG CTT GTG TTT AAA GAT TTT	398
Glu Lys Phe Ser Ser Asn Ser Thr Leu Ser Leu Val Phe Lys Asp Phe	
95 100 105	
AAA GAA GAT AAA GCC GCT TTA AGG CTT TTA GCC CTT ATG CCC CTT GTT	446
Lys Glu Asp Lys Ala Ala Leu Arg Leu Leu Ala Leu Met Pro Leu Val	
110 115 120 125	
TTT TCT CCT AAA GAG CCT TAAGGAATTT GCATGCAAGA AAAACAACCTT AAAACCAT	502
Phe Ser Pro Lys Glu Pro	
130	
TCAAAATAAG ATCGCTTCC	521

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:


```

Met Asn Glu Leu Ile Arg Tyr Gly Leu Ile Phe Leu Phe Phe Leu Lys
 1           5           10           15
Ala Phe Gly Leu Asp Tyr Gly Ile Asp Lys Thr Leu Glu Leu Lys Lys
          20           25           30
Asp Glu Val Phe Lys Ala Ile Ile Lys Asp Thr Ser Asn Glu Gln Thr
      35           40           45
Lys Glu Ile Thr Leu Tyr Trp Thr Leu Tyr Ala Asn Lys Gly Leu Val
 50           55           60
Ile Asn Met Arg Phe Asn His Phe Pro Tyr Gln Phe Ile Leu Tyr Thr
65           70           75           80
Asp His Ala Arg Asn Thr Tyr Asn Leu Lys Val Phe Glu Glu Lys Phe
          85           90           95
Ser Ser Asn Ser Thr Leu Ser Leu Val Phe Lys Asp Phe Lys Glu Asp
          100          105          110
Lys Ala Ala Leu Arg Leu Leu Ala Leu Met Pro Leu Val Phe Ser Pro
      115           120           125
Lys Glu Pro
    130

```

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 55...222
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

```

GCTCCCTCTA AAAGGGTTTT TAAACTATCT TGAGATTTAC CCAATTTATA GGTG ATG      57
                                     Met
                                     1

CTT TCA AAA CTC CCA TTT ACT GGT GTT TTA GCC TTA GTT TTA AAG GCT      105
Leu Ser Lys Leu Pro Phe Thr Gly Val Leu Ala Leu Val Leu Lys Ala
      5           10           15

GTC CAT GTT AGC TTA GCC GAA GAT AAA TCC AAA TTC ACC GCT TGC AAA      153
Val His Val Ser Leu Ala Glu Asp Lys Ser Lys Phe Thr Ala Cys Lys
      20           25           30

AAC CCT GCT AGT AAA ACC GAT ACC AAA ACC ATT TTT TTC ATT CAT TAT      201
Asn Pro Ala Ser Lys Thr Asp Thr Lys Thr Ile Phe Phe Ile His Tyr
      35           40           45

CCT TTA ATG TGG TCT TAT CAA TAACGCTTAT TATTTAGTG TAAATAAGCA CGCT      256
Pro Leu Met Trp Ser Tyr Gln
50           55

```

TACAACTAAA ACG

269

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

```

Met Leu Ser Lys Leu Pro Phe Thr Gly Val Leu Ala Leu Val Leu Lys
 1             5             10             15
Ala Val His Val Ser Leu Ala Glu Asp Lys Ser Lys Phe Thr Ala Cys
          20             25             30
Lys Asn Pro Ala Ser Lys Thr Asp Thr Lys Thr Ile Phe Phe Ile His
          35             40             45
Tyr Pro Leu Met Trp Ser Tyr Gln
50             55

```

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 66...611
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

```

AATGACTTTA GGGGATATTC TTAAAGAAAA ACTCTAAAGA GTGATTTTAA AAGCATGAGA      60
ATGGC ATG AGA TTT AAG GGT GTT GTT GCT TTT ATT TCC CTA GCT GTC GCT      110
  Met Arg Phe Lys Gly Val Val Ala Phe Ile Ser Leu Ala Val Ala
    1             5             10             15

CTT GGC GTT TTA GCC TAT TTG TTT TTA AGC GTT AAA AAA GAA ATG CCC      158
Leu Gly Val Leu Ala Tyr Leu Phe Leu Ser Val Lys Lys Glu Met Pro
          20             25             30

GCT ACT TCT CAT GCG ATC TCT CAA ACA CAT GCG ATC TCT CAA ACC AAT      206
Ala Thr Ser His Ala Ile Ser Gln Thr His Ala Ile Ser Gln Thr Asn
          35             40             45

GAA GGC CTC TCT CAA ACA GAT GCA AAA AGC CAT GAC ATC GAT CTA GAA      254
Glu Gly Leu Ser Gln Thr Asp Ala Lys Ser His Asp Ile Asp Leu Glu

```

50										55					60					
GAA	AAT	AGC	CCC	ACT	GAA	ACC	TCT	CAT	AAT	GAA	AAA	GCC	TCC	CAT	AAC	302				
Glu	Asn	Ser	Pro	Thr	Glu	Thr	Ser	His	Asn	Glu	Lys	Ala	Ser	His	Asn					
65					70					75										
GAA	GAA	GAT	CAC	AAT	AAC	GCC	CTT	TCT	CAA	AAT	CTT	GAT	GCG	CAA	GAA	350				
Glu	Glu	Asp	His	Asn	Asn	Ala	Leu	Ser	Gln	Asn	Leu	Asp	Ala	Gln	Glu					
80					85					90					95					
TCT	ATC	AAT	TAC	CCC	GTT	GTG	GAA	CAT	TAT	TCT	GAA	ATC	CCT	TTT	GAA	398				
Ser	Ile	Asn	Tyr	Pro	Val	Val	Glu	His	Tyr	Ser	Glu	Ile	Pro	Phe	Glu					
100					105					110										
GAA	AAA	AAA	AGG	GAA	TAT	TCA	AAG	CTT	ATC	ATT	AAG	GAT	TTA	AAG	GAC	446				
Glu	Lys	Lys	Arg	Glu	Tyr	Ser	Lys	Leu	Ile	Ile	Lys	Asp	Leu	Lys	Asp					
115					120					125										
TAT	CAA	TGG	TGG	TGC	TTA	AAA	GAA	ATC	CTC	AAA	AAA	GAA	CAG	ATT	GAT	494				
Tyr	Gln	Trp	Trp	Cys	Leu	Lys	Glu	Ile	Leu	Lys	Lys	Glu	Gln	Ile	Asp					
130					135					140										
TAC	GCT	TAC	GAT	AAC	ACC	AAA	AAC	CAA	CCT	AAC	CTC	ATC	ATC	TAT	TTA	542				
Tyr	Ala	Tyr	Asp	Asn	Thr	Lys	Asn	Gln	Pro	Asn	Leu	Ile	Ile	Tyr	Leu					
145					150					155										
GAT	GAA	AAT	AAA	AAA	GAA	CGC	TTG	CTG	GCT	GAT	TTA	GAC	TAT	TAT	AAA	590				
Asp	Glu	Asn	Lys	Lys	Glu	Arg	Leu	Leu	Ala	Asp	Leu	Asp	Tyr	Tyr	Lys					
160					165					170					175					
ATA	CGC	TAT	CAT	GCT	GTT	TTT	TAAATTCAAA	GGATAAAAAT	GTATCAAGTA	GCCA						645				
Ile	Arg	Tyr	His	Ala	Val	Phe														
180																				
TTTGCGACCC CATCCATGCT AAAGGC															671					

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

Met	Arg	Phe	Lys	Gly	Val	Val	Ala	Phe	Ile	Ser	Leu	Ala	Val	Ala	Leu
1				5					10					15	
Gly	Val	Leu	Ala	Tyr	Leu	Phe	Leu	Ser	Val	Lys	Lys	Glu	Met	Pro	Ala
		20						25					30		
Thr	Ser	His	Ala	Ile	Ser	Gln	Thr	His	Ala	Ile	Ser	Gln	Thr	Asn	Glu
		35					40					45			
Gly	Leu	Ser	Gln	Thr	Asp	Ala	Lys	Ser	His	Asp	Ile	Asp	Leu	Glu	Glu
	50					55				60					
Asn	Ser	Pro	Thr	Glu	Thr	Ser	His	Asn	Glu	Lys	Ala	Ser	His	Asn	Glu

```

65          70          75          80
Glu Asp His Asn Asn Ala Leu Ser Gln Asn Leu Asp Ala Gln Glu Ser
            85          90          95
Ile Asn Tyr Pro Val Val Glu His Tyr Ser Glu Ile Pro Phe Glu Glu
            100         105         110
Lys Lys Arg Glu Tyr Ser Lys Leu Ile Ile Lys Asp Leu Lys Asp Tyr
            115         120         125
Gln Trp Trp Cys Leu Lys Glu Ile Leu Lys Lys Glu Gln Ile Asp Tyr
            130         135         140
Ala Tyr Asp Asn Thr Lys Asn Gln Pro Asn Leu Ile Ile Tyr Leu Asp
            145         150         155         160
Glu Asn Lys Lys Glu Arg Leu Leu Ala Asp Leu Asp Tyr Tyr Lys Ile
            165         170         175
Arg Tyr His Ala Val Phe
            180

```

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 86...295
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

```

ACCCACAAAA CTAAAACCCA CTAACACAAT TAACCCTAAC AACACATAAA GATTGCCCAA      60
AGACGCGCAC AACACGCTCG CAACA ATG GTT GCA AAA ACA AAC ACA ATC CCC      112
                               Met Val Ala Lys Thr Asn Thr Ile Pro
                               1           5

CCC ATC GTA GGG GTA TCT TTT TTA TTC TGG TGG CTT GGC ACG AAG CTA      160
Pro Ile Val Gly Val Ser Phe Leu Phe Trp Trp Leu Gly Thr Lys Leu
10           15           20           25

GAA ATG GGC TGG TTA GCC TTT TTA GCC TTG GCC CAT AGA ATG AAT TTA      208
Glu Met Gly Trp Leu Ala Phe Leu Ala Leu Ala His Arg Met Asn Leu
           30           35           40

GGC ATT AAA AAA AGC GTG AGA AAA AAA GCT ATG AAA AAC CCT AAC CCT      256
Gly Ile Lys Lys Ser Val Arg Lys Lys Ala Met Lys Asn Pro Asn Pro
           45           50           55

GCT CTA AAA GTC AAA TAC TGG AAA AGA TTG ATA TTG AAA TAGCCATATA GT      307
Ala Leu Lys Val Lys Tyr Trp Lys Arg Leu Ile Leu Lys
           60           65           70

AAAGAATAGA GCATAAAATC CCCTAAAATC GCCA      341

```

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

```

Met Val Ala Lys Thr Asn Thr Ile Pro Pro Ile Val Gly Val Ser Phe
 1           5           10          15
Leu Phe Trp Trp Leu Gly Thr Lys Leu Glu Met Gly Trp Leu Ala Phe
 20          25          30
Leu Ala Leu Ala His Arg Met Asn Leu Gly Ile Lys Lys Ser Val Arg
 35          40          45
Lys Lys Ala Met Lys Asn Pro Asn Pro Ala Leu Lys Val Lys Tyr Trp
 50          55          60
Lys Arg Leu Ile Leu Lys
65          70

```

(2) INFORMATION FOR SEQ ID NO:333

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 58...2430
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

```

TTTTTTTTTT TTTTGATTT TTATTTTTTA AATTTTGA TTAAGGAGAG TTGTTGG ATG      60
                                     Met
                                     1

TTT TTA AGA GTA TAC CCA AAG CTT AGA TAC GCT TTA TGT TTC CCC CTA      108
Phe Leu Arg Val Tyr Pro Lys Leu Arg Tyr Ala Leu Cys Phe Pro Leu
      5           10          15

CTC GCT GAG ACT TGC TAT AGC GAA GAG CGG ACT TTA AAT AAG GTT ACC      156
Leu Ala Glu Thr Cys Tyr Ser Glu Glu Arg Thr Leu Asn Lys Val Thr
      20          25          30

ACC CAA GCT AAA AGG ATT TTC ACT TAC AAC AAT GAG TTT AAA GTA ACT      204
Thr Gln Ala Lys Arg Ile Phe Thr Tyr Asn Asn Glu Phe Lys Val Thr

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35	40	45	
TCT AAA GAA CTA GAT CAA CGC CAA AGC AAT GAA GTC AAG GAC TTG TTT Ser Lys Glu Leu Asp Gln Arg Gln Ser Asn Glu Val Lys Asp Leu Phe 50 55 60 65	252		
AGG ACT AAC CCT GAT GTG AAT GTG GGC GGA GGG AGC GTG ATG GGG CAG Arg Thr Asn Pro Asp Val Asn Val Gly Gly Gly Ser Val Met Gly Gln 70 75 80	300		
AAA ATC TAT GTG AGA GGC GTT GAA GAC AGG CTT TTA AGG GTT ACA GTG Lys Ile Tyr Val Arg Gly Val Glu Asp Arg Leu Leu Arg Val Thr Val 85 90 95	348		
GAT GGG GCT GCA CAA AAT GGC AAT ATC TAC CAC CAC CAA GGC AAC ACC Asp Gly Ala Ala Gln Asn Gly Asn Ile Tyr His His Gln Gly Asn Thr 100 105 110	396		
GTG ATT GAC CCT GGC ATG CTC AAA AGC GTG GAA GTT ACC AAA GGC GCG Val Ile Asp Pro Gly Met Leu Lys Ser Val Glu Val Thr Lys Gly Ala 115 120 125	444		
GCG AAT GCG AGC GCG GGG CCA GGA GCG ATT GCG GGA GTG ATT AAA ATG Ala Asn Ala Ser Ala Gly Pro Gly Ala Ile Ala Gly Val Ile Lys Met 130 135 140 145	492		
GAG ACT AAA GGA GCG GCT GAT TTT ATC CCT AGG GGG AAA AAT TAT GCT Glu Thr Lys Gly Ala Ala Asp Phe Ile Pro Arg Gly Lys Asn Tyr Ala 150 155 160	540		
GCC AGT GGG GCG GTG AGT TTT TAT ACC AAT TTT GGC GAT CGA GAG ACT Ala Ser Gly Ala Val Ser Phe Tyr Thr Asn Phe Gly Asp Arg Glu Thr 165 170 175	588		
TTC AGA TCG GCT TAT CAA AAC GCG CAT TTT GAT ATT ATC GCT TAC TAC Phe Arg Ser Ala Tyr Gln Asn Ala His Phe Asp Ile Ile Ala Tyr Tyr 180 185 190	636		
ACG CAC CAA AAC ATC TTC TAT TAT AGA AGC GGC GCT ACA GCG ATG AAA Thr His Gln Asn Ile Phe Tyr Tyr Arg Ser Gly Ala Thr Ala Met Lys 195 200 205	684		
AAC CTT TTC AAT CCC ACA CAA GCC GAT AAA GAG CCA GGA ACT CCT AGC Asn Leu Phe Asn Pro Thr Gln Ala Asp Lys Glu Pro Gly Thr Pro Ser 210 215 220 225	732		
GAG CAA AAC AAC GCT TTG ATT AAA ATG AAT GGT TAT TTG AGC GAC AGA Glu Gln Asn Asn Ala Leu Ile Lys Met Asn Gly Tyr Leu Ser Asp Arg 230 235 240	780		
GAC ACG CTC ACT TTC AGC TGG AAC ATG ACA CGA GAT AAC GCT ACA CGC Asp Thr Leu Thr Phe Ser Trp Asn Met Thr Arg Asp Asn Ala Thr Arg 245 250 255	828		
CCT TTA AGG AGT AAC GCT ATA GGG TTA GCC TAT CCT TGT GAA GCC CCC Pro Leu Arg Ser Asn Ala Ile Gly Leu Ala Tyr Pro Cys Glu Ala Pro 260 265 270	876		

TTT AGT CCT GAT AGT TCT CAA GGG TGT CCT AAT GTG TTA GAT AGT TTC	924
Phe Ser Pro Asp Ser Ser Gln Gly Cys Pro Asn Val Leu Asp Ser Phe	
275 280 285	
ACA AGA TAC ATG TAT CAC TCT ATT AAT AGT GCC AAC AAT CTT TCC TTA	972
Thr Arg Tyr Met Tyr His Ser Ile Asn Ser Ala Asn Asn Leu Ser Leu	
290 295 300 305	
CAA TAC AAA AGG GAA GCG GGA AAT TCT TTT GGC GAC CCA CGA TTA GAT	1020
Gln Tyr Lys Arg Glu Ala Gly Asn Ser Phe Gly Asp Pro Arg Leu Asp	
310 315 320	
TTT ACC CTT TAT ACA AGC ATC AGG AAC GCT CAG TTT GAT CCC CTA TTT	1068
Phe Thr Leu Tyr Thr Ser Ile Arg Asn Ala Gln Phe Asp Pro Leu Phe	
325 330 335	
GAT CCT AAT GGC GTT TAT GCT AAA TTC CCC ACT TCT TTA GCG AGC GCA	1116
Asp Pro Asn Gly Val Tyr Ala Lys Phe Pro Thr Ser Leu Ala Ser Ala	
340 345 350	
TGG GAA AAA GAA AAT TAC CCA TGC GTT GAA GGC GCT TAT TGC ACC CCA	1164
Trp Glu Lys Glu Asn Tyr Pro Cys Val Glu Gly Ala Tyr Cys Thr Pro	
355 360 365	
AGC TTT TCA GAT GTG GAT AAA CCA AGC TCA CAG CCT AGG AAT TTG TTT	1212
Ser Phe Ser Asp Val Asp Lys Pro Ser Ser Gln Pro Arg Asn Leu Phe	
370 375 380 385	
TTA AAC AAC ACC GGC TTA AAC CTT AAA GTC GCG CAT GTG ATT GAT GAA	1260
Leu Asn Asn Thr Gly Leu Asn Leu Lys Val Ala His Val Ile Asp Glu	
390 395 400	
GCC ACA GAC AGC CTT TTT GAA TAC GGA TTC AAC TAC CAA AAT TTG AGC	1308
Ala Thr Asp Ser Leu Phe Glu Tyr Gly Phe Asn Tyr Gln Asn Leu Ser	
405 410 415	
GTT TTT GAC GCT CGC ATC CCT AAA TCA GAA TTA TAC AGG CCT AAT CAA	1356
Val Phe Asp Ala Arg Ile Pro Lys Ser Glu Leu Tyr Arg Pro Asn Gln	
420 425 430	
GTT TAT ACT GAT GAT AAA GGA CAA AAA CAA ATC GCT TGC TCT CTT GTG	1404
Val Tyr Thr Asp Asp Lys Gly Gln Lys Gln Ile Ala Cys Ser Leu Val	
435 440 445	
AAT AAT AAC CCC AAT GAC CCC ACT CTG TGC CAA AGA GGG AAA GCG AAC	1452
Asn Asn Asn Pro Asn Asp Pro Thr Leu Cys Gln Arg Gly Lys Ala Asn	
450 455 460 465	
GGG AAT ATT TAT GGA GGC TAC GTG CAA GCG AAT TAC TCG CCT CAT AAA	1500
Gly Asn Ile Tyr Gly Gly Tyr Val Gln Ala Asn Tyr Ser Pro His Lys	
470 475 480	
ATC ATC ACT TTT GGA GCC GGG GTA AGG TGG GAC GCT TAC ACG CTT TAT	1548
Ile Ile Thr Phe Gly Ala Gly Val Arg Trp Asp Ala Tyr Thr Leu Tyr	
485 490 495	
GAT AAA GAC TGG AAC CAC CGC TAC ACT CAA GGC TTT AGC CCT AGC GCG	1596
Asp Lys Asp Trp Asn His Arg Tyr Thr Gln Gly Phe Ser Pro Ser Ala	

500					505					510						
GCT	CTT	GTG	CTA	AGC	CCC	ATT	GAG	CCT	TTA	TCT	TTA	AAA	ATC	ACT	TAT	1644
Ala	Leu	Val	Leu	Ser	Pro	Ile	Glu	Pro	Leu	Ser	Leu	Lys	Ile	Thr	Tyr	
515					520					525						
TCT	CAA	GTT	ACA	AGA	GGG	GTG	ATG	CCA	GGA	GAT	GGC	GTG	TAC	ATG	CGT	1692
Ser	Gln	Val	Thr	Arg	Gly	Val	Met	Pro	Gly	Asp	Gly	Val	Tyr	Met	Arg	
530					535					540					545	
CAA	AAC	GAT	TTA	CGA	TAC	GCC	AAA	AAC	ATC	AAG	CCT	GAA	GTG	GGC	TCT	1740
Gln	Asn	Asp	Leu	Arg	Tyr	Ala	Lys	Asn	Ile	Lys	Pro	Glu	Val	Gly	Ser	
550					555					560						
AAC	GCT	GAA	TTT	AAT	ATT	GAT	TAT	TCA	AGC	CAG	TAT	TTT	AGC	GGG	AGG	1788
Asn	Ala	Glu	Phe	Asn	Ile	Asp	Tyr	Ser	Ser	Gln	Tyr	Phe	Ser	Gly	Arg	
565					570					575						
GCT	GCG	GCG	TTT	TAT	CAG	GCT	TTG	GAT	AAT	TTC	ATC	TCA	CAA	TAC	GCA	1836
Ala	Ala	Ala	Phe	Tyr	Gln	Ala	Leu	Asp	Asn	Phe	Ile	Ser	Gln	Tyr	Ala	
580					585					590						
CAA	AAT	TTG	ATT	GTA	ACC	AAT	TTG	AGT	CAA	GCG	ATT	CGT	ATT	TAT	GGC	1884
Gln	Asn	Leu	Ile	Val	Thr	Asn	Leu	Ser	Gln	Ala	Ile	Arg	Ile	Tyr	Gly	
595					600					605						
TAT	GAA	GTG	GGT	GGG	ACT	TTC	AGA	TAC	AAG	GGC	GTG	AGT	TTG	AAT	GTA	1932
Tyr	Glu	Val	Gly	Gly	Thr	Phe	Arg	Tyr	Lys	Gly	Val	Ser	Leu	Asn	Val	
610					615					620					625	
GGG	GTC	TCG	CGC	ACC	TGG	CCC	ACC	ACT	AGG	GGG	TAT	TTA	ATG	GCG	GAT	1980
Gly	Val	Ser	Arg	Thr	Trp	Pro	Thr	Thr	Arg	Gly	Tyr	Leu	Met	Ala	Asp	
630					635					640						
AGC	TAT	GAG	CTT	GCC	GCA	AGC	ACC	GGT	AAT	GTT	TTT	ATC	ATC	AAA	TTG	2028
Ser	Tyr	Glu	Leu	Ala	Ala	Ser	Thr	Gly	Asn	Val	Phe	Ile	Ile	Lys	Leu	
645					650					655						
GAT	TAC	ACC	ATC	CCC	AAA	ACA	GGG	ATC	AAT	CTT	GCA	TGG	CTT	AGC	CGC	2076
Asp	Tyr	Thr	Ile	Pro	Lys	Thr	Gly	Ile	Asn	Leu	Ala	Trp	Leu	Ser	Arg	
660					665					670						
TTT	GTT	ACC	GGT	TTA	GAT	TAT	TGC	GGG	TTT	GAT	ATT	TAC	TTG	CCT	GAT	2124
Phe	Val	Thr	Gly	Leu	Asp	Tyr	Cys	Gly	Phe	Asp	Ile	Tyr	Leu	Pro	Asp	
675					680					685						
TAT	GGG	ACG	GCT	GAG	AAA	CCC	AAA	ACC	CCT	ACC	GAT	TTA	GCC	AAA	TGC	2172
Tyr	Gly	Thr	Ala	Glu	Lys	Pro	Lys	Thr	Pro	Thr	Asp	Leu	Ala	Lys	Cys	
690					695					700					705	
GGA	TCT	CAA	TTA	GGG	TTA	GTG	CAT	ATG	CAT	AAA	CCG	GGC	TAT	GGC	GTG	2220
Gly	Ser	Gln	Leu	Gly	Leu	Val	His	Met	His	Lys	Pro	Gly	Tyr	Gly	Val	
710					715					720						
AGT	AAT	TTT	TAT	ATC	AAT	TGG	AGT	CCT	AAA	ACC	AAA	AGC	CGC	TGG	AAG	2268
Ser	Asn	Phe	Tyr	Ile	Asn	Trp	Ser	Pro	Lys	Thr	Lys	Ser	Arg	Trp	Lys	
725					730					735						

GGT TTG TTG CTT TCA GCC GTG TTT AAT AAT GTT TTC AAC AAA TTC TAT 2316
 Gly Leu Leu Leu Ser Ala Val Phe Asn Asn Val Phe Asn Lys Phe Tyr
 740 745 750

GTG GAT CAA ACA AGC CCT TAT GTC ATG AGC CCG GAT ATG CCA GGC ACT 2364
 Val Asp Gln Thr Ser Pro Tyr Val Met Ser Pro Asp Met Pro Gly Thr
 755 760 765

GAC GCT GTT AAA AGA GCG ATC GCT GAG CCT GGG TTT AAC GCG CGT TTT 2412
 Asp Ala Val Lys Arg Ala Ile Ala Glu Pro Gly Phe Asn Ala Arg Phe
 770 775 780 785

GAA GTG GCT TAC AAA TGG TAGTTAATGG AGCTTTAAGC GTTGCGCATG CGTGATAG 2468
 Glu Val Ala Tyr Lys Trp
 790

CAACGGCTAT CGC 2481

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

Met Phe Leu Arg Val Tyr Pro Lys Leu Arg Tyr Ala Leu Cys Phe Pro
 1 5 10 15
 Leu Leu Ala Glu Thr Cys Tyr Ser Glu Glu Arg Thr Leu Asn Lys Val
 20 25 30
 Thr Thr Gln Ala Lys Arg Ile Phe Thr Tyr Asn Asn Glu Phe Lys Val
 35 40 45
 Thr Ser Lys Glu Leu Asp Gln Arg Gln Ser Asn Glu Val Lys Asp Leu
 50 55 60
 Phe Arg Thr Asn Pro Asp Val Asn Val Gly Gly Gly Ser Val Met Gly
 65 70 75 80
 Gln Lys Ile Tyr Val Arg Gly Val Glu Asp Arg Leu Leu Arg Val Thr
 85 90 95
 Val Asp Gly Ala Ala Gln Asn Gly Asn Ile Tyr His His Gln Gly Asn
 100 105 110
 Thr Val Ile Asp Pro Gly Met Leu Lys Ser Val Glu Val Thr Lys Gly
 115 120 125
 Ala Ala Asn Ala Ser Ala Gly Pro Gly Ala Ile Ala Gly Val Ile Lys
 130 135 140
 Met Glu Thr Lys Gly Ala Ala Asp Phe Ile Pro Arg Gly Lys Asn Tyr
 145 150 155 160
 Ala Ala Ser Gly Ala Val Ser Phe Tyr Thr Asn Phe Gly Asp Arg Glu
 165 170 175
 Thr Phe Arg Ser Ala Tyr Gln Asn Ala His Phe Asp Ile Ile Ala Tyr
 180 185 190
 Tyr Thr His Gln Asn Ile Phe Tyr Tyr Arg Ser Gly Ala Thr Ala Met
 195 200 205
 Lys Asn Leu Phe Asn Pro Thr Gln Ala Asp Lys Glu Pro Gly Thr Pro

210	215	220
Ser Glu Gln Asn Asn Ala Leu Ile Lys Met Asn Gly Tyr Leu Ser Asp		
225	230	235
Arg Asp Thr Leu Thr Phe Ser Trp Asn Met Thr Arg Asp Asn Ala Thr		240
	245	250
Arg Pro Leu Arg Ser Asn Ala Ile Gly Leu Ala Tyr Pro Cys Glu Ala		255
	260	265
Pro Phe Ser Pro Asp Ser Ser Gln Gly Cys Pro Asn Val Leu Asp Ser		270
	275	280
Phe Thr Arg Tyr Met Tyr His Ser Ile Asn Ser Ala Asn Asn Leu Ser		285
	290	295
Leu Gln Tyr Lys Arg Glu Ala Gly Asn Ser Phe Gly Asp Pro Arg Leu		300
305	310	315
Asp Phe Thr Leu Tyr Thr Ser Ile Arg Asn Ala Gln Phe Asp Pro Leu		320
	325	330
Phe Asp Pro Asn Gly Val Tyr Ala Lys Phe Pro Thr Ser Leu Ala Ser		335
	340	345
Ala Trp Glu Lys Glu Asn Tyr Pro Cys Val Glu Gly Ala Tyr Cys Thr		350
	355	360
Pro Ser Phe Ser Asp Val Asp Lys Pro Ser Ser Gln Pro Arg Asn Leu		365
	370	375
Phe Leu Asn Asn Thr Gly Leu Asn Leu Lys Val Ala His Val Ile Asp		380
385	390	395
Glu Ala Thr Asp Ser Leu Phe Glu Tyr Gly Phe Asn Tyr Gln Asn Leu		400
	405	410
Ser Val Phe Asp Ala Arg Ile Pro Lys Ser Glu Leu Tyr Arg Pro Asn		415
	420	425
Gln Val Tyr Thr Asp Asp Lys Gly Gln Lys Gln Ile Ala Cys Ser Leu		430
	435	440
Val Asn Asn Asn Pro Asn Asp Pro Thr Leu Cys Gln Arg Gly Lys Ala		445
	450	455
Asn Gly Asn Ile Tyr Gly Gly Tyr Val Gln Ala Asn Tyr Ser Pro His		460
465	470	475
Lys Ile Ile Thr Phe Gly Ala Gly Val Arg Trp Asp Ala Tyr Thr Leu		480
	485	490
Tyr Asp Lys Asp Trp Asn His Arg Tyr Thr Gln Gly Phe Ser Pro Ser		495
	500	505
Ala Ala Leu Val Leu Ser Pro Ile Glu Pro Leu Ser Leu Lys Ile Thr		510
	515	520
Tyr Ser Gln Val Thr Arg Gly Val Met Pro Gly Asp Gly Val Tyr Met		525
	530	535
Arg Gln Asn Asp Leu Arg Tyr Ala Lys Asn Ile Lys Pro Glu Val Gly		540
545	550	555
Ser Asn Ala Glu Phe Asn Ile Asp Tyr Ser Ser Gln Tyr Phe Ser Gly		560
	565	570
Arg Ala Ala Ala Phe Tyr Gln Ala Leu Asp Asn Phe Ile Ser Gln Tyr		575
	580	585
Ala Gln Asn Leu Ile Val Thr Asn Leu Ser Gln Ala Ile Arg Ile Tyr		590
	595	600
Gly Tyr Glu Val Gly Gly Thr Phe Arg Tyr Lys Gly Val Ser Leu Asn		605
	610	615
Val Gly Val Ser Arg Thr Trp Pro Thr Thr Arg Gly Tyr Leu Met Ala		620
625	630	635
Asp Ser Tyr Glu Leu Ala Ala Ser Thr Gly Asn Val Phe Ile Ile Lys		640
	645	650
Leu Asp Tyr Thr Ile Pro Lys Thr Gly Ile Asn Leu Ala Trp Leu Ser		655
	660	665
Arg Phe Val Thr Gly Leu Asp Tyr Cys Gly Phe Asp Ile Tyr Leu Pro		670

675	680	685
Asp Tyr Gly Thr Ala Glu Lys	Pro Lys Thr Pro Thr	Asp Leu Ala Lys
690	695	700
Cys Gly Ser Gln Leu Gly Leu	Val His Met His Lys	Pro Gly Tyr Gly
705	710	715
Val Ser Asn Phe Tyr Ile Asn	Trp Ser Pro Lys Thr	Lys Ser Arg Trp
725	730	735
Lys Gly Leu Leu Leu Ser Ala	Val Phe Asn Asn Val Phe	Asn Lys Phe
740	745	750
Tyr Val Asp Gln Thr Ser Pro	Tyr Val Met Ser Pro Asp	Met Pro Gly
755	760	765
Thr Asp Ala Val Lys Arg Ala	Ile Ala Glu Pro Gly Phe	Asn Ala Arg
770	775	780
Phe Glu Val Ala Tyr Lys Trp		
785	790	

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 120...428
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

GTCGGTCGGG TAATGTTCAA ATTCACAAAT GAGTCTGAAG ACAAAGAAGT CTTGATCTAG	60
AAGCCGAAAT TCTCATACCG CACTTAGAAT TGCGTCAAAA ACAAATTGAT GCGCTGTTG	119
GTG CAC GAT ATT ACC AAG CTA TGT TAC ACC AAA CCA CTA GGG TGT GTT	167
Val His Asp Ile Thr Lys Leu Cys Tyr Thr Lys Pro Leu Gly Cys Val	
1 5 10 15	
GTG CTG TTC AGC AAG GAT ACT GAT CTT GTG CCT GTG TTA GAA TCC GCT	215
Val Leu Phe Ser Lys Asp Thr Asp Leu Val Pro Val Leu Glu Ser Ala	
20 25 30	
TGG GAG AAA GGC TTT GAA GTC TTC ATT GCT AAC ATT CAA GAA TGC CCC	263
Trp Glu Lys Gly Phe Glu Val Phe Ile Ala Asn Ile Gln Glu Cys Pro	
35 40 45	
AAT TCT GTC CCT TCA GAC TTG AAG AAG TCT TGC AAT GTG AGG GAA CGC	311
Asn Ser Val Pro Ser Asp Leu Lys Lys Ser Cys Asn Val Arg Glu Arg	
50 55 60	
AGT GTC GCT GAA ATT GTA GAT AAC TTG CCC AAA AAT CAG CAC ACT CCC	359
Ser Val Ala Glu Ile Val Asp Asn Leu Pro Lys Asn Gln His Thr Pro	
65 70 75 80	

AAG AAA AAG AAC TTT TCC ACC AAC GAG CCT TTT AAC AAC CCA TTT AAA	407
Lys Lys Lys Asn Phe Ser Thr Asn Glu Pro Phe Asn Asn Pro Phe Lys	
85 90 95	
 GAC CAA CTC TTT AAG AAG AAC TAACACGATC CCCACACCAA GGGGACAAAA AAGCA	463
Asp Gln Leu Phe Lys Lys Asn	
100	
 CCCATTTTAA AAGG	477

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

[illegible]

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEOUENCE CHARACTERISTICS:

- (A) LENGTH: 685 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 220...624
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

TCTTTTGAAA TTGCCTGATG TGGAAAAAGA AATGCCCAA GAGACGACTC AAAAAAGCTT 60

TTTTTCGCAC AAACACTTTG TTTTGGGGC TTGGGGATCT TTTTTTATGT GGGGGGAGAA	120
NTGGCGATTG GCTCATCTT GGTGCTAAGC TTTGAAAAGC TTTTGAATTT AGACTCTCAA	180
TCAAGCGCGC ATTACTTGGT GTATTATTGG GGAGGCGCG ATG GTG GGC CGT TTC	234
Met Val Gly Arg Phe	
1 5	
TTA GGC AGT GTG TTG ATG AAT AAA ATT GCC CCT AAT AAA TAC TTG GCT	282
Leu Gly Ser Val Leu Met Asn Lys Ile Ala Pro Asn Lys Tyr Leu Ala	
10 15 20	
TTC AAC GCC TTA AGC TCT ATT GTT CTC ATC GCT TTA GCC ATT ATC ATT	330
Phe Asn Ala Leu Ser Ser Ile Val Leu Ile Ala Leu Ala Ile Ile Ile	
25 30 35	
GGA GGC AAG ATC GCT TTA TTC GCT CTG ACT TTT GTG GGC TTT TTC AAC	378
Gly Gly Lys Ile Ala Leu Phe Ala Leu Thr Phe Val Gly Phe Phe Asn	
40 45 50	
TCT ATC ATG TTC CCT ACC ATC TTT TCT TTG GCT ACG CTC AAT TTA GGG	426
Ser Ile Met Phe Pro Thr Ile Phe Ser Leu Ala Thr Leu Asn Leu Gly	
55 60 65	
CAT CTC ACT TCT AAA GCT TCT GGG GTG ATT AGC ATG GCG ATT GTG GGA	474
His Leu Thr Ser Lys Ala Ser Gly Val Ile Ser Met Ala Ile Val Gly	
70 75 80 85	
GGG GCG TTA ATC CCC CCC ATT CAA GGT GCG GTT ACA GAC ATG CTA ACA	522
Gly Ala Leu Ile Pro Pro Ile Gln Gly Ala Val Thr Asp Met Leu Thr	
90 95 100	
GCA ACC GAA TCA AAT TTG CTC TAC GCT TAT GGT GTG CCG TTG TTG TGC	570
Ala Thr Glu Ser Asn Leu Leu Tyr Ala Tyr Gly Val Pro Leu Leu Cys	
105 110 115	
TAT TTT TAT ATT CTC TTC TTT GCG CTT AAA GGG TAT AAG CAA GAA GAA	618
Tyr Phe Tyr Ile Leu Phe Phe Ala Leu Lys Gly Tyr Lys Gln Glu Glu	
120 125 130	
AAC TCC TAAAAAAAGG GGGGGTTTCT TTCTTCTTTC CTTTCTTTTA TCTTGTTTAA AA	676
Asn Ser	
135	
AATCAGTAA	685

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

Met Val Gly Arg Phe Leu Gly Ser Val Leu Met Asn Lys Ile Ala Pro

1	5	10	15
Asn Lys Tyr Leu Ala Phe Asn Ala Leu Ser Ser Ile Val Leu Ile Ala			
	20	25	30
Leu Ala Ile Ile Ile Gly Gly Lys Ile Ala Leu Phe Ala Leu Thr Phe			
	35	40	45
Val Gly Phe Phe Asn Ser Ile Met Phe Pro Thr Ile Phe Ser Leu Ala			
	50	55	60
Thr Leu Asn Leu Gly His Leu Thr Ser Lys Ala Ser Gly Val Ile Ser			
	65	70	75
Met Ala Ile Val Gly Gly Ala Leu Ile Pro Pro Ile Gln Gly Ala Val			
	85	90	95
Thr Asp Met Leu Thr Ala Thr Glu Ser Asn Leu Leu Tyr Ala Tyr Gly			
	100	105	110
Val Pro Leu Leu Cys Tyr Phe Tyr Ile Leu Phe Phe Ala Leu Lys Gly			
	115	120	125
Tyr Lys Gln Glu Glu Asn Ser			
	130	135	

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 58...765
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

ACCGATCACT AAAACCAATG TAACTTACCG CTCTTTACAG CGTAAGTGAG AAAAGGA ATG	60
	Met
	1
CAT TTG AAT ACG GAT TTT AGC CAT ATC ACC GAT ATA GAG GGC ATG CGT	108
His Leu Asn Thr Asp Phe Ser His Ile Thr Asp Ile Glu Gly Met Arg	
	5 10 15
TTT ATC AAT GAA GAA GAC GCT TTG AAC AAA TTG ATT AAT GAA ATC CAC	156
Phe Ile Asn Glu Glu Asp Ala Leu Asn Lys Leu Ile Asn Glu Ile His	
	20 25 30
ACG CGC CAC ATT GAT TTA AAA GAT TCC ATC ATG CTC GCT TTG AGT TTT	204
Thr Arg His Ile Asp Leu Lys Asp Ser Ile Met Leu Ala Leu Ser Phe	
	35 40 45
AAC GCT CTG TAT TTA GCT CAC GCT TTA GCG CAA AAA TTT GGA GCG ACT	252
Asn Ala Leu Tyr Leu Ala His Ala Leu Ala Gln Lys Phe Gly Ala Thr	
	50 55 60 65
TAT GAT ATA CTT TTT TTA GAA CCT ATC CTA GCC CCT TTA AAC TCA AAA	300

Tyr	Asp	Ile	Leu	Phe	Leu	Glu	Pro	Ile	Leu	Ala	Pro	Leu	Asn	Ser	Lys	
				70					75					80		
TGC	GAG	ATC	GCT	TTA	GTG	AGT	GAG	AGC	ATG	GAT	ATA	GTG	ATG	AAT	GAA	348
Cys	Glu	Ile	Ala	Leu	Val	Ser	Glu	Ser	Met	Asp	Ile	Val	Met	Asn	Glu	
			85					90					95			
AGT	TTG	ATC	AAT	TCC	TTT	GAC	ATC	ACT	TTA	GAC	TAT	GTT	TAT	GGG	GAA	396
Ser	Leu	Ile	Asn	Ser	Phe	Asp	Ile	Thr	Leu	Asp	Tyr	Val	Tyr	Gly	Glu	
		100					105					110				
GCC	AAG	CGA	GCT	TAT	GAA	GAA	GAC	ATT	TTG	TCT	CAC	ATC	TAT	CAG	TAT	444
Ala	Lys	Arg	Ala	Tyr	Glu	Glu	Asp	Ile	Leu	Ser	His	Ile	Tyr	Gln	Tyr	
	115					120					125					
CGC	AAA	GGC	AAT	GCG	ATC	AAA	AGC	TTA	AAA	GAT	AAA	AAT	ATT	TTT	ATC	492
Arg	Lys	Gly	Asn	Ala	Ile	Lys	Ser	Leu	Lys	Asp	Lys	Asn	Ile	Phe	Ile	
130					135					140					145	
GTA	GAT	AGG	GGG	ATT	GAA	ACC	GGG	TTT	AGA	GCA	GGG	TTA	GGC	GTG	CAA	540
Val	Asp	Arg	Gly	Ile	Glu	Thr	Gly	Phe	Arg	Ala	Gly	Leu	Gly	Val	Gln	
				150				155						160		
ACT	TGC	TTG	AAA	AAA	GAA	TGC	CAA	GAC	ATT	TAT	ATT	TTA	ACC	CCC	ATT	588
Thr	Cys	Leu	Lys	Lys	Glu	Cys	Gln	Asp	Ile	Tyr	Ile	Leu	Thr	Pro	Ile	
			165					170					175			
GTC	GCG	CAA	AAT	GTC	GCT	CAA	GGC	TTA	GAA	AGT	TTG	TGC	GAT	GGG	GTG	636
Val	Ala	Gln	Asn	Val	Ala	Gln	Gly	Leu	Glu	Ser	Leu	Cys	Asp	Gly	Val	
		180					185					190				
ATT	AGT	GTG	TAT	CGC	CCT	GAA	TGT	TTT	GTC	TCT	GTG	GAG	CAT	CAT	TAT	684
Ile	Ser	Val	Tyr	Arg	Pro	Glu	Cys	Phe	Val	Ser	Val	Glu	His	His	Tyr	
	195					200					205					
AAA	GAA	CTC	AAG	CGA	TTA	AGC	AAT	GAA	GAA	GTT	GAA	AAA	TAC	TTG	GGC	732
Lys	Glu	Leu	Lys	Arg	Leu	Ser	Asn	Glu	Glu	Val	Glu	Lys	Tyr	Leu	Gly	
210					215				220						225	
GCT	AAC	AAC	ATG	CCT	AAT	TTA	AAA	AAG	GAA	CAT	TAAATATGGA	TTTTATCACC				785
Ala	Asn	Asn	Met	Pro	Asn	Leu	Lys	Lys	Glu	His						
				230				235								
ATCAATTCTA	GTAACAAAAC	CGAA														809

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

```

Met His Leu Asn Thr Asp Phe Ser His Ile Thr Asp Ile Glu Gly Met
 1          5          10          15
Arg Phe Ile Asn Glu Glu Asp Ala Leu Asn Lys Leu Ile Asn Glu Ile
          20          25          30
His Thr Arg His Ile Asp Leu Lys Asp Ser Ile Met Leu Ala Leu Ser
          35          40          45
Phe Asn Ala Leu Tyr Leu Ala His Ala Leu Ala Gln Lys Phe Gly Ala
          50          55          60
Thr Tyr Asp Ile Leu Phe Leu Glu Pro Ile Leu Ala Pro Leu Asn Ser
65          70          75          80
Lys Cys Glu Ile Ala Leu Val Ser Glu Ser Met Asp Ile Val Met Asn
          85          90          95
Glu Ser Leu Ile Asn Ser Phe Asp Ile Thr Leu Asp Tyr Val Tyr Gly
          100          105          110
Glu Ala Lys Arg Ala Tyr Glu Glu Asp Ile Leu Ser His Ile Tyr Gln
          115          120          125
Tyr Arg Lys Gly Asn Ala Ile Lys Ser Leu Lys Asp Lys Asn Ile Phe
          130          135          140
Ile Val Asp Arg Gly Ile Glu Thr Gly Phe Arg Ala Gly Leu Gly Val
          145          150          155          160
Gln Thr Cys Leu Lys Lys Glu Cys Gln Asp Ile Tyr Ile Leu Thr Pro
          165          170          175
Ile Val Ala Gln Asn Val Ala Gln Gly Leu Glu Ser Leu Cys Asp Gly
          180          185          190
Val Ile Ser Val Tyr Arg Pro Glu Cys Phe Val Ser Val Glu His His
          195          200          205
Tyr Lys Glu Leu Lys Arg Leu Ser Asn Glu Glu Val Glu Lys Tyr Leu
          210          215          220
Gly Ala Asn Asn Met Pro Asn Leu Lys Lys Glu His
          225          230          235

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(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 70...285
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

```

TAACACAAGC CACCATGAGC ATACTATCGC CATAGTTGGC AATAAAGCAG TGATTCTTAC      60
GGAGCGTTA ATG GCA AGA GAT GAT GTT ATA GAA GTG GAT GGG AAA GTG ATT      111
  Met Ala Arg Asp Asp Val Ile Glu Val Asp Gly Lys Val Ile
    1          5          10

GAG GCG TTG CCT AAC GCT ACT TTT AAG GTG GAG TTA GAC AAT AAG CAT      159
Glu Ala Leu Pro Asn Ala Thr Phe Lys Val Glu Leu Asp Asn Lys His
15          20          25          30

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GTG GTG TTG TGC CGT ATT TCT GGA AAG ATG CGC ATG CAC TAT ATT AGG 207
 Val Val Leu Cys Arg Ile Ser Gly Lys Met Arg Met His Tyr Ile Arg
 35 40 45

ATT GCT TTA GGC GAT AGG GTT AAG CTA GAG CTT ACG CCC TAT AGC TTA 255
 Ile Ala Leu Gly Asp Arg Val Lys Leu Glu Leu Thr Pro Tyr Ser Leu
 50 55 60

GAC AAA GGT CGG ATA ACT TTT AGA TAT AAA TGAATTTAAG GGTTATTTCA ATG 308
 Asp Lys Gly Arg Ile Thr Phe Arg Tyr Lys
 65 70

AAAATATGTT AATATAA 325

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

Met Ala Arg Asp Asp Val Ile Glu Val Asp Gly Lys Val Ile Glu Ala
 1 5 10 15
 Leu Pro Asn Ala Thr Phe Lys Val Glu Leu Asp Asn Lys His Val Val
 20 25 30
 Leu Cys Arg Ile Ser Gly Lys Met Arg Met His Tyr Ile Arg Ile Ala
 35 40 45
 Leu Gly Asp Arg Val Lys Leu Glu Leu Thr Pro Tyr Ser Leu Asp Lys
 50 55 60
 Gly Arg Ile Thr Phe Arg Tyr Lys
 65 70

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 52...309
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

ATCGCTCAAA TTTCAACGAC CATGCTTGTT AAAAAAACT AAAGGAATGT T ATG CAA 57

Met Gln
1

GAT GAA TTA TTT GAA ACC GAA AAA ATC CCC CCA AAA AAC ACT AAA AAT	105
Asp Glu Leu Phe Glu Thr Glu Lys Ile Pro Pro Lys Asn Thr Lys Asn	
5 10 15	
ACT AAA AAC GCC CCT AAA AAA AGT TTT GAA GAG CAT GTT CAT TCC CTA	153
Thr Lys Asn Ala Pro Lys Lys Ser Phe Glu Glu His Val His Ser Leu	
20 25 30	
GAG CGA GCC ATA GAT CGC TTG AAT GAT CCC AAT TTA TCC TTA AAA GAC	201
Glu Arg Ala Ile Asp Arg Leu Asn Asp Pro Asn Leu Ser Leu Lys Asp	
35 40 45 50	
GGG ATG GAT TTG TAT AAA ACG GCC ATG CAA GAG TTG TTT TTG GCT CAA	249
Gly Met Asp Leu Tyr Lys Thr Ala Met Gln Glu Leu Phe Leu Ala Gln	
55 60 65	
AAG CTT TTA GAA AAC GCT TAT TTA GAG CAT GAA AAA CTC CAA ACG CCA	297
Lys Leu Leu Glu Asn Ala Tyr Leu Glu His Glu Lys Leu Gln Thr Pro	
70 75 80	
GAC CAA AAG GCT TAAAGCATGC GAGTGTTCG TTTGCAATTA GAATCTTTTA AAGAA	354
Asp Gln Lys Ala	
85	
AATCTC	360

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

Met Gln Asp Glu Leu Phe Glu Thr Glu Lys Ile Pro Pro Lys Asn Thr	
1 5 10 15	
Lys Asn Thr Lys Asn Ala Pro Lys Lys Ser Phe Glu Glu His Val His	
20 25 30	
Ser Leu Glu Arg Ala Ile Asp Arg Leu Asn Asp Pro Asn Leu Ser Leu	
35 40 45	
Lys Asp Gly Met Asp Leu Tyr Lys Thr Ala Met Gln Glu Leu Phe Leu	
50 55 60	
Ala Gln Lys Leu Leu Glu Asn Ala Tyr Leu Glu His Glu Lys Leu Gln	
65 70 75 80	
Thr Pro Asp Gln Lys Ala	
85	

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 841 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 46...795
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

ATGACTAAAA AGATATAATT CATTCAAAAT TAAACAAGGA TTACA ATG AAA CTG ATT	57
Met Lys Leu Ile	
1	
TCA TGG AAT GTG AAC GGG TTA AGG GCT TGC ATG ACT AAG GGC TTT ATG	105
Ser Trp Asn Val Asn Gly Leu Arg Ala Cys Met Thr Lys Gly Phe Met	
5 10 15 20	
GAT TTT TTC AAT AGC GTT GAT GCG GAT GTT TTT TGC ATT CAA GAA TCT	153
Asp Phe Phe Asn Ser Val Asp Ala Asp Val Phe Cys Ile Gln Glu Ser	
25 30 35	
AAA ATG CAG CAA GAA CAA AAC ACC TTT GAA TTT AAA GGG TAT TTT GAT	201
Lys Met Gln Gln Glu Gln Asn Thr Phe Glu Phe Lys Gly Tyr Phe Asp	
40 45 50	
TTT TGG AAT TGC GCG ATT AAA AAG GGC TAT TCT GGG GTG GTA ACT TTC	249
Phe Trp Asn Cys Ala Ile Lys Lys Gly Tyr Ser Gly Val Val Thr Phe	
55 60 65	
ACT AAA AAA GAG CCT TTA AGC GTG AGC TAT GGT ATT AAT ATG GAA GAG	297
Thr Lys Lys Glu Pro Leu Ser Val Ser Tyr Gly Ile Asn Met Glu Glu	
70 75 80	
CAT GAC AAA GAA GGG CGC GTA ATA ACT TGC GAA TTT GAG TCG TTT TAT	345
His Asp Lys Glu Gly Arg Val Ile Thr Cys Glu Phe Glu Ser Phe Tyr	
85 90 95 100	
TTG GTG AAT GTT TAT ACC CCT AAT TCC CAA CAA GCC CTA TCC AGG CTT	393
Leu Val Asn Val Tyr Thr Pro Asn Ser Gln Gln Ala Leu Ser Arg Leu	
105 110 115	
AGT TAT CGC ATG AGT TGG GAA GTG GAG TTT AAG AAA TTT TTA AAA GCT	441
Ser Tyr Arg Met Ser Trp Glu Val Glu Phe Lys Lys Phe Leu Lys Ala	
120 125 130	
TTA GAG TTG AAA AAA CCG GTC ATT GTG TGT GGG GAT TTG AAT GTG GCT	489
Leu Glu Leu Lys Lys Pro Val Ile Val Cys Gly Asp Leu Asn Val Ala	
135 140 145	
CAC AAT GAA ATT GAT TTA GAA AAC CCC AAA ACC AAC CGA AAA AAT GCC	537
His Asn Glu Ile Asp Leu Glu Asn Pro Lys Thr Asn Arg Lys Asn Ala	

150		155		160	
GGC TTT AGC GAT GAA GAG AGA GAA AAA TTC AGC GAG CTT TTG AAC GCC	585				
Gly Phe Ser Asp Glu Glu Arg Glu Lys Phe Ser Glu Leu Leu Asn Ala					
165		170		175	180
GGT TTT ATT GAC ACT TTC CGT TAT TTT TAC CCT AAC AAA GAA AAG GCT	633				
Gly Phe Ile Asp Thr Phe Arg Tyr Phe Tyr Pro Asn Lys Glu Lys Ala					
		185		190	195
TAC ACC TGG TGG AGT TAC ATG CAA CAA GCA AGG GAT AAA AAC ATT GGT	681				
Tyr Thr Trp Trp Ser Tyr Met Gln Gln Ala Arg Asp Lys Asn Ile Gly					
		200		205	210
TGG CGC ATT GAT TAT TTT TTA TGC TCT AAC CCT TTA AAA ACG CGC TTA	729				
Trp Arg Ile Asp Tyr Phe Leu Cys Ser Asn Pro Leu Lys Thr Arg Leu					
		215		220	225
AAA GAC GCT TTA ATC TAT AAA GAT ATT TTA GGG AGC GAT CAT TGC CCG	777				
Lys Asp Ala Leu Ile Tyr Lys Asp Ile Leu Gly Ser Asp His Cys Pro					
		230		235	240
GTA GGG TTG GAA TTA GTT TAAAGGTAGA AAGTGTGCGA AATAAAGACA GAAAAAAG	833				
Val Gly Leu Glu Leu Val					
245		250			
CCTTACAA	841				

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Met	Lys	Leu	Ile	Ser	Trp	Asn	Val	Asn	Gly	Leu	Arg	Ala	Cys	Met	Thr
1				5					10					15	
Lys	Gly	Phe	Met	Asp	Phe	Phe	Asn	Ser	Val	Asp	Ala	Asp	Val	Phe	Cys
			20					25					30		
Ile	Gln	Glu	Ser	Lys	Met	Gln	Gln	Glu	Gln	Asn	Thr	Phe	Glu	Phe	Lys
		35					40					45			
Gly	Tyr	Phe	Asp	Phe	Trp	Asn	Cys	Ala	Ile	Lys	Lys	Gly	Tyr	Ser	Gly
	50					55				60					
Val	Val	Thr	Phe	Thr	Lys	Lys	Glu	Pro	Leu	Ser	Val	Ser	Tyr	Gly	Ile
65					70				75					80	
Asn	Met	Glu	Glu	His	Asp	Lys	Glu	Gly	Arg	Val	Ile	Thr	Cys	Glu	Phe
				85					90				95		
Glu	Ser	Phe	Tyr	Leu	Val	Asn	Val	Tyr	Thr	Pro	Asn	Ser	Gln	Gln	Ala
			100					105					110		
Leu	Ser	Arg	Leu	Ser	Tyr	Arg	Met	Ser	Trp	Glu	Val	Glu	Phe	Lys	Lys
		115					120					125			
Phe	Leu	Lys	Ala	Leu	Glu	Leu	Lys	Lys	Pro	Val	Ile	Val	Cys	Gly	Asp

130	135	140
Leu Asn Val Ala His Asn Glu Ile Asp Leu Glu Asn Pro Lys Thr Asn		
145	150	155
Arg Lys Asn Ala Gly Phe Ser Asp Glu Glu Arg Glu Lys Phe Ser Glu		160
	165	170
Leu Leu Asn Ala Gly Phe Ile Asp Thr Phe Arg Tyr Phe Tyr Pro Asn		175
	180	185
Lys Glu Lys Ala Tyr Thr Trp Trp Ser Tyr Met Gln Gln Ala Arg Asp		190
	195	200
Lys Asn Ile Gly Trp Arg Ile Asp Tyr Phe Leu Cys Ser Asn Pro Leu		205
	210	215
Lys Thr Arg Leu Lys Asp Ala Leu Ile Tyr Lys Asp Ile Leu Gly Ser		220
225	230	235
Asp His Cys Pro Val Gly Leu Glu Leu Val		240
	245	250

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 62...571
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

AGAATGCGAG CGTTAAAAAA GAAATTTATG TGCCTAATAA GCTTGTTAAT TTTGTTATCG	60
C ATG AGG GCT TTA CTT TTT TTT ATT TTG TTA CTT TGG TTC AAG GGT TGT	109
Met Arg Ala Leu Leu Phe Phe Ile Leu Leu Leu Trp Phe Lys Gly Cys	
1 5 10 15	
GGG TAT AAG CCT ATT GCA GCT TAC GCT CAA AAC GCT TTA GGC GAT AGC	157
Gly Tyr Lys Pro Ile Ala Ala Tyr Ala Gln Asn Ala Leu Gly Asp Ser	
20 25 30	
GTA TAC GTG AAA CTC ATT GTG AAT TTG CCT AAC CCT GAA AAC TCT GTA	205
Val Tyr Val Lys Leu Ile Val Asn Leu Pro Asn Pro Glu Asn Ser Val	
35 40 45	
GAG TTT AAG GAT TTG ATG AAT CGT TTA GTC GTG CAA CGC TTC CAA AGC	253
Glu Phe Lys Asp Leu Met Asn Arg Leu Val Val Gln Arg Phe Gln Ser	
50 55 60	
CGC TTA GCG AGT GAA AAG GAT GCG GAT TCT ATC ATT ATT ATA GAA ATC	301
Arg Leu Ala Ser Glu Lys Asp Ala Asp Ser Ile Ile Ile Ile Glu Ile	
65 70 75 80	
ACG AAT GTA ACC GAT ACG AGT ATC ACG CAA AAT AAA GAA GGC TTC ACG	349
Thr Asn Val Thr Asp Thr Ser Ile Thr Gln Asn Lys Glu Gly Phe Thr	

85													90				95				
ACT	TTC	TAT	CGC	GCA	ACC	GTG	TCT	GTG	AAT	TAC	ACC	TAC	GAT	AAT	AAA	397					
Thr	Phe	Tyr	Arg	Ala	Thr	Val	Ser	Val	Asn	Tyr	Thr	Tyr	Asp	Asn	Lys						
			100							105				110							
AGA	GGC	ACA	CAA	AAG	ACT	TTT	CAA	GAT	AGC	GGG	TAT	TAC	AAT	TAC	GCT	445					
Arg	Gly	Thr	Gln	Lys	Thr	Phe	Gln	Asp	Ser	Gly	Tyr	Tyr	Asn	Tyr	Ala						
			115							120				125							
GTG	AAT	TTG	CAA	GAC	CCC	CTT	AAT	ACC	TAC	CAG	AAC	CGC	TAT	TAT	GCT	493					
Val	Asn	Leu	Gln	Asp	Pro	Leu	Asn	Thr	Tyr	Gln	Asn	Arg	Tyr	Tyr	Ala						
			130							135				140							
ATC	AAT	CAG	GCT	GTG	GAA	CAG	ACT	TTG	ACT	AAA	TTT	GTG	GCT	CAA	ATC	541					
Ile	Asn	Gln	Ala	Val	Glu	Gln	Thr	Leu	Thr	Lys	Phe	Val	Ala	Gln	Ile						
			145							150				160							
GCT	TAT	GAG	GGG	AAA	TTC	AAT	AAT	GAA	AAA	TAGCCCTTTG	AATGGATTGA	ATG				594					
Ala	Tyr	Glu	Gly	Lys	Phe	Asn	Asn	Glu	Lys												
						165				170											
GACTAAAGGC GTTTTTAGAA ACAA															618						

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

Met	Arg	Ala	Leu	Leu	Phe	Phe	Ile	Leu	Leu	Leu	Trp	Phe	Lys	Gly	Cys
1				5					10					15	
Gly	Tyr	Lys	Pro	Ile	Ala	Ala	Tyr	Ala	Gln	Asn	Ala	Leu	Gly	Asp	Ser
			20					25					30		
Val	Tyr	Val	Lys	Leu	Ile	Val	Asn	Leu	Pro	Asn	Pro	Glu	Asn	Ser	Val
		35					40					45			
Glu	Phe	Lys	Asp	Leu	Met	Asn	Arg	Leu	Val	Val	Gln	Arg	Phe	Gln	Ser
	50					55					60				
Arg	Leu	Ala	Ser	Glu	Lys	Asp	Ala	Asp	Ser	Ile	Ile	Ile	Ile	Glu	Ile
65					70				75					80	
Thr	Asn	Val	Thr	Asp	Thr	Ser	Ile	Thr	Gln	Asn	Lys	Glu	Gly	Phe	Thr
			85					90						95	
Thr	Phe	Tyr	Arg	Ala	Thr	Val	Ser	Val	Asn	Tyr	Thr	Tyr	Asp	Asn	Lys
			100					105					110		
Arg	Gly	Thr	Gln	Lys	Thr	Phe	Gln	Asp	Ser	Gly	Tyr	Tyr	Asn	Tyr	Ala
		115					120					125			
Val	Asn	Leu	Gln	Asp	Pro	Leu	Asn	Thr	Tyr	Gln	Asn	Arg	Tyr	Tyr	Ala
	130					135					140				
Ile	Asn	Gln	Ala	Val	Glu	Gln	Thr	Leu	Thr	Lys	Phe	Val	Ala	Gln	Ile
145					150					155					160
Ala	Tyr	Glu	Gly	Lys	Phe	Asn	Asn	Glu	Lys						

165

170

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 61...1224
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

AATACCCATA AAATACCTTA AGAGAACGCC TATTCAAAAA CCAAAAATAA GGAAATCCTA	60
ATG ACT ACA GAC AGA AAT TTG TTT TTT TGC GCT TCG CTA TTG ATT TTT	108
Met Thr Thr Asp Arg Asn Leu Phe Phe Cys Ala Ser Leu Leu Ile Phe	
1 5 10 15	
TTG GGG GTA TTG ATG AGC TAT TCG CTC TCA ACT TAC ACC ACA GTG GTG	156
Leu Gly Val Leu Met Ser Tyr Ser Leu Ser Thr Tyr Thr Thr Val Val	
20 25 30	
CTG TAT CAT TAT GGG GAG TTC CAT TTT TTC ATA CGC CAG CTT GTG AGC	204
Leu Tyr His Tyr Gly Glu Phe His Phe Phe Ile Arg Gln Leu Val Ser	
35 40 45	
GCG ATC ATA GGG ATT GTT ATC ATG TGG GGG TTG TCT AGG GTT GAT CCT	252
Ala Ile Ile Gly Ile Val Ile Met Trp Gly Leu Ser Arg Val Asp Pro	
50 55 60	
AGC AAG TGG TTT AGC CGT TTG GGG TTT TTT CTT CTT TTT GTC CCA CCA	300
Ser Lys Trp Phe Ser Arg Leu Gly Phe Phe Leu Leu Phe Val Pro Pro	
65 70 75 80	
TTA CTC ATT ATT GGC ATG TTT TTT TTG CCA GAA AGC CTT TCT AGC AGT	348
Leu Leu Ile Ile Gly Met Phe Phe Leu Pro Glu Ser Leu Ser Ser Ser	
85 90 95	
GCT GGG GGG GCG AAG CGA TGG ATT CGT TTG GGG TTT TTT TCT CTA GCG	396
Ala Gly Gly Ala Lys Arg Trp Ile Arg Leu Gly Phe Phe Ser Leu Ala	
100 105 110	
CCT TTG GAG TTT TTG AAG ATT GGT TTC ACC TTT TTT CTT GCG TGG AGT	444
Pro Leu Glu Phe Leu Lys Ile Gly Phe Thr Phe Phe Leu Ala Trp Ser	
115 120 125	
TTG TCT CGC ACT TTT GTG GCA AAA GAA AAG GCT AAT GTT AAA GAA GAA	492
Leu Ser Arg Thr Phe Val Ala Lys Glu Lys Ala Asn Val Lys Glu Glu	
130 135 140	

CTC	ATC	ACT	TTT	GTG	CCT	TAT	TCA	GTG	GTG	TTT	GTA	GCC	TTA	GCG	ATT	540
Leu	Ile	Thr	Phe	Val	Pro	Tyr	Ser	Val	Val	Phe	Val	Ala	Leu	Ala	Ile	
145					150					155					160	
GGG	GTG	GGG	GTT	TTG	CAA	AAC	GAT	TTG	GGG	CAG	ATT	GTT	CTT	TTG	GGG	588
Gly	Val	Gly	Val	Leu	Gln	Asn	Asp	Leu	Gly	Gln	Ile	Val	Leu	Leu	Gly	
				165					170						175	
GCG	GTT	TTA	GCG	GTG	TTG	TTG	GTT	TTT	TCT	GGG	GGG	AGC	GTG	CAT	TTG	636
Ala	Val	Leu	Ala	Val	Leu	Leu	Val	Phe	Ser	Gly	Gly	Ser	Val	His	Leu	
			180					185					190			
TTT	GGC	TTG	ATT	ATT	TCA	GGG	GCG	TTT	GCG	ATC	AGC	GTT	TTA	GCG	ATT	684
Phe	Gly	Leu	Ile	Ile	Ser	Gly	Ala	Phe	Ala	Ile	Ser	Val	Leu	Ala	Ile	
		195					200					205				
GTT	ACA	AGC	GAG	CAT	AGG	ATT	TTG	CGC	CTG	AAA	TTG	TGG	TGG	TCT	AAT	732
Val	Thr	Ser	Glu	His	Arg	Ile	Leu	Arg	Leu	Lys	Leu	Trp	Trp	Ser	Asn	
	210					215					220					
TTG	CAA	AAT	TCG	CTT	TTC	ACG	CTC	TTG	CCG	GAT	AGA	TTA	GCG	AAC	GCT	780
Leu	Gln	Asn	Ser	Leu	Phe	Thr	Leu	Leu	Pro	Asp	Arg	Leu	Ala	Asn	Ala	
225					230					235					240	
CTT	AGA	ATA	AGC	GAC	TTG	CCC	GAA	TCC	TAT	CAG	GTC	TTT	CAT	GCA	GGC	828
Leu	Arg	Ile	Ser	Asp	Leu	Pro	Glu	Ser	Tyr	Gln	Val	Phe	His	Ala	Gly	
				245					250					255		
AAT	GCC	ATG	CAT	AAT	GGG	GGG	TTG	TTT	GGG	CAA	GGG	CTT	GGG	CTT	GGG	876
Asn	Ala	Met	His	Asn	Gly	Gly	Leu	Phe	Gly	Gln	Gly	Leu	Gly	Leu	Gly	
			260					265					270			
CAA	ATC	AAG	CTT	GGG	TTT	TTG	AGC	GAA	GTG	CAT	ACG	GAC	ATG	GTC	TTA	924
Gln	Ile	Lys	Leu	Gly	Phe	Leu	Ser	Glu	Val	His	Thr	Asp	Met	Val	Leu	
		275					280					285				
GCT	GGG	ATC	GCC	GAA	GAA	TGG	GGG	TTT	TTG	GGG	CTA	TGC	GTT	TGT	TTT	972
Ala	Gly	Ile	Ala	Glu	Glu	Trp	Gly	Phe	Leu	Gly	Leu	Cys	Val	Cys	Phe	
	290					295					300					
ATT	TTG	TTT	TCT	GTT	TTG	ATT	GTT	TTG	ATT	TTT	AGG	ATC	GCT	AAC	CGC	1020
Ile	Leu	Phe	Ser	Val	Leu	Ile	Val	Leu	Ile	Phe	Arg	Ile	Ala	Asn	Arg	
305					310					315					320	
TTG	AAA	GAG	CCA	AAA	TAT	TCG	CTA	TTT	TGC	GTG	GGC	GTG	GTG	CTG	CTT	1068
Leu	Lys	Glu	Pro	Lys	Tyr	Ser	Leu	Phe	Cys	Val	Gly	Val	Val	Leu	Leu	
				325					330					335		
ATT	AGT	TTT	TCT	TTG	GTG	ATC	AAC	GCC	TTT	GGG	GTG	GGC	GGG	ATT	CTT	1116
Ile	Ser	Phe	Ser	Leu	Val	Ile	Asn	Ala	Phe	Gly	Val	Gly	Gly	Ile	Leu	
			340					345					350			
CCG	GTT	AAA	GGT	CTA	GCG	GTG	CCG	TTT	TTG	AGC	TAT	GGA	GGG	AGT	TCG	1164
Pro	Val	Lys	Gly	Leu	Ala	Val	Pro	Phe	Leu	Ser	Tyr	Gly	Gly	Ser	Ser	
		355					360					365				
CTT	CTA	GCG	AAT	TGT	ATC	GCT	ATA	GGG	CTT	GTT	CTA	AGC	CTA	GCG	CGA	1212
Leu	Leu	Ala	Asn	Cys	Ile	Ala	Ile	Gly	Leu	Val	Leu	Ser	Leu	Ala	Arg	

290		295		300
Ile Leu Phe Ser Val	Leu Ile Val Leu Ile Phe Arg	Ile Ala Asn Arg		
305		310		320
Leu Lys Glu Pro Lys Tyr Ser Leu Phe Cys Val Gly Val Val Leu Leu				
		325		335
Ile Ser Phe Ser Leu Val Ile Asn Ala Phe Gly Val Gly Gly Ile Leu				
		340		350
Pro Val Lys Gly Leu Ala Val Pro Phe Leu Ser Tyr Gly Gly Ser Ser				
		355		365
Leu Leu Ala Asn Cys Ile Ala Ile Gly Leu Val Leu Ser Leu Ala Arg				
		370		380
Tyr Thr Lys Gly				
385				

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 961 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...908
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

AGAACAGTAT CTATTTTGTG TCGGTTGTA TATTTAATTA GGAGTTTGGT GTG AAA	56
Val Lys	
1	
CGG ATT TTA TTT TTT TTA GTA GCT ACG ACT TTT TTG TTG AGA GCA GAA	104
Arg Ile Leu Phe Phe Leu Val Ala Thr Thr Phe Leu Leu Arg Ala Glu	
5 10 15	
ACG GAT TCT GCC ACT ATT AAC ACT ACA GTT GAT CCC AAT GTT ATG TTT	152
Thr Asp Ser Ala Thr Ile Asn Thr Thr Val Asp Pro Asn Val Met Phe	
20 25 30	
TCT GAA AGC TCC ACA GGG AAT GTG AAA AAA GAC CGC AAG AGG GTT TTA	200
Ser Glu Ser Ser Thr Gly Asn Val Lys Lys Asp Arg Lys Arg Val Leu	
35 40 45 50	
AAG AGC ATG GTT AAT TTG GAA AAA GAG CGC GTG AAG AAT TTT AAC CGG	248
Lys Ser Met Val Asn Leu Glu Lys Glu Arg Val Lys Asn Phe Asn Arg	
55 60 65	
TAT TCT GAA ACC AAG ATG AGT AAG GGC GAC TTA TCC GCT TTT GGA GCT	296
Tyr Ser Glu Thr Lys Met Ser Lys Gly Asp Leu Ser Ala Phe Gly Ala	
70 75 80	
TTC TTT AAG GGG AGT TTG GAA AGT TGT GTG GAT CAA AAG ATT TGT TAT	344

Phe	Phe	Lys	Gly	Ser	Leu	Glu	Ser	Cys	Val	Asp	Gln	Lys	Ile	Cys	Tyr	
	85						90					95				
TAT	GAG	CAT	AAA	GAT	GGC	AAG	GTT	TCT	TTT	GTG	GTG	AAT	GAC	AGG	GAG	392
Tyr	Glu	His	Lys	Asp	Gly	Lys	Val	Ser	Phe	Val	Val	Asn	Asp	Arg	Glu	
	100					105					110					
AAG	TTT	TAT	AAA	CAT	GTG	CTT	AAA	GAC	TTA	GGG	ACA	GAG	CTT	TCG	CTC	440
Lys	Phe	Tyr	Lys	His	Val	Leu	Lys	Asp	Leu	Gly	Thr	Glu	Leu	Ser	Leu	
	115				120					125					130	
CCT	TTG	TTT	AAC	TGG	CTT	TAC	AAA	GGC	TCG	GAT	TTT	GGG	GCT	TTG	CAT	488
Pro	Leu	Phe	Asn	Trp	Leu	Tyr	Lys	Gly	Ser	Asp	Phe	Gly	Ala	Leu	His	
			135						140					145		
GAG	CAG	TTT	GGG	GAT	ATG	TAT	GAT	GGG	TAT	ATC	AAA	TAC	TTG	ATC	AGT	536
Glu	Gln	Phe	Gly	Asp	Met	Tyr	Asp	Gly	Tyr	Ile	Lys	Tyr	Leu	Ile	Ser	
			150					155					160			
ATG	GTT	AGA	ATA	AGC	CAA	AAA	GAA	AAG	GCT	AGA	AAA	GTG	GAT	GCA	ATC	584
Met	Val	Arg	Ile	Ser	Gln	Lys	Glu	Lys	Ala	Arg	Lys	Val	Asp	Ala	Ile	
		165					170					175				
GTT	CTT	AAG	AAA	ATG	GAA	GAA	CAA	GCT	GAG	AAA	GAC	ACT	AAG	GCA	GCG	632
Val	Leu	Lys	Lys	Met	Glu	Glu	Gln	Ala	Glu	Lys	Asp	Thr	Lys	Ala	Ala	
	180					185					190					
TTT	CAA	AAG	AGG	AGC	AGT	GGG	GAG	CTT	GAA	AGC	CAT	ACT	GAT	AGC	CCT	680
Phe	Gln	Lys	Arg	Ser	Ser	Gly	Glu	Leu	Glu	Ser	His	Thr	Asp	Ser	Pro	
	195				200					205					210	
GAA	TTT	ATA	AGC	TCT	TCT	AAG	AGG	ACA	CAG	AAC	GCT	TCT	AAT	TCG	GAT	728
Glu	Phe	Ile	Ser	Ser	Ser	Lys	Arg	Thr	Gln	Asn	Ala	Ser	Asn	Ser	Asp	
				215					220					225		
CTC	AAT	TCT	ATG	ACC	AAT	GCT	AAC	GCG	CTC	AAA	GAA	ACA	GCT	TCA	AAA	776
Leu	Asn	Ser	Met	Thr	Asn	Ala	Asn	Ala	Leu	Lys	Glu	Thr	Ala	Ser	Lys	
			230					235					240			
GAG	CCA	GAG	GCT	TCT	TCA	AAA	AAA	GAG	AAA	AAG	TCT	AAG	AAA	AAA	CGT	824
Glu	Pro	Glu	Ala	Ser	Ser	Lys	Lys	Glu	Lys	Lys	Ser	Lys	Lys	Lys	Arg	
		245					250					255				
CGC	CTT	TCA	AAG	AAA	GAA	AAA	CAA	CAA	CAA	GCC	TTG	CAA	CAA	GAG	TTT	872
Arg	Leu	Ser	Lys	Lys	Glu	Lys	Gln	Gln	Gln	Ala	Leu	Gln	Gln	Glu	Phe	
	260					265					270					
GAA	AAA	CAA	ATT	AGC	GAC	TCT	AGT	AAG	TCT	GAA	AAA	TAGTAATAAT AGTTAA				924
Glu	Lys	Gln	Ile	Ser	Asp	Ser	Ser	Lys	Ser	Glu	Lys					
	275				280					285						
GCTTACCTTT TTAGGGGGCT TTCAATAAAT CTCTTAA																961

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 286 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

Val	Lys	Arg	Ile	Leu	Phe	Phe	Leu	Val	Ala	Thr	Thr	Phe	Leu	Leu	Arg	1	5	10	15
Ala	Glu	Thr	Asp	Ser	Ala	Thr	Ile	Asn	Thr	Thr	Val	Asp	Pro	Asn	Val	20	25	30	
Met	Phe	Ser	Glu	Ser	Ser	Thr	Gly	Asn	Val	Lys	Lys	Asp	Arg	Lys	Arg	35	40	45	
Val	Leu	Lys	Ser	Met	Val	Asn	Leu	Glu	Lys	Glu	Arg	Val	Lys	Asn	Phe	50	55	60	
Asn	Arg	Tyr	Ser	Glu	Thr	Lys	Met	Ser	Lys	Gly	Asp	Leu	Ser	Ala	Phe	65	70	75	80
Gly	Ala	Phe	Phe	Lys	Gly	Ser	Leu	Glu	Ser	Cys	Val	Asp	Gln	Lys	Ile	85	90	95	
Cys	Tyr	Tyr	Glu	His	Lys	Asp	Gly	Lys	Val	Ser	Phe	Val	Val	Asn	Asp	100	105	110	
Arg	Glu	Lys	Phe	Tyr	Lys	His	Val	Leu	Lys	Asp	Leu	Gly	Thr	Glu	Leu	115	120	125	
Ser	Leu	Pro	Leu	Phe	Asn	Trp	Leu	Tyr	Lys	Gly	Ser	Asp	Phe	Gly	Ala	130	135	140	
Leu	His	Glu	Gln	Phe	Gly	Asp	Met	Tyr	Asp	Gly	Tyr	Ile	Lys	Tyr	Leu	145	150	155	160
Ile	Ser	Met	Val	Arg	Ile	Ser	Gln	Lys	Glu	Lys	Ala	Arg	Lys	Val	Asp	165	170	175	
Ala	Ile	Val	Leu	Lys	Lys	Met	Glu	Glu	Gln	Ala	Glu	Lys	Asp	Thr	Lys	180	185	190	
Ala	Ala	Phe	Gln	Lys	Arg	Ser	Ser	Gly	Glu	Leu	Glu	Ser	His	Thr	Asp	195	200	205	
Ser	Pro	Glu	Phe	Ile	Ser	Ser	Ser	Lys	Arg	Thr	Gln	Asn	Ala	Ser	Asn	210	215	220	
Ser	Asp	Leu	Asn	Ser	Met	Thr	Asn	Ala	Asn	Ala	Leu	Lys	Glu	Thr	Ala	225	230	235	240
Ser	Lys	Glu	Pro	Glu	Ala	Ser	Ser	Lys	Lys	Glu	Lys	Lys	Ser	Lys	Lys	245	250	255	
Lys	Arg	Arg	Leu	Ser	Lys	Lys	Glu	Lys	Gln	Gln	Gln	Ala	Leu	Gln	Gln	260	265	270	
Glu	Phe	Glu	Lys	Gln	Ile	Ser	Asp	Ser	Ser	Lys	Ser	Glu	Lys			275	280	285	

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1555 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...1499

ATG CGC AAA GAA TTT GAA AGC TTT AAA ATG GGG ATT AGT GGG GTT AAT	680
Met Arg Lys Glu Phe Glu Ser Phe Lys Met Gly Ile Ser Gly Val Asn	
195 200 205 210	
TTT GCT ATC GCT AAC GAA GGA GCG ATC TGG TTA GTG GAA AAT GAA GGC	728
Phe Ala Ile Ala Asn Glu Gly Ala Ile Trp Leu Val Glu Asn Glu Gly	
215 220 225	
AAT GGC AGA ATG AGC ACC ACT GCA TGC GAT GTG CAT GTC GCA ATT TGT	776
Asn Gly Arg Met Ser Thr Thr Ala Cys Asp Val His Val Ala Ile Cys	
230 235 240	
GGG ATT GAA AAA TTA GTA GAA AGC TTT GAT GAT GCG GCG ATT TTA AAC	824
Gly Ile Glu Lys Leu Val Glu Ser Phe Asp Asp Ala Ala Ile Leu Asn	
245 250 255	
AAT TTG CTC GCC CCA AGC GCT GTG GGT GTG CCT ATC ACT TGC TAT CAA	872
Asn Leu Leu Ala Pro Ser Ala Val Gly Val Pro Ile Thr Cys Tyr Gln	
260 265 270	
AAC ATT ATC ACA GGC CCT AGA AAA GAG GGC GAT TTA GAC GGC CCT AAA	920
Asn Ile Ile Thr Gly Pro Arg Lys Glu Gly Asp Leu Asp Gly Pro Lys	
275 280 285 290	
GAA GCC CAC ATC ATT TTA TTA GAC AAC AAC CGC TCT AAT ATT TTG GCT	968
Glu Ala His Ile Ile Leu Leu Asp Asn Asn Arg Ser Asn Ile Leu Ala	
295 300 305	
GAT GAA AAG TAT TAT CGC GCT CTT TCA TGC ATC CGT TGC GGG ACT TGT	1016
Asp Glu Lys Tyr Tyr Arg Ala Leu Ser Cys Ile Arg Cys Gly Thr Cys	
310 315 320	
TTG AAC CAC TGC CCT GTG TAT GAT AAA ATC GGT GGG CAT GCC TAT CTT	1064
Leu Asn His Cys Pro Val Tyr Asp Lys Ile Gly Gly His Ala Tyr Leu	
325 330 335	
TCT ACT TAT CCT GGC CCT ATA GGC GTG GTG GTA TCC CCC CAA CTC TTT	1112
Ser Thr Tyr Pro Gly Pro Ile Gly Val Val Val Ser Pro Gln Leu Phe	
340 345 350	
GGC TTG AAT AAT TAC GGG CAT ATC CCT AAT TTG TGC AGT CTT TGC GGG	1160
Gly Leu Asn Asn Tyr Gly His Ile Pro Asn Leu Cys Ser Leu Cys Gly	
355 360 365 370	
CGT TGC ACT GAA GTA TGC CCC GTA GAA ATC CCT TTA GCC GAA CTC ATT	1208
Arg Cys Thr Glu Val Cys Pro Val Glu Ile Pro Leu Ala Glu Leu Ile	
375 380 385	
AGG GAT TTA CGA TCC GAT AAA GTG GGC GAG GGC AGG GGT GTA ATT AAG	1256
Arg Asp Leu Arg Ser Asp Lys Val Gly Glu Gly Arg Gly Val Ile Lys	
390 395 400	
GGG GCT AAA AGC ACC CAA CAC AGC GGG ATG GAA AAA TTC TCT ATG AAA	1304
Gly Ala Lys Ser Thr Gln His Ser Gly Met Glu Lys Phe Ser Met Lys	
405 410 415	
ATG TTT GCC AAA ATG GCA AGC GAT GGG GCT AAG TGG CGT TTC CAA TTG	1352
Met Phe Ala Lys Met Ala Ser Asp Gly Ala Lys Trp Arg Phe Gln Leu	

420	425	430	
AAA ATG GCT CAA TTT TTC TCG CCT TTA GGC AAG CTT TTA GCT CCC ATA			1400
Lys Met Ala Gln Phe Phe Ser Pro Leu Gly Lys Leu Leu Ala Pro Ile			
435	440	445	450
CTG CCT TTA GTC AAA GAG TGG GCG AGC GTT AGG ACC TTA CCC AAT ATG			1448
Leu Pro Leu Val Lys Glu Trp Ala Ser Val Arg Thr Leu Pro Asn Met			
	455	460	465
GAC ACG AGC TTG CAT GCA AAA GTC CAG CAC TTA GAA GGG GTG ATT TAT			1496
Asp Thr Ser Leu His Ala Lys Val Gln His Leu Glu Gly Val Ile Tyr			
	470	475	480
GAG TAAAGAGCTT ATTTTAAAGC GCATTAAAGA AGCCAGAGCC AAGCATGCCA TTCAGG			1555
Glu			

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

Met	Ile	Met	Glu	Lys	Tyr	His	Ser	Asp	Gln	Glu	Tyr	Glu	Glu	Ile	Ile
1				5					10					15	
Thr	Asp	Gln	Leu	Gly	Asp	Met	Gln	Leu	Arg	Glu	Asn	Leu	Arg	Ser	Ala
		20						25					30		
Met	Asp	Thr	Leu	Arg	Ala	Asn	Arg	Lys	Asn	Leu	Leu	Lys	Asn	Arg	Tyr
		35					40					45			
Ser	Glu	Trp	Glu	Asn	Leu	Arg	Glu	Leu	Gly	Lys	Glu	Val	Lys	Leu	Lys
	50					55				60					
Ile	Leu	Ser	Arg	Leu	Asp	Glu	Tyr	Leu	Glu	Leu	Phe	Glu	Lys	Asn	Ala
65				70					75					80	
Thr	Gln	Asn	Gly	Phe	Lys	Ile	His	Tyr	Ala	Lys	Asp	Gly	Asp	Glu	Ala
			85					90					95		
Asn	Glu	Ile	Ile	Tyr	Asn	Leu	Ala	Lys	Glu	Lys	Asn	Ile	Lys	Arg	Ile
		100						105					110		
Leu	Lys	Gln	Lys	Ser	Met	Ala	Ser	Glu	Glu	Ile	Gly	Leu	Asn	His	Tyr
		115					120					125			
Leu	Lys	Glu	Lys	Gly	Ile	Gln	Ala	Gln	Glu	Thr	Asp	Leu	Gly	Glu	Leu
	130					135					140				
Ile	Ile	Gln	Leu	Ile	Asn	Glu	His	Pro	Val	His	Ile	Val	Val	Pro	Ala
145				150						155				160	
Ile	His	Lys	Asn	Arg	Lys	Gln	Ile	Gly	Lys	Ile	Phe	Glu	Glu	Lys	Leu
			165					170						175	
Asn	Ala	Ala	Tyr	Glu	Glu	Glu	Pro	Glu	Lys	Leu	Asn	Ala	Ile	Ala	Arg
		180					185						190		
Lys	His	Met	Arg	Lys	Glu	Phe	Glu	Ser	Phe	Lys	Met	Gly	Ile	Ser	Gly
	195						200					205			
Val	Asn	Phe	Ala	Ile	Ala	Asn	Glu	Gly	Ala	Ile	Trp	Leu	Val	Glu	Asn

210		215		220
Glu Gly Asn Gly Arg Met Ser Thr Thr Ala Cys Asp Val His Val Ala				
225		230		235
Ile Cys Gly Ile Glu Lys Leu Val Glu Ser Phe Asp Asp Ala Ala Ile				240
	245		250	255
Leu Asn Asn Leu Leu Ala Pro Ser Ala Val Gly Val Pro Ile Thr Cys				
	260		265	270
Tyr Gln Asn Ile Ile Thr Gly Pro Arg Lys Glu Gly Asp Leu Asp Gly				
	275		280	285
Pro Lys Glu Ala His Ile Ile Leu Leu Asp Asn Asn Arg Ser Asn Ile				
	290		295	300
Leu Ala Asp Glu Lys Tyr Tyr Arg Ala Leu Ser Cys Ile Arg Cys Gly				
305		310		315
Thr Cys Leu Asn His Cys Pro Val Tyr Asp Lys Ile Gly Gly His Ala				320
	325		330	335
Tyr Leu Ser Thr Tyr Pro Gly Pro Ile Gly Val Val Val Ser Pro Gln				
	340		345	350
Leu Phe Gly Leu Asn Asn Tyr Gly His Ile Pro Asn Leu Cys Ser Leu				
	355		360	365
Cys Gly Arg Cys Thr Glu Val Cys Pro Val Glu Ile Pro Leu Ala Glu				
	370		375	380
Leu Ile Arg Asp Leu Arg Ser Asp Lys Val Gly Glu Gly Arg Gly Val				
385		390		395
Ile Lys Gly Ala Lys Ser Thr Gln His Ser Gly Met Glu Lys Phe Ser				
	405		410	415
Met Lys Met Phe Ala Lys Met Ala Ser Asp Gly Ala Lys Trp Arg Phe				
	420		425	430
Gln Leu Lys Met Ala Gln Phe Phe Ser Pro Leu Gly Lys Leu Leu Ala				
	435		440	445
Pro Ile Leu Pro Leu Val Lys Glu Trp Ala Ser Val Arg Thr Leu Pro				
	450		455	460
Asn Met Asp Thr Ser Leu His Ala Lys Val Gln His Leu Glu Gly Val				
465		470		475
Ile Tyr Glu				480

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 294...1577
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

GTATCGCCAC	TTTGCGTAAC	AGGATGTTGA	AAGTGGGTAA	AAGCCGCTAA	TTTCTTTTTA	60
GTGGGTCGTT	TTTGAAAATC	TTTTAGTCT	TTTAAAGCGT	CTTTTTTTTT	AATGGGTGTT	120
TTGGGTTAGT	CTATAAGACT	CCCATTTCAA	GCTCTCCTAT	CTCTTATGAT	CCCTACACTA	180

CCCCATTGG	GAGCTTG	TAT	GCTGAAAAAT	TAAAAGAAAA	CCCTAACCAT	AGCGCGGCCA	240									
TTCTTTTAGA	AGATGGCTTT	GACGCTCTGT	TGCATAGAGT	GGGACTTATT	AGA	ATG	296									
						Met										
						1										
AGC	CAA	AAA	AGC	ATT	GAC	ATG	CAA	ACT	TAT	ATC	TAT	AAA	AAC	GAC	CTT	344
Ser	Gln	Lys	Ser	Ile	Asp	Met	Gln	Thr	Tyr	Ile	Tyr	Lys	Asn	Asp	Leu	
			5					10					15			
TCT	TCT	CAA	GTG	ATT	GCT	AAA	GAA	CTT	TTA	AAT	GCG	GCC	AAT	CGT	GGG	392
Ser	Ser	Gln	Val	Ile	Ala	Lys	Glu	Leu	Leu	Asn	Ala	Ala	Asn	Arg	Gly	
		20					25					30				
GTA	AAA	GTG	CGC	ATC	CTT	TTA	GAC	GAT	AAC	GGA	TTG	GAT	TCG	GAT	TTT	440
Val	Lys	Val	Arg	Ile	Leu	Leu	Asp	Asp	Asn	Gly	Leu	Asp	Ser	Asp	Phe	
	35					40					45					
TCA	GAT	ATT	ATG	CTC	TTA	AAT	TTC	CAT	AAA	AAC	ATT	GAG	GTG	AAA	ATT	488
Ser	Asp	Ile	Met	Leu	Leu	Asn	Phe	His	Lys	Asn	Ile	Glu	Val	Lys	Ile	
	50				55					60					65	
TTT	AAC	CCC	TAC	TAT	ATC	CGC	AAT	AAA	GGC	TTG	CGT	TAT	TTT	GAA	ATG	536
Phe	Asn	Pro	Tyr	Tyr	Ile	Arg	Asn	Lys	Gly	Leu	Arg	Tyr	Phe	Glu	Met	
				70					75					80		
CTT	GCG	GAT	TAT	GAG	CGC	ATT	AAA	AAA	CGC	ATG	CAC	AAC	AAG	CTT	TTC	584
Leu	Ala	Asp	Tyr	Glu	Arg	Ile	Lys	Lys	Arg	Met	His	Asn	Lys	Leu	Phe	
			85					90					95			
ATC	GTG	GAT	AAT	TTC	GCT	GTC	ATT	ATA	GGG	GGG	CGC	AAT	ATT	GGG	GAC	632
Ile	Val	Asp	Asn	Phe	Ala	Val	Ile	Ile	Gly	Gly	Arg	Asn	Ile	Gly	Asp	
		100					105					110				
AAT	TAT	TTT	GAT	AAC	GAT	TTA	GAC	ACG	AAT	TTT	TTA	GAT	TTA	GAC	GCT	680
Asn	Tyr	Phe	Asp	Asn	Asp	Leu	Asp	Thr	Asn	Phe	Leu	Asp	Leu	Asp	Ala	
		115				120					125					
TTG	TTT	TTT	GGG	GGG	GTT	GCT	TCA	AAA	GCC	AAA	GAA	AGC	TTT	GAA	CGC	728
Leu	Phe	Phe	Gly	Gly	Val	Ala	Ser	Lys	Ala	Lys	Glu	Ser	Phe	Glu	Arg	
	130				135				140						145	
TAT	TGG	AGA	TTC	CAC	CGC	TCT	ATC	CCT	GTT	TCA	TTA	CTA	AGA	ACC	CAT	776
Tyr	Trp	Arg	Phe	His	Arg	Ser	Ile	Pro	Val	Ser	Leu	Leu	Arg	Thr	His	
				150					155					160		
AAA	AGA	CTC	AAA	AAC	AAC	GCT	AAA	GAA	ATC	GCT	AAA	CTC	CAT	GAA	AAA	824
Lys	Arg	Leu	Lys	Asn	Asn	Ala	Lys	Glu	Ile	Ala	Lys	Leu	His	Glu	Lys	
			165					170					175			
ATC	CCT	ATC	AGC	GCT	GAA	GAC	AAA	AAC	CAG	TTT	GAA	AAA	AAA	GTC	AAT	872
Ile	Pro	Ile	Ser	Ala	Glu	Asp	Lys	Asn	Gln	Phe	Glu	Lys	Lys	Val	Asn	
		180					185					190				
GAT	TTT	ATA	GAT	CGT	TTC	CAA	AAA	TAC	CAA	TAC	CCC	ATT	TAT	TAT	GGG	920
Asp	Phe	Ile	Asp	Arg	Phe	Gln	Lys	Tyr	Gln	Tyr	Pro	Ile	Tyr	Tyr	Gly	
	195					200					205					
AAT	GCC	ATT	TTT	TTA	GCC	GAT	TCA	CCC	AAA	AAA	ATT	GAC	ACG	CCC	TTG	968

Asn	Ala	Ile	Phe	Leu	Ala	Asp	Ser	Pro	Lys	Lys	Ile	Asp	Thr	Pro	Leu	
210					215					220					225	
TAT	TCG	CCT	ATC	AAA	ATC	GCT	TTT	GAG	AAA	GCC	CTT	AAA	AAC	GCT	AAG	1016
Tyr	Ser	Pro	Ile	Lys	Ile	Ala	Phe	Glu	Lys	Ala	Leu	Lys	Asn	Ala	Lys	
				230					235					240		
GAC	TCC	GTT	TTT	ATC	GCT	TCA	TCG	TAT	TTT	ATT	CCA	GGC	AAA	AAG	ATG	1064
Asp	Ser	Val	Phe	Ile	Ala	Ser	Ser	Tyr	Phe	Ile	Pro	Gly	Lys	Lys	Met	
			245					250					255			
ATG	AAA	ATC	TTT	AAA	AAT	CAA	ATT	TCT	AAG	GGG	ATT	GAA	TTG	AAC	ATC	1112
Met	Lys	Ile	Phe	Lys	Asn	Gln	Ile	Ser	Lys	Gly	Ile	Glu	Leu	Asn	Ile	
		260					265				270					
CTT	ACC	AAT	TCC	CTT	TCA	TCT	ACT	GAT	GCG	ATA	GTG	GTC	TAT	GGG	GCA	1160
Leu	Thr	Asn	Ser	Leu	Ser	Ser	Thr	Asp	Ala	Ile	Val	Val	Tyr	Gly	Ala	
	275					280					285					
TGG	GAA	AGG	TAT	CGC	AAC	CAA	TTA	GTG	CGA	ATG	GGC	GCG	AAT	GTC	TAT	1208
Trp	Glu	Arg	Tyr	Arg	Asn	Gln	Leu	Val	Arg	Met	Gly	Ala	Asn	Val	Tyr	
290					295				300					305		
GAA	ATA	CGA	AAC	GAT	TTT	TTC	AAC	CGC	CAG	ATT	AAA	GGG	CGC	TTT	AGC	1256
Glu	Ile	Arg	Asn	Asp	Phe	Phe	Asn	Arg	Gln	Ile	Lys	Gly	Arg	Phe	Ser	
			310					315						320		
ACC	AAA	CAT	TCC	TTG	CAT	GGC	AAG	ACG	ATT	GTT	TTT	GAT	GAC	AAT	TTA	1304
Thr	Lys	His	Ser	Leu	His	Gly	Lys	Thr	Ile	Val	Phe	Asp	Asp	Asn	Leu	
			325					330					335			
ACG	CTT	CTA	GGG	AGT	TTC	AAT	ATT	GAT	CCG	CGC	TCT	GCA	TAC	ATC	AAC	1352
Thr	Leu	Leu	Gly	Ser	Phe	Asn	Ile	Asp	Pro	Arg	Ser	Ala	Tyr	Ile	Asn	
		340					345					350				
ACT	GAA	AGC	GCG	GTT	TTG	TTT	GAC	AAC	CCG	TCT	TTT	GCT	AAA	AGG	GTG	1400
Thr	Glu	Ser	Ala	Val	Leu	Phe	Asp	Asn	Pro	Ser	Phe	Ala	Lys	Arg	Val	
	355					360					365					
CGT	TTG	TCG	CTT	AAA	GAT	CAT	GCC	CAA	CAA	TCA	TGG	CAT	TTG	GTG	GTG	1448
Arg	Leu	Ser	Leu	Lys	Asp	His	Ala	Gln	Gln	Ser	Trp	His	Leu	Val	Val	
370				375					380					385		
TAT	CGG	CAT	AGA	GTG	ATT	TGG	GAA	GCG	GTG	GAA	GAA	GGC	ATT	TTA	ATC	1496
Tyr	Arg	His	Arg	Val	Ile	Trp	Glu	Ala	Val	Glu	Glu	Gly	Ile	Leu	Ile	
				390					395					400		
CAT	GAA	AAA	ACT	TCG	CCT	GAC	ACT	TCC	TTC	TTT	TTG	CGC	TTG	ATT	AAA	1544
His	Glu	Lys	Thr	Ser	Pro	Asp	Thr	Ser	Phe	Phe	Leu	Arg	Leu	Ile	Lys	
			405					410					415			
GAA	TGG	TCT	AAA	GTC	CTT	CCT	GAA	AGA	GAG	CTT	TAAACTTTT	AATGCGCTTT				1597
Glu	Trp	Ser	Lys	Val	Leu	Pro	Glu	Arg	Glu	Leu						
	420						425									
ATTTT	TCGAA	AAAGCGATGT	TATTGGTAAC	GGC												1630

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

Met	Ser	Gln	Lys	Ser	Ile	Asp	Met	Gln	Thr	Tyr	Ile	Tyr	Lys	Asn	Asp	1	5	10	15
Leu	Ser	Ser	Gln	Val	Ile	Ala	Lys	Glu	Leu	Leu	Asn	Ala	Ala	Asn	Arg	20	25	30	
Gly	Val	Lys	Val	Arg	Ile	Leu	Leu	Asp	Asp	Asn	Gly	Leu	Asp	Ser	Asp	35	40	45	
Phe	Ser	Asp	Ile	Met	Leu	Leu	Asn	Phe	His	Lys	Asn	Ile	Glu	Val	Lys	50	55	60	
Ile	Phe	Asn	Pro	Tyr	Tyr	Ile	Arg	Asn	Lys	Gly	Leu	Arg	Tyr	Phe	Glu	65	70	75	80
Met	Leu	Ala	Asp	Tyr	Glu	Arg	Ile	Lys	Lys	Arg	Met	His	Asn	Lys	Leu	85	90	95	
Phe	Ile	Val	Asp	Asn	Phe	Ala	Val	Ile	Ile	Gly	Gly	Arg	Asn	Ile	Gly	100	105	110	
Asp	Asn	Tyr	Phe	Asp	Asn	Asp	Leu	Asp	Thr	Asn	Phe	Leu	Asp	Leu	Asp	115	120	125	
Ala	Leu	Phe	Phe	Gly	Gly	Val	Ala	Ser	Lys	Ala	Lys	Glu	Ser	Phe	Glu	130	135	140	
Arg	Tyr	Trp	Arg	Phe	His	Arg	Ser	Ile	Pro	Val	Ser	Leu	Leu	Arg	Thr	145	150	155	160
His	Lys	Arg	Leu	Lys	Asn	Asn	Ala	Lys	Glu	Ile	Ala	Lys	Leu	His	Glu	165	170	175	
Lys	Ile	Pro	Ile	Ser	Ala	Glu	Asp	Lys	Asn	Gln	Phe	Glu	Lys	Lys	Val	180	185	190	
Asn	Asp	Phe	Ile	Asp	Arg	Phe	Gln	Lys	Tyr	Gln	Tyr	Pro	Ile	Tyr	Tyr	195	200	205	
Gly	Asn	Ala	Ile	Phe	Leu	Ala	Asp	Ser	Pro	Lys	Lys	Ile	Asp	Thr	Pro	210	215	220	
Leu	Tyr	Ser	Pro	Ile	Lys	Ile	Ala	Phe	Glu	Lys	Ala	Leu	Lys	Asn	Ala	225	230	235	240
Lys	Asp	Ser	Val	Phe	Ile	Ala	Ser	Ser	Tyr	Phe	Ile	Pro	Gly	Lys	Lys	245	250	255	
Met	Met	Lys	Ile	Phe	Lys	Asn	Gln	Ile	Ser	Lys	Gly	Ile	Glu	Leu	Asn	260	265	270	
Ile	Leu	Thr	Asn	Ser	Leu	Ser	Ser	Thr	Asp	Ala	Ile	Val	Val	Tyr	Gly	275	280	285	
Ala	Trp	Glu	Arg	Tyr	Arg	Asn	Gln	Leu	Val	Arg	Met	Gly	Ala	Asn	Val	290	295	300	
Tyr	Glu	Ile	Arg	Asn	Asp	Phe	Phe	Asn	Arg	Gln	Ile	Lys	Gly	Arg	Phe	305	310	315	320
Ser	Thr	Lys	His	Ser	Leu	His	Gly	Lys	Thr	Ile	Val	Phe	Asp	Asp	Asn	325	330	335	
Leu	Thr	Leu	Leu	Gly	Ser	Phe	Asn	Ile	Asp	Pro	Arg	Ser	Ala	Tyr	Ile	340	345	350	
Asn	Thr	Glu	Ser	Ala	Val	Leu	Phe	Asp	Asn	Pro	Ser	Phe	Ala	Lys	Arg	355	360	365	
Val	Arg	Leu	Ser	Leu	Lys	Asp	His	Ala	Gln	Gln	Ser	Trp	His	Leu	Val				

370	375	380
Val Tyr Arg His Arg	Val Ile Trp Glu Ala	Val Glu Glu Gly Ile Leu
385	390	395
Ile His Glu Lys Thr	Ser Pro Asp Thr Ser Phe	Phe Leu Arg Leu Ile
405	410	415
Lys Glu Trp Ser Lys	Val Leu Pro Glu Arg	Glu Leu
420	425	

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 79...510
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

AACTCTTTTG GTGTAGGATA GCGATCAAGG TTTTATGAA AATAAAAGCC TAAAACAATT	60
TTAAAAAAG GACTTTTG ATG AAA ACA TTT GAA ATT CTA AAA CAT TTG CAA	111
Met Lys Thr Phe Glu Ile Leu Lys His Leu Gln	
1 5 10	
GCG GAT GCG ATC GTG TTA TTT ATG AAA GTG CAT AAC TTC CAT TGG AAT	159
Ala Asp Ala Ile Val Leu Phe Met Lys Val His Asn Phe His Trp Asn	
15 20 25	
GTG AAA GGC ACC GAT TTT TTC AAT GTG CAT AAA GCC ACT GAA GAA ATT	207
Val Lys Gly Thr Asp Phe Phe Asn Val His Lys Ala Thr Glu Glu Ile	
30 35 40	
TAT GAA GAG TTT GCG GAC ATG TTT GAC GAT CTC GCT GAA AGG ATC GTT	255
Tyr Glu Glu Phe Ala Asp Met Phe Asp Asp Leu Ala Glu Arg Ile Val	
45 50 55	
CAA TTA GGG CAT CAC CCC TTA GTC ACT TTA TCC GAA GCG ATC AAA CTC	303
Gln Leu Gly His His Pro Leu Val Thr Leu Ser Glu Ala Ile Lys Leu	
60 65 70 75	
ACT CGT GTT AAA GAA GAA ACT AAA ACG AGC TTC CAC TCT AAA GAC ATC	351
Thr Arg Val Lys Glu Glu Thr Lys Thr Ser Phe His Ser Lys Asp Ile	
80 85 90	
TTT AAA GAA ATT CTA GAG GAC TAC AAA TAT CTA GAA AAA GAA TTT AAA	399
Phe Lys Glu Ile Leu Glu Asp Tyr Lys Tyr Leu Glu Lys Glu Phe Lys	
95 100 105	
GAG CTC TCT AAC ACC GCT GAA AAA GAA GGC GAT AAA GTT ACC GTA ACT	447
Glu Leu Ser Asn Thr Ala Glu Lys Glu Gly Asp Lys Val Thr Val Thr	

110 115 120

TAT GCG GAT GAT CAA TTA GCC AAG TTG CAA AAA TCC ATT TGG ATG CTG 495
 Tyr Ala Asp Asp Gln Leu Ala Lys Leu Gln Lys Ser Ile Trp Met Leu
 125 130 135

CAA GCC CAT TTG GCT TAAGCGACCA AAAAGAAGCC AGCATGAGAG ATTACAGCGA 550
 Gln Ala His Leu Ala
 140

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

Met Lys Thr Phe Glu Ile Leu Lys His Leu Gln Ala Asp Ala Ile Val
 1 5 10 15
 Leu Phe Met Lys Val His Asn Phe His Trp Asn Val Lys Gly Thr Asp
 20 25 30
 Phe Phe Asn Val His Lys Ala Thr Glu Glu Ile Tyr Glu Glu Phe Ala
 35 40 45
 Asp Met Phe Asp Asp Leu Ala Glu Arg Ile Val Gln Leu Gly His His
 50 55 60
 Pro Leu Val Thr Leu Ser Glu Ala Ile Lys Leu Thr Arg Val Lys Glu
 65 70 75 80
 Glu Thr Lys Thr Ser Phe His Ser Lys Asp Ile Phe Lys Glu Ile Leu
 85 90 95
 Glu Asp Tyr Lys Tyr Leu Glu Lys Glu Phe Lys Glu Leu Ser Asn Thr
 100 105 110
 Ala Glu Lys Glu Gly Asp Lys Val Thr Val Thr Tyr Ala Asp Asp Gln
 115 120 125
 Leu Ala Lys Leu Gln Lys Ser Ile Trp Met Leu Gln Ala His Leu Ala
 130 135 140

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...323
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

CTTTTTTCTC TTCCACTTTT TCCACTTTTT TAAGAGCCTT GTGTTTATGA TTG GGC 56
 Leu Gly
 1

TTT TTG GGT TCA GGT TTG GGT TTT GGT TTA GGC TCA GGC TTA GGC TTT 104
 Phe Leu Gly Ser Gly Leu Gly Phe Gly Leu Gly Ser Gly Leu Gly Phe
 5 10 15

TCT ATA GGT TTT GGC GGG GTT GGC GGG GTT GGC GGA GTT GGG GGT GTG 152
 Ser Ile Gly Phe Gly Gly Val Gly Gly Val Gly Gly Val Gly Gly Val
 20 25 30

GGA GGC GTT GGA GGT TTT TGG GGG CCA GCC AGC GTG GGT TTA GGA GCG 200
 Gly Gly Val Gly Gly Phe Trp Gly Pro Ala Ser Val Gly Leu Gly Ala
 35 40 45 50

CCC TGG GTG TTT TTA CTG GGA TCT TGC GAA TGG CCT CTT TTT AAA ACC 248
 Pro Trp Val Phe Leu Leu Gly Ser Cys Glu Trp Pro Leu Phe Lys Thr
 55 60 65

AAT AAA TTT TCA GGA TTT AAT TTA ACA AGC TTG GGT TTT GAA GGA AAA 296
 Asn Lys Phe Ser Gly Phe Asn Leu Thr Ser Leu Gly Phe Glu Gly Lys
 70 75 80

AAA TCT TCT CTG TGT TCA AAT AAA AAA TAAATCAACC AGTGTAAACAA TACAGAC 350
 Lys Ser Ser Leu Cys Ser Asn Lys Lys
 85 90

AGAATGAGAG AAAAGAAAAA ATTCCT 376

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

Leu Gly Phe Leu Gly Ser Gly Leu Gly Phe Gly Leu Gly Ser Gly Leu
 1 5 10 15
 Gly Phe Ser Ile Gly Phe Gly Gly Val Gly Gly Val Gly Gly Val Gly
 20 25 30
 Gly Val Gly Gly Val Gly Gly Phe Trp Gly Pro Ala Ser Val Gly Leu
 35 40 45
 Gly Ala Pro Trp Val Phe Leu Leu Gly Ser Cys Glu Trp Pro Leu Phe
 50 55 60
 Lys Thr Asn Lys Phe Ser Gly Phe Asn Leu Thr Ser Leu Gly Phe Glu
 65 70 75 80
 Gly Lys Lys Ser Ser Leu Cys Ser Asn Lys Lys
 85 90

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2890 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 458...2836
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

TCAAAATT	TAAGTTAATTTT	AATAATTATT	TTTATAGTAT	GCATCGGTTT	GAATTAAATG	60
AGAAAGGT	TAACAAATGAA	TGGTTATTTG	AGAGTAAAAA	CCTCTTATTT	TTTAGCGTTG	120
AACGCTTT	GACTTTTGTG	TTTTAACTCT	TTGGTGGGCG	CGAAAGAACA	GCATCACACT	180
TTGCAAAA	AGTGACAACCAC	TGAGCAAAAA	TTCAATCCAA	GCGCGCCGCT	TTCATGGCAA	240
AGCGAAGA	GATGCGTAATTC	CACAAGCTCT	CGCACGGTGA	TTTCCAACAA	GGAACTCAAA	300
AAAACGGG	GGAATTTGAATAT	TGAAAACGCC	TTGCAAAACG	TGCCAGGGAT	TCAAATCAGA	360
GACGCTAC	AGGCACAGGCGT	GCTGCCTAAA	ATTTCGGTGC	TCAAAATTTA	AGTTAATTTT	420
AATAATTATT	TTTATAGTAT	GCATCGGTTT	GAATTAA	ATG AGA AAG GTT ATC ACA		475
				Met Arg Lys Val Ile Thr		
				1	5	
ATG AAT GGT	TAT TTG AGA	GTA AAA ACC	TCT TAT TTT	TTA GCG TTG	AAC	523
Met Asn Gly	Tyr Leu Arg	Val Lys Thr	Ser Tyr Phe	Leu Ala Leu	Asn	
	10	15		20		
GCT TTG ACT	TTT TTG TCT	TTT AAC TCT	TTG GTG GGC	GCG AAA GAA	CAG	571
Ala Leu Thr	Phe Leu Ser	Phe Asn Ser	Leu Val Gly	Ala Lys Glu	Gln	
	25	30		35		
CAT CAC ACT	TTG CAA AAA	GTG ACA ACC	ACT GAG CAA	AAA TTC AAT	CCA	619
His His Thr	Leu Gln Lys	Val Thr Thr	Thr Glu Gln	Lys Phe Asn	Pro	
	40	45		50		
AGC GCG CCG	CTT TCA TGG	CAA AGC GAA	GAG ATG CGT	AAT TCC ACA	AGC	667
Ser Ala Pro	Leu Ser Trp	Gln Ser Glu	Glu Met Arg	Asn Ser Thr	Ser	
	55	60	65	70		
TCT CGC ACG	GTG ATT TCC	AAC AAG GAA	CTC AAA AAA	ACG GGG AAT	TTG	715
Ser Arg Thr	Val Ile Ser	Asn Lys Glu	Leu Lys Lys	Thr Gly Asn	Leu	
	75	80		85		
AAT ATT GAA	AAC GCC TTG	CAA AAC GTG	CCA GGG ATT	CAA ATC AGA	GAC	763
Asn Ile Glu	Asn Ala Leu	Gln Asn Val	Pro Gly Ile	Gln Ile Arg	Asp	
	90	95		100		
GCT ACA GGC	ACA GGC GTG	CTG CCT AAA	ATT TCG GTG	CGC GGT TTT	GGT	811
Ala Thr Gly	Thr Gly Val	Leu Pro Lys	Ile Ser Val	Arg Gly Phe	Gly	
	105	110		115		
GGG GGC GGT	AAC GGG CAT	AGC AAT ACC	AAC ATG ATT	TTA GTC AAT	GGT	859

Gly	Gly	Gly	Asn	Gly	His	Ser	Asn	Thr	Asn	Met	Ile	Leu	Val	Asn	Gly	
120						125					130					
ATC	CCC	ATT	TAT	GGC	GCG	CCG	TAT	TCC	AAT	ATT	GAA	CTG	GCG	ATT	TTC	907
Ile	Pro	Ile	Tyr	Gly	Ala	Pro	Tyr	Ser	Asn	Ile	Glu	Leu	Ala	Ile	Phe	
135					140					145					150	
CCT	GTA	ACT	TTC	CAG	TCA	GTG	GAT	AGG	ATT	GAT	GTG	ATT	AAA	GGG	GGC	955
Pro	Val	Thr	Phe	Gln	Ser	Val	Asp	Arg	Ile	Asp	Val	Ile	Lys	Gly	Gly	
				155					160					165		
ACG	AGC	GTG	CAA	TAC	GGC	CCT	AAT	ACT	TTT	GGA	GGC	GTG	GTG	AAT	ATC	1003
Thr	Ser	Val	Gln	Tyr	Gly	Pro	Asn	Thr	Phe	Gly	Gly	Val	Val	Asn	Ile	
			170					175					180			
ATC	ACT	AAA	GAA	ATC	CCT	AAA	GAG	TGG	GAA	AAT	CAA	GCG	GCT	GAA	AGG	1051
Ile	Thr	Lys	Glu	Ile	Pro	Lys	Glu	Trp	Glu	Asn	Gln	Ala	Ala	Glu	Arg	
		185					190					195				
ATC	ACT	TTT	TGG	GGG	CGA	TCC	TCT	AAT	GGG	AAT	TTT	GTA	GAT	CCC	AAA	1099
Ile	Thr	Phe	Trp	Gly	Arg	Ser	Ser	Asn	Gly	Asn	Phe	Val	Asp	Pro	Lys	
	200					205					210					
GAA	AAA	GGC	AAG	CCT	TTA	GCC	CAA	ACT	TTA	GGA	AAC	CAA	ATG	CTG	TTT	1147
Glu	Lys	Gly	Lys	Pro	Leu	Ala	Gln	Thr	Leu	Gly	Asn	Gln	Met	Leu	Phe	
215					220					225					230	
AAC	ACT	TAC	GGG	CGA	ACG	GCT	GGA	ATG	TTG	GGT	AAG	CAT	GTA	GGA	ATT	1195
Asn	Thr	Tyr	Gly	Arg	Thr	Ala	Gly	Met	Leu	Gly	Lys	His	Val	Gly	Ile	
				235					240					245		
AGC	GCT	CAA	GGC	AAT	TGG	ATT	AAC	GGG	CAA	GGT	TTC	AGG	CAA	AAC	AGC	1243
Ser	Ala	Gln	Gly	Asn	Trp	Ile	Asn	Gly	Gln	Gly	Phe	Arg	Gln	Asn	Ser	
			250					255					260			
CCC	ACA	AAG	GTG	CAA	AAC	TAC	TTG	CTT	GAT	GCG	GTT	TAT	AAG	ATT	AAT	1291
Pro	Thr	Lys	Val	Gln	Asn	Tyr	Leu	Leu	Asp	Ala	Val	Tyr	Lys	Ile	Asn	
		265					270					275				
GCG	ACC	AAT	ACT	TTT	AAA	GCT	TAT	TAC	CAA	TAT	TAT	CAA	TAC	AAC	TCT	1339
Ala	Thr	Asn	Thr	Phe	Lys	Ala	Tyr	Tyr	Gln	Tyr	Tyr	Gln	Tyr	Asn	Ser	
	280					285					290					
TAC	CAT	CCA	GGC	ACT	TTG	AGT	GCA	CAA	GAT	TAT	GCT	TAT	AAC	CGC	TTC	1387
Tyr	His	Pro	Gly	Thr	Leu	Ser	Ala	Gln	Asp	Tyr	Ala	Tyr	Asn	Arg	Phe	
	295				300					305					310	
ATT	AAT	GAG	CGC	CCT	GAC	AAT	CAA	GAT	GGA	GGG	CGA	GCC	AAG	CGC	TTT	1435
Ile	Asn	Glu	Arg	Pro	Asp	Asn	Gln	Asp	Gly	Gly	Arg	Ala	Lys	Arg	Phe	
				315					320					325		
GGG	ATC	GTG	TAT	CAA	AAT	TAT	TTT	GGC	GAT	CCG	GAT	AGG	AAA	GTG	GGG	1483
Gly	Ile	Val	Tyr	Gln	Asn	Tyr	Phe	Gly	Asp	Pro	Asp	Arg	Lys	Val	Gly	
			330					335					340			
GGA	GAT	TTT	AAA	TTC	ACT	TAT	TTC	ACG	CAT	GAC	ATG	AGT	AGG	GAT	TTT	1531
Gly	Asp	Phe	Lys	Phe	Thr	Tyr	Phe	Thr	His	Asp	Met	Ser	Arg	Asp	Phe	
		345					350					355				

GGG TTT TCC AAC CAA TAC CAA AGC GTG TAT ATG AGC AGT CAA AAC AAG Gly Phe Ser Asn Gln Tyr Gln Ser Val Tyr Met Ser Ser Gln Asn Lys 360 365 370	1579
ATT TTA CCT TTT AAA GGC AAG GGA AAA ATT AGC GCG ACT AAC CCT AAT Ile Leu Pro Phe Lys Gly Lys Gly Lys Ile Ser Ala Thr Asn Pro Asn 375 380 385 390	1627
TGC GGT TTG TAT TCT TAT AGC GAC ACG AAC AGC CCT TGT TGG CAA TTT Cys Gly Leu Tyr Ser Tyr Ser Asp Thr Asn Ser Pro Cys Trp Gln Phe 395 400 405	1675
TTT GAC AAT ATC CGC CGA TCC GTG GTG AAT GCC TTT GAG CCA AAA CTC Phe Asp Asn Ile Arg Arg Ser Val Val Asn Ala Phe Glu Pro Lys Leu 410 415 420	1723
AAT CTT ATC GTC AAT ACC GGT AAA GTC AAA CAA ACT TTT AAT ATG GGA Asn Leu Ile Val Asn Thr Gly Lys Val Lys Gln Thr Phe Asn Met Gly 425 430 435	1771
ATG CGC TTT TTA ACT GAA GAT TTA TAC CGC CGA TCC ACC ACC AGG AAA Met Arg Phe Leu Thr Glu Asp Leu Tyr Arg Arg Ser Thr Thr Arg Lys 440 445 450	1819
AAC CCT AGC ATG CCT AAT AAT GGG AGT GGT TTT GAT GCA GGA ACT TCA Asn Pro Ser Met Pro Asn Asn Gly Ser Gly Phe Asp Ala Gly Thr Ser 455 460 465 470	1867
CTC AAT AAT TTC AAC AAT TAT ACC GCT GTG TAT GCC AGC GAT GAG ATC Leu Asn Asn Phe Asn Asn Tyr Thr Ala Val Tyr Ala Ser Asp Glu Ile 475 480 485	1915
AAT TTC AAT AAC GGC ATG CTA ACG ATC ACG CCG GGC TTG AGA TAC ACT Asn Phe Asn Asn Gly Met Leu Thr Ile Thr Pro Gly Leu Arg Tyr Thr 490 495 500	1963
TTT TTA AAT TAC GAA AAA AAA GAC GCT CCT CCT TTT AAA GCA GGC CAA Phe Leu Asn Tyr Glu Lys Lys Asp Ala Pro Pro Phe Lys Ala Gly Gln 505 510 515	2011
ACA GGA AAA ACC ATT AAA GAT CGT TAT AAC CAA TGG AAT CCA GCA GTG Thr Gly Lys Thr Ile Lys Asp Arg Tyr Asn Gln Trp Asn Pro Ala Val 520 525 530	2059
AAT GTC GGC TAT AAA CCC ATT AAA GAA TTG TTG TTT TAT TTC AAT TAC Asn Val Gly Tyr Lys Pro Ile Lys Glu Leu Leu Phe Tyr Phe Asn Tyr 535 540 545 550	2107
CAA AGA AGC TAC ATT CCG CCT CAA TTC AGC AAT ATC GGT AGT TTT GTA Gln Arg Ser Tyr Ile Pro Pro Gln Phe Ser Asn Ile Gly Ser Phe Val 555 560 565	2155
GGC ACA AGC ACG GAT TAT TTT CAA ATC TTT AAT GTC ATG GAA GGC GGC Gly Thr Ser Thr Asp Tyr Phe Gln Ile Phe Asn Val Met Glu Gly Gly 570 575 580	2203
TCA AGA TAT TAT TTT AAC AAC CAA GTG AGT TTT AAC GCG AAT TAT TTT Ser Arg Tyr Tyr Phe Asn Asn Gln Val Ser Phe Asn Ala Asn Tyr Phe	2251

585					590					595						
GTG	ATT	TTT	GCG	AAT	AAC	TAT	TTT	ACC	GGG	CGC	TAT	GGG	GAT	AAT	AAA	2299
Val	Ile	Phe	Ala	Asn	Asn	Tyr	Phe	Thr	Gly	Arg	Tyr	Gly	Asp	Asn	Lys	
600						605					610					
GAG	CCG	GTC	AAT	GCG	AGA	TCG	CAA	GGC	GTG	GAG	CTA	GAG	TTG	TAT	TAC	2347
Glu	Pro	Val	Asn	Ala	Arg	Ser	Gln	Gly	Val	Glu	Leu	Glu	Leu	Tyr	Tyr	
615					620					625					630	
ACG	CCG	ATT	AGA	GGG	CTT	AAT	TTC	CAT	GCG	GCT	TAC	ACT	TTC	ATA	GAT	2395
Thr	Pro	Ile	Arg	Gly	Leu	Asn	Phe	His	Ala	Ala	Tyr	Thr	Phe	Ile	Asp	
				635					640					645		
GCC	AAT	ATC	ACA	AGC	CAC	ACG	ATG	GTT	ACT	AAC	CCC	GCT	AAT	CCT	AAA	2443
Ala	Asn	Ile	Thr	Ser	His	Thr	Met	Val	Thr	Asn	Pro	Ala	Asn	Pro	Lys	
			650					655					660			
GGG	CCT	AAA	AAA	GAT	ATT	TTT	GGC	AAA	AAG	CTC	CCT	TTT	GTA	AGC	CCG	2491
Gly	Pro	Lys	Lys	Asp	Ile	Phe	Gly	Lys	Lys	Leu	Pro	Phe	Val	Ser	Pro	
		665					670					675				
CAC	CAA	TTC	ATT	TTA	GAC	GCG	AGC	TAC	ACT	TAC	GCT	AAA	ACC	ACG	ATT	2539
His	Gln	Phe	Ile	Leu	Asp	Ala	Ser	Tyr	Thr	Tyr	Ala	Lys	Thr	Thr	Ile	
		680				685					690					
GGG	TTG	AGT	TCT	TTC	TTT	TAT	AGC	CGA	ACT	TAT	AGC	GAT	GTG	TTA	AAC	2587
Gly	Leu	Ser	Ser	Phe	Phe	Tyr	Ser	Arg	Thr	Tyr	Ser	Asp	Val	Leu	Asn	
695					700					705					710	
ACC	GTG	CCT	TTT	ATT	CAA	TAC	GCG	CCC	ACG	ATC	AAA	AAT	GGT	GCT	ATC	2635
Thr	Val	Pro	Phe	Ile	Gln	Tyr	Ala	Pro	Thr	Ile	Lys	Asn	Gly	Ala	Ile	
				715					720					725		
ACT	ACC	AAA	ACA	GCG	GGC	ATG	ACG	CCA	TGG	TAT	TGG	GTG	TGG	AAT	TTG	2683
Thr	Thr	Lys	Thr	Ala	Gly	Met	Thr	Pro	Trp	Tyr	Trp	Val	Trp	Asn	Leu	
			730					735						740		
CAA	ATT	TCT	ACC	ACT	TTT	TGG	GAA	CGC	AAA	AAG	CAA	AGC	GTT	AAT	GCG	2731
Gln	Ile	Ser	Thr	Thr	Phe	Trp	Glu	Arg	Lys	Lys	Gln	Ser	Val	Asn	Ala	
		745					750					755				
AGC	TTG	CAA	ATC	AAT	AAC	ATT	TTT	AAC	ATG	AAA	TAT	TGG	TTT	AGC	GGG	2779
Ser	Leu	Gln	Ile	Asn	Asn	Ile	Phe	Asn	Met	Lys	Tyr	Trp	Phe	Ser	Gly	
	760					765					770					
ATA	GGC	ACT	AGC	CTA	ACG	GGA	AAG	AAG	CCG	CGC	CTC	CTA	GGA	GCA	TCA	2827
Ile	Gly	Thr	Ser	Leu	Thr	Gly	Lys	Lys	Pro	Arg	Leu	Leu	Gly	Ala	Ser	
775					780					785					790	
CAG	CGT	ATG	TGAGCTATCA	TTTTTAATTT	TAGGGTTGTA	ATGTTTTGAG	AAGTTGGGC									2885
Gln	Arg	Met														
GTAAA																2890

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

Met	Arg	Lys	Val	Ile	Thr	Met	Asn	Gly	Tyr	Leu	Arg	Val	Lys	Thr	Ser	1	5	10	15
Tyr	Phe	Leu	Ala	Leu	Asn	Ala	Leu	Thr	Phe	Leu	Ser	Phe	Asn	Ser	Leu	20	25	30	
Val	Gly	Ala	Lys	Glu	Gln	His	His	Thr	Leu	Gln	Lys	Val	Thr	Thr	Thr	35	40	45	
Glu	Gln	Lys	Phe	Asn	Pro	Ser	Ala	Pro	Leu	Ser	Trp	Gln	Ser	Glu	Glu	50	55	60	
Met	Arg	Asn	Ser	Thr	Ser	Ser	Arg	Thr	Val	Ile	Ser	Asn	Lys	Glu	Leu	65	70	75	80
Lys	Lys	Thr	Gly	Asn	Leu	Asn	Ile	Glu	Asn	Ala	Leu	Gln	Asn	Val	Pro	85	90	95	
Gly	Ile	Gln	Ile	Arg	Asp	Ala	Thr	Gly	Thr	Gly	Val	Leu	Pro	Lys	Ile	100	105	110	
Ser	Val	Arg	Gly	Phe	Gly	Gly	Gly	Asn	Gly	His	Ser	Asn	Thr	Asn		115	120	125	
Met	Ile	Leu	Val	Asn	Gly	Ile	Pro	Ile	Tyr	Gly	Ala	Pro	Tyr	Ser	Asn	130	135	140	
Ile	Glu	Leu	Ala	Ile	Phe	Pro	Val	Thr	Phe	Gln	Ser	Val	Asp	Arg	Ile	145	150	155	160
Asp	Val	Ile	Lys	Gly	Gly	Thr	Ser	Val	Gln	Tyr	Gly	Pro	Asn	Thr	Phe	165	170	175	
Gly	Gly	Val	Val	Asn	Ile	Ile	Thr	Lys	Glu	Ile	Pro	Lys	Glu	Trp	Glu	180	185	190	
Asn	Gln	Ala	Glu	Arg	Ile	Thr	Phe	Trp	Gly	Arg	Ser	Ser	Asn	Gly		195	200	205	
Asn	Phe	Val	Asp	Pro	Lys	Glu	Lys	Gly	Lys	Pro	Leu	Ala	Gln	Thr	Leu	210	215	220	
Gly	Asn	Gln	Met	Leu	Phe	Asn	Thr	Tyr	Gly	Arg	Thr	Ala	Gly	Met	Leu	225	230	235	240
Gly	Lys	His	Val	Gly	Ile	Ser	Ala	Gln	Gly	Asn	Trp	Ile	Asn	Gly	Gln	245	250	255	
Gly	Phe	Arg	Gln	Asn	Ser	Pro	Thr	Lys	Val	Gln	Asn	Tyr	Leu	Leu	Asp	260	265	270	
Ala	Val	Tyr	Lys	Ile	Asn	Ala	Thr	Asn	Thr	Phe	Lys	Ala	Tyr	Tyr	Gln	275	280	285	
Tyr	Tyr	Gln	Tyr	Asn	Ser	Tyr	His	Pro	Gly	Thr	Leu	Ser	Ala	Gln	Asp	290	295	300	
Tyr	Ala	Tyr	Asn	Arg	Phe	Ile	Asn	Glu	Arg	Pro	Asp	Asn	Gln	Asp	Gly	305	310	315	320
Gly	Arg	Ala	Lys	Arg	Phe	Gly	Ile	Val	Tyr	Gln	Asn	Tyr	Phe	Gly	Asp	325	330	335	
Pro	Asp	Arg	Lys	Val	Gly	Gly	Asp	Phe	Lys	Phe	Thr	Tyr	Phe	Thr	His	340	345	350	
Asp	Met	Ser	Arg	Asp	Phe	Gly	Phe	Ser	Asn	Gln	Tyr	Gln	Ser	Val	Tyr	355	360	365	
Met	Ser	Ser	Gln	Asn	Lys	Ile	Leu	Pro	Phe	Lys	Gly	Lys	Gly	Lys	Ile				

370		375		380
Ser Ala Thr Asn Pro Asn Cys Gly Leu Tyr Ser Tyr Ser Asp Thr Asn				
385		390		400
Ser Pro Cys Trp Gln Phe Phe Asp Asn Ile Arg Arg Ser Val Val Asn				
	405		410	415
Ala Phe Glu Pro Lys Leu Asn Leu Ile Val Asn Thr Gly Lys Val Lys				
	420		425	430
Gln Thr Phe Asn Met Gly Met Arg Phe Leu Thr Glu Asp Leu Tyr Arg				
	435		440	445
Arg Ser Thr Thr Arg Lys Asn Pro Ser Met Pro Asn Asn Gly Ser Gly				
	450		455	460
Phe Asp Ala Gly Thr Ser Leu Asn Asn Phe Asn Asn Tyr Thr Ala Val				
465		470		480
Tyr Ala Ser Asp Glu Ile Asn Phe Asn Asn Gly Met Leu Thr Ile Thr				
	485		490	495
Pro Gly Leu Arg Tyr Thr Phe Leu Asn Tyr Glu Lys Lys Asp Ala Pro				
	500		505	510
Pro Phe Lys Ala Gly Gln Thr Gly Lys Thr Ile Lys Asp Arg Tyr Asn				
	515		520	525
Gln Trp Asn Pro Ala Val Asn Val Gly Tyr Lys Pro Ile Lys Glu Leu				
	530		535	540
Leu Phe Tyr Phe Asn Tyr Gln Arg Ser Tyr Ile Pro Pro Gln Phe Ser				
545		550		560
Asn Ile Gly Ser Phe Val Gly Thr Ser Thr Asp Tyr Phe Gln Ile Phe				
	565		570	575
Asn Val Met Glu Gly Gly Ser Arg Tyr Tyr Phe Asn Asn Gln Val Ser				
	580		585	590
Phe Asn Ala Asn Tyr Phe Val Ile Phe Ala Asn Asn Tyr Phe Thr Gly				
	595		600	605
Arg Tyr Gly Asp Asn Lys Glu Pro Val Asn Ala Arg Ser Gln Gly Val				
	610		615	620
Glu Leu Glu Leu Tyr Tyr Thr Pro Ile Arg Gly Leu Asn Phe His Ala				
625		630		640
Ala Tyr Thr Phe Ile Asp Ala Asn Ile Thr Ser His Thr Met Val Thr				
	645		650	655
Asn Pro Ala Asn Pro Lys Gly Pro Lys Lys Asp Ile Phe Gly Lys Lys				
	660		665	670
Leu Pro Phe Val Ser Pro His Gln Phe Ile Leu Asp Ala Ser Tyr Thr				
	675		680	685
Tyr Ala Lys Thr Thr Ile Gly Leu Ser Ser Phe Phe Tyr Ser Arg Thr				
	690		695	700
Tyr Ser Asp Val Leu Asn Thr Val Pro Phe Ile Gln Tyr Ala Pro Thr				
705		710		720
Ile Lys Asn Gly Ala Ile Thr Thr Lys Thr Ala Gly Met Thr Pro Trp				
	725		730	735
Tyr Trp Val Trp Asn Leu Gln Ile Ser Thr Thr Phe Trp Glu Arg Lys				
	740		745	750
Lys Gln Ser Val Asn Ala Ser Leu Gln Ile Asn Asn Ile Phe Asn Met				
	755		760	765
Lys Tyr Trp Phe Ser Gly Ile Gly Thr Ser Leu Thr Gly Lys Lys Pro				
	770		775	780
Arg Leu Leu Gly Ala Ser Gln Arg Met				
785		790		

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 406 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 51...353
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

TCGTCTTTTG TCGGTTCAAA AAAATCTCTC GACTTAAAAA AACCTATTAA	ATC AAG	56
	Ile Lys	
	1	
ATA ATC TAT CAA ATC ATC AAG TTT TTT CGT TCT AAG AAT TTT ATT TTG		104
Ile Ile Tyr Gln Ile Ile Lys Phe Phe Arg Ser Lys Asn Phe Ile Leu		
5 10 15		
TTT TTT AGA ATA GCA ACG ATA AAG TTC TTC TTT TAT CTC ATT TGG GAA		152
Phe Phe Arg Ile Ala Thr Ile Lys Phe Phe Phe Tyr Leu Ile Trp Glu		
20 25 30		
TTT TTG AAT GTT ATA GAC AAT TTC ACT ATC TCT TTG ATT TTG TTT ATA		200
Phe Leu Asn Val Ile Asp Asn Phe Thr Ile Ser Leu Ile Leu Phe Ile		
35 40 45 50		
TTT TTT AGC CCC ATA CCA AAG AAA TAT TTG ATA AAA AAT AAG AAA AAT		248
Phe Phe Ser Pro Ile Pro Lys Lys Tyr Leu Ile Lys Asn Lys Lys Asn		
55 60 65		
AGC GTA AAA GAA AAA GAA AAT AAA GAA AAA AGA AAG AGA AAA AGA AAG		296
Ser Val Lys Glu Lys Glu Asn Lys Glu Lys Arg Lys Arg Lys Arg Lys		
70 75 80		
GAT TTT GTT TTG GGT GTA TTG GAA AAT AGA CTC AAA AAT CAA TTG AAA		344
Asp Phe Val Leu Gly Val Leu Glu Asn Arg Leu Lys Asn Gln Leu Lys		
85 90 95		
AAC CCC TTT TAGATTAAAA ATAAAAACAA TAAGCGAAAC GACAAAAGCA AGCAGAAAA		402
Asn Pro Phe		
100		
GAAG		406

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

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Ile Lys Ile Ile Tyr Gln Ile Ile Lys Phe Phe Arg Ser Lys Asn Phe
 1           5           10           15
Ile Leu Phe Phe Arg Ile Ala Thr Ile Lys Phe Phe Phe Tyr Leu Ile
          20           25           30
Trp Glu Phe Leu Asn Val Ile Asp Asn Phe Thr Ile Ser Leu Ile Leu
      35           40           45
Phe Ile Phe Phe Ser Pro Ile Pro Lys Lys Tyr Leu Ile Lys Asn Lys
      50           55           60
Lys Asn Ser Val Lys Glu Lys Glu Asn Lys Glu Lys Arg Lys Arg Lys
      65           70           75           80
Arg Lys Asp Phe Val Leu Gly Val Leu Glu Asn Arg Leu Lys Asn Gln
          85           90           95
Leu Lys Asn Pro Phe
          100

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(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 89...1087
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

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GATTTTGTGA AAAATAGTTT CATTTTACT GCTTGATTT CCTTAATGGT GTTATAATCG      60
CTCCATAAAT CATACAAAAA GGATCGTT ATG TTA GTT ACT CGC TTT AAA AAA      112
          Met Leu Val Thr Arg Phe Lys Lys
          1           5

GCT TTA ATC TCT TAT TCT TTA GGC GCG CTT CTT GTT TCA TCG TTA TTG      160
Ala Leu Ile Ser Tyr Ser Leu Gly Ala Leu Leu Val Ser Ser Leu Leu
      10           15           20

GGC GTG GCT AGT GCT TCC AAT CAA GAA ATC CAA GTC AAA GAT TAT TTT      208
Gly Val Ala Ser Ala Ser Asn Gln Glu Ile Gln Val Lys Asp Tyr Phe
      25           30           35           40

GGG GAT CAA GCC ATC AAG CTT CCT GTT TCT AAA ATA ATC TAC TTG GGT      256
Gly Asp Gln Ala Ile Lys Leu Pro Val Ser Lys Ile Ile Tyr Leu Gly
          45           50           55

AGC TTT GCA GAA GTG CCT GCT ATG TTC CAT ACT TGG GAT AGG GTC GTG      304
Ser Phe Ala Glu Val Pro Ala Met Phe His Thr Trp Asp Arg Val Val
          60           65           70

GGA ATT TCG GAT TAC GCT TTT AAA TCT GAT ATT GTT AAA GCT ACT CTC      352
Gly Ile Ser Asp Tyr Ala Phe Lys Ser Asp Ile Val Lys Ala Thr Leu

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75	80	85	
AAA GAT CCT AAA CGC ATT AAA TCC ATG AGC AGT GAT CAT GTG GCG GCG Lys Asp Pro Lys Arg Ile Lys Ser Met Ser Ser Asp His Val Ala Ala 90 95 100			400
TTG AAT GTG GAG CTT TTA AAA AAG CTT GGC CCC GAT CTT GTG GTA ACC Leu Asn Val Glu Leu Leu Lys Lys Leu Gly Pro Asp Leu Val Val Thr 105 110 115 120			448
TTT GTG GGC AAC CCT AAA GCG GTA GAG CAT GCG AAA AAA TTT GGT ATA Phe Val Gly Asn Pro Lys Ala Val Glu His Ala Lys Lys Phe Gly Ile 125 130 135			496
TTA TTT CTT TCT TTC CAA GAA AAA ACC ATT GCA GAA GTC ATG GAA GAT Leu Phe Leu Ser Phe Gln Glu Lys Thr Ile Ala Glu Val Met Glu Asp 140 145 150			544
ATT GAC GCT CAA GCT AAA GCC TTA GAA ATT GAT GCT TCT AAA AAA CTG Ile Asp Ala Gln Ala Lys Ala Leu Glu Ile Asp Ala Ser Lys Lys Leu 155 160 165			592
GCC AAA ATG CAA GAA ACT TTG GAT TTT ATT GCT GAG CGT TTG AAA GGT Ala Lys Met Gln Glu Thr Leu Asp Phe Ile Ala Glu Arg Leu Lys Gly 170 175 180			640
GTC AAA AAG AAA AAA GGG GTG GAG CTT TTC CAT AAG GCC AAT AAG ATC Val Lys Lys Lys Lys Gly Val Glu Leu Phe His Lys Ala Asn Lys Ile 185 190 195 200			688
AGC GGC CAT CAA GCC CTT GAT TCA GAC ATT TTA GAA AAA GGA GGC ATA Ser Gly His Gln Ala Leu Asp Ser Asp Ile Leu Glu Lys Gly Gly Ile 205 210 215			736
GAC AAT TTT GGC TTG AAA TAT GTC AAA TTT GGG CGT GCT GAC ATT AGC Asp Asn Phe Gly Leu Lys Tyr Val Lys Phe Gly Arg Ala Asp Ile Ser 220 225 230			784
GTG GAA AAA ATC GTT AAA GAA AAC CCT GAG ATT ATC TTT ATT TGG TGG Val Glu Lys Ile Val Lys Glu Asn Pro Glu Ile Ile Phe Ile Trp Trp 235 240 245			832
ATA AGC CCA CTC ACG CCT GAA GAT GTG TTA AAC AAC CCC AAA TTT GCT Ile Ser Pro Leu Thr Pro Glu Asp Val Leu Asn Asn Pro Lys Phe Ala 250 255 260			880
ACC ATC AAA GCC ATT AAA AAC AAG CAG GTT TAT AAA CTC CCC ACA ATG Thr Ile Lys Ala Ile Lys Asn Lys Gln Val Tyr Lys Leu Pro Thr Met 265 270 275 280			928
GAT ATT GGC GGG CCT AGA GCC CCA CTC ATA AGT CTT TTT ATC GCT CTA Asp Ile Gly Gly Pro Arg Ala Pro Leu Ile Ser Leu Phe Ile Ala Leu 285 290 295			976
AAA GCC CAC CCT GAA GCC TTT AAG GGC GTG GAT ATT AAT GCG ATT GTT Lys Ala His Pro Glu Ala Phe Lys Gly Val Asp Ile Asn Ala Ile Val 300 305 310			1024

AAA GAC TAC TAT AAA GTG GTT TTT GAT TTG AAT GAT GCA GAG GTT GAA 1072
 Lys Asp Tyr Tyr Lys Val Val Phe Asp Leu Asn Asp Ala Glu Val Glu
 315 320 325

CCC TTT TTA TGG CAT TAATTTTAA AAAAGGGCTG ATATTTTATAG CCCTTTGTGT A 1128
 Pro Phe Leu Trp His
 330

TCGCGCTAGG ATTAG 1143

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

Met	Leu	Val	Thr	Arg	Phe	Lys	Lys	Ala	Leu	Ile	Ser	Tyr	Ser	Leu	Gly	1	5	10	15
Ala	Leu	Leu	Val	Ser	Ser	Leu	Leu	Gly	Val	Ala	Ser	Ala	Ser	Asn	Gln	20	25	30	
Glu	Ile	Gln	Val	Lys	Asp	Tyr	Phe	Gly	Asp	Gln	Ala	Ile	Lys	Leu	Pro	35	40	45	
Val	Ser	Lys	Ile	Ile	Tyr	Leu	Gly	Ser	Phe	Ala	Glu	Val	Pro	Ala	Met	50	55	60	
Phe	His	Thr	Trp	Asp	Arg	Val	Val	Gly	Ile	Ser	Asp	Tyr	Ala	Phe	Lys	65	70	75	80
Ser	Asp	Ile	Val	Lys	Ala	Thr	Leu	Lys	Asp	Pro	Lys	Arg	Ile	Lys	Ser	85	90	95	
Met	Ser	Ser	Asp	His	Val	Ala	Ala	Leu	Asn	Val	Glu	Leu	Leu	Lys	Lys	100	105	110	
Leu	Gly	Pro	Asp	Leu	Val	Val	Thr	Phe	Val	Gly	Asn	Pro	Lys	Ala	Val	115	120	125	
Glu	His	Ala	Lys	Lys	Phe	Gly	Ile	Leu	Phe	Leu	Ser	Phe	Gln	Glu	Lys	130	135	140	
Thr	Ile	Ala	Glu	Val	Met	Glu	Asp	Ile	Asp	Ala	Gln	Ala	Lys	Ala	Leu	145	150	155	160
Glu	Ile	Asp	Ala	Ser	Lys	Lys	Leu	Ala	Lys	Met	Gln	Glu	Thr	Leu	Asp	165	170	175	
Phe	Ile	Ala	Glu	Arg	Leu	Lys	Gly	Val	Lys	Lys	Lys	Lys	Gly	Val	Glu	180	185	190	
Leu	Phe	His	Lys	Ala	Asn	Lys	Ile	Ser	Gly	His	Gln	Ala	Leu	Asp	Ser	195	200	205	
Asp	Ile	Leu	Glu	Lys	Gly	Gly	Ile	Asp	Asn	Phe	Gly	Leu	Lys	Tyr	Val	210	215	220	
Lys	Phe	Gly	Arg	Ala	Asp	Ile	Ser	Val	Glu	Lys	Ile	Val	Lys	Glu	Asn	225	230	235	240
Pro	Glu	Ile	Ile	Phe	Ile	Trp	Trp	Ile	Ser	Pro	Leu	Thr	Pro	Glu	Asp	245	250	255	
Val	Leu	Asn	Asn	Pro	Lys	Phe	Ala	Thr	Ile	Lys	Ala	Ile	Lys	Asn	Lys	260	265	270	
Gln	Val	Tyr	Lys	Leu	Pro	Thr	Met	Asp	Ile	Gly	Gly	Pro	Arg	Ala	Pro				

275	280	285
Leu Ile Ser Leu Phe Ile Ala	Leu Lys Ala His Pro	Glu Ala Phe Lys
290	295	300
Gly Val Asp Ile Asn Ala Ile	Val Lys Asp Tyr Tyr	Lys Val Val Phe
305	310	315
Asp Leu Asn Asp Ala Glu	Val Glu Pro Phe Leu	Trp His
325	330	

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 898 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...845
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

GGGGGGTTAT AGTAAAAACA TGCAAGTAAT TTAAAGTTAA TTAAAGATAA	TTA GGC	56
	Leu Gly	
	1	
ACA ATA GCC ACA AAA AGT TTA AGG CTG TAT TTG AAA ACT CTA TTT AGT		104
Thr Ile Ala Thr Lys Ser Leu Arg Leu Tyr Leu Lys Thr Leu Phe Ser		
5	10	15
ATT TAT CTC TTT TTA TCG TTG AAC CCA CTC TTT TTA GAA GCT AAT GAA		152
Ile Tyr Leu Phe Leu Ser Leu Asn Pro Leu Phe Leu Glu Ala Asn Glu		
20	25	30
ATC ACT TGG TCT AAA TTC TTG GAA AAT TTT AAA AAC AAG AAT GAT GAT		200
Ile Thr Trp Ser Lys Phe Leu Glu Asn Phe Lys Asn Lys Asn Asp Asp		
35	40	45
GAC AAA CCT AAA CCC CTA ACT ATT GAT AAA AAC AAT GAA AAA CAG CAA		248
Asp Lys Pro Lys Pro Leu Thr Ile Asp Lys Asn Asn Glu Lys Gln Gln		
55	60	65
ATC TTA GAC AAA AAC CAG CAA ATC TTA AAA AGG GCT TTG GAA AAA AGC		296
Ile Leu Asp Lys Asn Gln Gln Ile Leu Lys Arg Ala Leu Glu Lys Ser		
70	75	80
CTT AAA TTC TTT TTC ATT TTT GGA TAC AAC TAT TCG CAA GCC ACT TTT		344
Leu Lys Phe Phe Phe Ile Phe Gly Tyr Asn Tyr Ser Gln Ala Thr Phe		
85	90	95
TCA ACT TCT AAC CAA ACC TTG ACT TTT GTA GCC AAT AGC ATA GGG TTT		392
Ser Thr Ser Asn Gln Thr Leu Thr Phe Val Ala Asn Ser Ile Gly Phe		
100	105	110

AAC ACC GCT ACC GGT TTA GAG CAT TTT TTA AGA AAC CAC CCT AAA GTC	440
Asn Thr Ala Thr Gly Leu Glu His Phe Leu Arg Asn His Pro Lys Val	
115 120 125 130	
GGT TTT AGA ATC TTT AGC GTC TAT AAC TAT TTC CAT TCT GTT TCC CTC	488
Gly Phe Arg Ile Phe Ser Val Tyr Asn Tyr Phe His Ser Val Ser Leu	
135 140 145	
TCC CAG CCT CAA ACC TTA ATG GTG CAA AAT TAT GGG GGC GCG TTA GAT	536
Ser Gln Pro Gln Thr Leu Met Val Gln Asn Tyr Gly Gly Ala Leu Asp	
150 155 160	
TTT TCT TGG ATT TTT GTA GAT AAA AAT ATT TAT CGC TTT AGG AGT TAT	584
Phe Ser Trp Ile Phe Val Asp Lys Asn Ile Tyr Arg Phe Arg Ser Tyr	
165 170 175	
TTA GGG ATC GCT TTA GAA CAA GGG GTG TTG TTA GTG GAT ACG ATT AAA	632
Leu Gly Ile Ala Leu Glu Gln Gly Val Leu Leu Val Asp Thr Ile Lys	
180 185 190	
CCA GGT GCT ATC ACA ACG ATT ATC CCA AGA ACC AAA AAA ACC TTT TTT	680
Pro Gly Ala Ile Thr Thr Ile Ile Pro Arg Thr Lys Lys Thr Phe Phe	
195 200 205 210	
CAA GCC CCT TTG CGT TTT GGT TTT ATC GTG GAT TTT ATC GGC TAT TTG	728
Gln Ala Pro Leu Arg Phe Gly Phe Ile Val Asp Phe Ile Gly Tyr Leu	
215 220 225	
TCT TTG CAA TTA GGG ATT GAA ATG CCT TTA GTG AGG AAT GTT TTT TAC	776
Ser Leu Gln Leu Gly Ile Glu Met Pro Leu Val Arg Asn Val Phe Tyr	
230 235 240	
ACC TAC AAC AAC CAT CAA GAA AGA TTC AAA CCA CGA TTT AAC GCT AAT	824
Thr Tyr Asn Asn His Gln Glu Arg Phe Lys Pro Arg Phe Asn Ala Asn	
245 250 255	
CTT TCT TTA ATC GTT TCG TTT TAGCCCCCCT TTTCCCCTTT TAAATAAGCC CATG	879
Leu Ser Leu Ile Val Ser Phe	
260 265	
ATTTTCCTAG GGTATTTTA	898

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

Leu Gly Thr Ile Ala Thr Lys Ser Leu Arg Leu Tyr Leu Lys Thr Leu
1 5 10 15
Phe Ser Ile Tyr Leu Phe Leu Ser Leu Asn Pro Leu Phe Leu Glu Ala

Asn	Glu	Ile	Thr	Trp	Ser	Lys	Phe	Leu	Glu	Asn	Phe	Lys	Asn	Lys	Asn	20	25	30
			35				40					45						
Asp	Asp	Asp	Lys	Pro	Lys	Pro	Leu	Thr	Ile	Asp	Lys	Asn	Asn	Glu	Lys			
	50					55					60							
Gln	Gln	Ile	Leu	Asp	Lys	Asn	Gln	Gln	Ile	Leu	Lys	Arg	Ala	Leu	Glu			
65					70					75					80			
Lys	Ser	Leu	Lys	Phe	Phe	Phe	Ile	Phe	Gly	Tyr	Asn	Tyr	Ser	Gln	Ala			
				85					90					95				
Thr	Phe	Ser	Thr	Ser	Asn	Gln	Thr	Leu	Thr	Phe	Val	Ala	Asn	Ser	Ile			
			100					105					110					
Gly	Phe	Asn	Thr	Ala	Thr	Gly	Leu	Glu	His	Phe	Leu	Arg	Asn	His	Pro			
		115					120					125						
Lys	Val	Gly	Phe	Arg	Ile	Phe	Ser	Val	Tyr	Asn	Tyr	Phe	His	Ser	Val			
	130					135					140							
Ser	Leu	Ser	Gln	Pro	Gln	Thr	Leu	Met	Val	Gln	Asn	Tyr	Gly	Gly	Ala			
145					150					155					160			
Leu	Asp	Phe	Ser	Trp	Ile	Phe	Val	Asp	Lys	Asn	Ile	Tyr	Arg	Phe	Arg			
				165				170						175				
Ser	Tyr	Leu	Gly	Ile	Ala	Leu	Glu	Gln	Gly	Val	Leu	Leu	Val	Asp	Thr			
			180					185						190				
Ile	Lys	Pro	Gly	Ala	Ile	Thr	Thr	Ile	Ile	Pro	Arg	Thr	Lys	Lys	Thr			
		195					200					205						
Phe	Phe	Gln	Ala	Pro	Leu	Arg	Phe	Gly	Phe	Ile	Val	Asp	Phe	Ile	Gly			
	210					215					220							
Tyr	Leu	Ser	Leu	Gln	Leu	Gly	Ile	Glu	Met	Pro	Leu	Val	Arg	Asn	Val			
225					230					235					240			
Phe	Tyr	Thr	Tyr	Asn	Asn	His	Gln	Glu	Arg	Phe	Lys	Pro	Arg	Phe	Asn			
				245				250						255				
Ala	Asn	Leu	Ser	Leu	Ile	Val	Ser	Phe										
			260					265										

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 742 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 51...689
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

GCACTTCACG	CATTCCATAA	ACGATATTGA	TTATTGCTA	GACAGCTTGA	AAA AAG	56
					Lys Lys	
					1	
CAG TTA AAA AAT TGC GTT AAG CTA AAA CTA TTT TTA AGG AAA AAT TTG						104
Gln Leu Lys Asn Cys Val Lys Leu Lys Leu Phe Leu Arg Lys Asn Leu						
5		10		15		

GAT ATT TTA GAT TTG AAC AAA GCG CAA GCG GTG CAA CAA AAT GAA CAA	152
Asp Ile Leu Asp Leu Asn Lys Ala Gln Ala Val Gln Gln Asn Glu Gln	
20 25 30	
GAG GTA GAG GAT AAA GAG CGA GAG TCT AAA GAG CCG GTG GTT TTA GAA	200
Glu Val Glu Asp Lys Glu Arg Glu Ser Lys Glu Pro Val Val Leu Glu	
35 40 45 50	
GAT TTG AGC GCT TTA GCG TGG CTT GAA TTA GAA GAG TTT AGC CGC CTT	248
Asp Leu Ser Ala Leu Ala Trp Leu Glu Leu Glu Glu Phe Ser Arg Leu	
55 60 65	
TCA GGG CTT CCT AAA GAA AGG ATT TTG GAA TTA GTG AAT CTT GGT AAA	296
Ser Gly Leu Pro Lys Glu Arg Ile Leu Glu Leu Val Asn Leu Gly Lys	
70 75 80	
ATC AAG AGC AAA ATA AGC AGC AAC AAG CTT TTA ATT GAT GCG AGC AGC	344
Ile Lys Ser Lys Ile Ser Ser Asn Lys Leu Leu Ile Asp Ala Ser Ser	
85 90 95	
GGG ACA AAC GCT TTA ATC AAA AAG GTA GAA AAT AGT TTG ATT TCT ATG	392
Gly Thr Asn Ala Leu Ile Lys Lys Val Glu Asn Ser Leu Ile Ser Met	
100 105 110	
GAT ATG AAC GGG CGT TCT TTA GAA CCT GTG TTT GTG GAA AAG ACC ATT	440
Asp Met Asn Gly Arg Ser Leu Glu Pro Val Phe Val Glu Lys Thr Ile	
115 120 125 130	
AAC ACG ATT TTA AAC TTG CAT GAT AAG GTC ATT GGC GCT AAA GAT GAA	488
Asn Thr Ile Leu Asn Leu His Asp Lys Val Ile Gly Ala Lys Asp Glu	
135 140 145	
ACG ATT TCA GCC TTT AAA AAT GAA AAC ATG TTT TTA AAA GAC GCT TTA	536
Thr Ile Ser Ala Phe Lys Asn Glu Asn Met Phe Leu Lys Asp Ala Leu	
150 155 160	
ATC TCT ATG CAA GAA GTC TAT GAA GAA GAT AAA AAA ACC ATT GAT CTT	584
Ile Ser Met Gln Glu Val Tyr Glu Glu Asp Lys Lys Thr Ile Asp Leu	
165 170 175	
TTG CGC GAT GAA CTC AAT CAA GCG AGA GAA GAA ATT GAA TTT ATG AAG	632
Leu Arg Asp Glu Leu Asn Gln Ala Arg Glu Glu Ile Glu Phe Met Lys	
180 185 190	
AGG AAA TAC CGC TTG ATG TGG GGG AAA GTC GCT GAC ATG AGC AGC GTG	680
Arg Lys Tyr Arg Leu Met Trp Gly Lys Val Ala Asp Met Ser Ser Val	
195 200 205 210	
AAT AAA AAG TAGTTTTTAAA TTAACGCCCA TGCTGAGGGC TTATTAGCGG TAATTTTAG	738
Asn Lys Lys	

GTGA

742

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

Lys	Lys	Gln	Leu	Lys	Asn	Cys	Val	Lys	Leu	Lys	Leu	Phe	Leu	Arg	Lys
1				5				10						15	
Asn	Leu	Asp	Ile	Leu	Asp	Leu	Asn	Lys	Ala	Gln	Ala	Val	Gln	Gln	Asn
		20					25						30		
Glu	Gln	Glu	Val	Glu	Asp	Lys	Glu	Arg	Glu	Ser	Lys	Glu	Pro	Val	Val
		35				40						45			
Leu	Glu	Asp	Leu	Ser	Ala	Leu	Ala	Trp	Leu	Glu	Leu	Glu	Glu	Phe	Ser
	50					55				60					
Arg	Leu	Ser	Gly	Leu	Pro	Lys	Glu	Arg	Ile	Leu	Glu	Leu	Val	Asn	Leu
65					70				75					80	
Gly	Lys	Ile	Lys	Ser	Lys	Ile	Ser	Ser	Asn	Lys	Leu	Leu	Ile	Asp	Ala
			85					90						95	
Ser	Ser	Gly	Thr	Asn	Ala	Leu	Ile	Lys	Lys	Val	Glu	Asn	Ser	Leu	Ile
		100					105					110			
Ser	Met	Asp	Met	Asn	Gly	Arg	Ser	Leu	Glu	Pro	Val	Phe	Val	Glu	Lys
		115					120					125			
Thr	Ile	Asn	Thr	Ile	Leu	Asn	Leu	His	Asp	Lys	Val	Ile	Gly	Ala	Lys
	130					135					140				
Asp	Glu	Thr	Ile	Ser	Ala	Phe	Lys	Asn	Glu	Asn	Met	Phe	Leu	Lys	Asp
145					150				155					160	
Ala	Leu	Ile	Ser	Met	Gln	Glu	Val	Tyr	Glu	Glu	Asp	Lys	Lys	Thr	Ile
			165					170						175	
Asp	Leu	Leu	Arg	Asp	Glu	Leu	Asn	Gln	Ala	Arg	Glu	Glu	Ile	Glu	Phe
		180					185						190		
Met	Lys	Arg	Lys	Tyr	Arg	Leu	Met	Trp	Gly	Lys	Val	Ala	Asp	Met	Ser
		195				200						205			
Ser	Val	Asn	Lys	Lys											
	210														